GenCore version 5.1.6

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 2, 2005, 13:09:41 ; Search time 315.379 Seconds
(without alignments)
6013.950 Million cell updates/sec

Title: US-09-945-326-1
Perfect score: 4504
Sequence: 1 cgtgtgtgtgtccctgggc.........actgtaaaaaaaaaaaa 2452

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3195	70.9	628	4	AAU23008	Aau23008 Novel hum
2	3171	70.4	628	8	ADM87776	Adm87776 Human EST
3	3153	70.0	621	4	AAB73691	Aab73691 Human oxi
4	3153	70.0	621	4	AAB94839	Aab94839 Human pro
5	3153	70.0	621	5	AAE21680	Aae21680 Human acy
6	3153	70.0	621	7	ADJ69253	Adj69253 Human hea
7	3153	70.0	621	7	ADJ70247	Adj70247 Human hea
8	3153	70.0	621	8	ADM87327	Adm87327 Human pro
9	2864	63.6	565	3	AAB41800	Aab41800 Human ORF
10	2526	56.1	498	4	AAB94077	Aab94077 Human pro
11	1537	34.1	306	4	AAU23012	Novel hum
12	1365	30.3	653	5	ABB06991	Rat very
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14	1360	30.2	655	5	ABB06992	Mouse ver
15	1345	29.9	655	5	ABB06993	Bovine ve
16	1321	29.3	655	5	ABB06988	Human MD2
17	1321	29.3	655	7	ADJ68728	Human hea
18	1321	29.1	655	8	ABM81815	Tumour-as
19	1312	29.1	655	7	ADJ68514	Human hea
20	1297.5	28.8	618	7	ADC14242	Human enz
21	1295.5	28.8	655	4	ABB63264	Drosophil
22	1210.5	26.9	613	8	ADN22791	Bacterial
23	1135	25.2	527	7	ADC14245	Human enz
24	1022	22.7	202	4	AAU23009	Novel hum
25	954	21.2	188	7	ADJ70246	Human hea
26	954	21.2	188	8	ADJ69636	Human hea
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28	835.5	18.6	360	7	ADC14211	Human enz
29	821	18.2	594	8	ADS28396	Bacterial
30	818	18.2	169	6	ABP76260	Human GEN
31	816	18.1	581	8	ADS30391	Bacterial
32	815.5	18.1	594	8	ADS44855	Bacterial
33	799	17.7	585	8	ADN27112	Bacterial
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35	765	17.0	583	8	ADS21350	Bacterial
36	704	15.6	373	8	ADS27581	Bacterial
37	699	15.5	382	8	ADS27762	Bacterial
38	691.5	15.4	390	7	ABO77312	Pseudomon
39	690	15.3	379	8	ADS28427	Bacterial
40	686.5	15.2	377	8	ADN27173	Bacterial
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42	678	15.1	381	8	ADS27885	Bacterial
43	675.5	15.0	379	8	ADS27580	Bacterial
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45	658	14.6	380	8	ADS28426	Bacterial

ALIGNMENTS

RESULT 1
AAU23008
ID AAU23008 standard; protein; 628 AA.
AC AAU23008;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #94.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.

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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-465566/50.
DR   N-PSDB; AAS40878.
XX
PT   Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT   treating neural, immune system, muscular, reproductive, pulmonary,
PT   cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS   Claim 11; SEQ ID NO 1004; 1180pp; English.
XX
CC   The present invention relates to the isolation of novel human enzyme
CC   polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC   encoding them. The enzyme polypeptides of the invention may comprise the
CC   functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC   isomerases or ligases. The sequences of the invention are useful in the
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CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. Note: The sequence
CC   the novel human enzyme polypeptides of the invention. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX.
SQ   Sequence 628 AA;

Alignment Scores:
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Best Local Similarity: 100.00%         Mismatches:       0
Query Match:          70.94%           Indels:           0
DB:                                    Gaps:             0

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Qy    286 GTGAAAAAATTCTTCACTGAAGAGAGTGGACTCCCGAAAAAATTGACCAGGAAGGAAAATC 345
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Qy    466 ATGGATGGTGCGCTCCACCTGTGACCGAGAGCACTAGGGGAGACCATCAGC 525
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Qy    826 GTCACTAATGGGAAACCGAAGATAAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTC 885
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Db    501 LeuAlaAspSerAlaAsnLysPheGluGluAsnHisMetGluMetGlyLysThrValGlu 520

Qy   1606 ACACTGCTGCTCCATCAACCTGTATGGCATGAGCGGCCGGCCGTCGCGGCCGCTCC 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 ThrLeuLeuLeuArgPheLysGlyMetThrAlaValLeuSerArgAlaSerArgSer 540

Qy   1666 GCCAACATCCTCATCAACGCTATGGATGCCATGACGCGGGGTG 1725
          |||||||||||||||||||||||||||||||||||||||||||
Db    541 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 560

Qy   1726 ATCCGGCATTGGCTCCCAACCACGACCAGAGTTCTTCTTGCCCAACAACACCTTCTCGGTG 1785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuLeuAlaAsnThrPheCysVal 580

Qy   1786 GAAGCTTACTTGCAGAATCTCTTCAGCTCTTCAGCTGGACAAGTAATGCTCCAGAAAAC 1845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn 600
```

```
Qy   1846  CTAGATGAGCAGATTAAGAAAGTGTCCAGCAGATCCTTGAGAAGCCAGCCTATATCTGT 1905
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  LeuAspGluGlnIleLysLysValSerGlnIleLeuGluLysProAlaTyrIleCys    620

Qy   1906  GCCCACCCTCTGGACAGGACATGC 1929
           ||||||||||||||||||||||||
Db    621  AlaHisProLeuAspArgThrCys 628
```

RESULT 2
ADM87776
ID   ADM87776 standard; protein; 628 AA.
XX
AC   ADM87776;
XX
DT   03-JUN-2004 (first entry)
XX
DE   Human EST derived amino acid sequence SEQ ID NO:869.
XX
KW   respiratory; cytostatic; antiarthritic; antiinflammatory;
KW   gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW   antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW   chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW   inflammatory condition; arthritis; inflammatory bowel disease;
KW   Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW   graft versus host disease; human; expressed sequence tag; EST.
XX
OS   Homo sapiens.
XX
XX
PN   WO200409934-A2.
XX
PD   29-JAN-2004.
XX
PF   19-JUL-2002; 2002WO-US022858.
XX
PR   21-JUL-2001; 2001US-0306971P.
PR   28-MAR-2002; 2002US-00112944.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI   Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
DR   WPI; 2004-143291/14.
DR   N-PSDB; ADM87558.
XX
PT   New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT   cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT   Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT   versus host disease.
XX
PS   Example 2; SEQ ID NO 869; 591pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I): (a)
CC   comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC   which encodes a polypeptide with biological activity, where the
CC   polynucleotide hybridises to (I) under stringent hybridisation conditions
CC   or has greater than 99% sequence identity with (I). (I) has respiratory,
CC   cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
CC   antibacterial, immunosuppressive, antidiabetic and antirheumatic
CC   activities, and can be used in gene therapy. (I) can be used for
CC   generating polynucleotides encoding chimeric or fusion proteins and
CC   heterologous protein sequences. The polynucleotides can be used to
CC   express recombinant protein for analysis, characterisation or therapeutic
CC   use; as markers for tissues in which the corresponding protein is
CC   preferentially expressed; as molecular weight markers on gels; as
CC   chromosome markers or tags to identify chromosomes or to map related gene
CC   positions; to compare with endogenous DNA sequences in patients to
CC   identify potential genetic disorders; as probes to hybridise and discover
CC   genes, related DNA sequences; as a source of information to derive PCR
CC   primers for genetic fingerprinting; as a probe to subtract-out known
CC   sequences in the process of discovering other novel polynucleotides; for
CC   selecting and making oligomers for attachment to a gene chip or other
CC   support, including for examination of expression patterns; to raise anti-
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CC   protein antibodies using DNA immunisation techniques; and as an antigen
CC   to raise anti-DNA antibodies or elicit another immune response. The
CC   polynucleotides and polypeptides can also be used as nutritional sources
CC   or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC   source, as a nitrogen source or as a source of carbohydrates. The
CC   polynucleotides and polypeptides can also be used treat cancer. The
CC   compositions are useful for promoting better or faster closure of non-
CC   healing wounds, for the generation and regeneration of tissues, for gut
CC   protection or regeneration and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues, and conditions resulting from
CC   systemic cytokine damage. The compositions can also be used to treat
CC   inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC   Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC   or graft versus host disease. The present sequence represents an
CC   expressed sequence tag (EST) derived amino acid sequence from the present
CC   invention. N.B. The sequences for this patent were obtained from the
CC   USPTO web site from an equivalent US patent US20040048249A1.
XX
SQ   Sequence 628 AA;
```

Alignment Scores:
```
Pred. No.:                          Length:                628
Score:               4.23e-285      Matches:               623
Percent Similarity:  3171.00        Conservative:            2
Best Local Similarity: 99.52%       Mismatches:              3
Query Match:         99.20%         Indels:                  0
DB:                  70.40%         Gaps:                    0
                        8
```

US-09-945-326-1 (1-2452) x ADM87776 (1-628)

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Qy    46  GGCTGGGAACATCGGGCAGCATGAGCGGCTGCGGCTCTTCCTGCCACCACGGCTGCG 105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GlyTrpGlyThrSerGlySerMetSerGlyCysGlyLeuPheLeuArgThrThrAlaAla 20

Qy   106  GCTCCGTGCCTGCCGGGGTCTTGGTGTCTCTACCGGCAACCGGCGGCTACTGCGCCACCAGC 165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21  AlaArgAlaCysArgGlyLeuValValSerThrAlaAsnArgArgLeuLeuArgThrSer 40

Qy   166  CCGCCTGCTACGAGCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGAAGTT 225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41  ProProValArgAlaPheAlaLysGluLeuPheLeuGlyLysSerIleLysLysLysGluVal 60

Qy   226  TTCCCATTCCAGAAGTAGCCAAGATGAACTAATGAAATCAGTTCTTGGGACCC 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  PheProPheProGluValSerGlnAspAspLeuLeuAsnGluIleAsnGlnPheLeuGlyPro 80

Qy   286  GTGGAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAGGAGGAAAATC 345
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81  ValGluLysPhePheThrGluGluValAspSerArgLysIleAspSerGlnGluGlyLysIle 100

Qy   346  CCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAA 405
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101  ProAspGluThrLeuGluLysLeuLysSerLeuGlyLeuPheGlyLeuGlnValProGlu 120

Qy   406  GAATATGGTGGCCTGGCTTCTCCAACACCATGGTCCAAGACTAGCAGACTAGGGGAGATCATCAGC 465
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GluTyrGlyGlyLeuGlyPhePheSerAsnThrMetTyrSerArgLeuGlyThrLeuSer 140

Qy   466  ATGGATGGGTCCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATC 525
          |||||||||||||||||||||||||||||||||||||||||||::::|||||||||||||
Db   141  MetAspGlySerIleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIle 160

Qy   526  ATCTTGGCTGCCACTGAGGAGCAGAGACAGAAAGCCAAATACTTGCCTAAACTGGGCTCCGGGGAG 585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161  IleLeuAlaAlaThrGluGluGlnGlnArgGlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGlu 180

Qy   586  CACATTGCAGCCCTTCGCCTCCACGGAGCCAGCCAGTGGGAGCCGATGCAGCCTCAATCCGG 645
          :::|||||||||||||||||||||||||||||||::::::|||||||||||||||||||||
Db   181  AlaLeuAlaAlaPheCysLeuThrGluThrProAlaAsnGlySerAspAlaAla***IleArg 200

Qy   646  AGCAGAGCCACCACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGG 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201  SerArgAlaThrLeuSerGluLysThrArgArgHisTyrIleLeuAsnGlySerLysValTrp 220
```

Qy   1786 GAAGCTTACTTGCAGAAATCTCTTCAGCCTCTCCTCAGCTGGACAAGTATGCTCCAGAAAAC 1845
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581   GluAlaTyrLeuGlnLysIleSerGlnProLeuLeuSerGlnLeuAspLysTyrAlaProGluAsn 600

Qy   1846 CTAGATGAGCAGATTAAGAAAGTGTCCAGCAGATCCTTGAGAGCCGAGCCTATATCTGT 1905
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601   LeuAspGluGlnIleLysLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCys 620

Qy   1906 GCCCACCCTCTGGACAGGACATGC 1929
           ||||||||||||||||||||||
Db   621   AlaHisProLeuAspArgThrCys 628

RESULT 3
AAB73691
ID   AAB73691 standard; protein; 621 AA.
XX
AC   AAB73691;
XX
DT   11-SEP-2001 (first entry)
XX
DE   Human oxidoreductase protein ORP-24.
XX
KW   Human oxidoreductase protein; ORP; cell proliferative disorder;
KW   arteriosclerosis; cirrhosis; psoriasis; cancer; endocrine disorder;
KW   diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhoea;
KW   osteoporosis; metabolic disorder; obesity; phenylketonuria;
KW   hypercholesterolaemia; reproductive disorder; infertility;
KW   ovulatory defect; menstrual cycle defect; endometriosis;
KW   polycystic ovary disease; spermatogenesis disruption; impotence;
KW   neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW   Huntington's disease; Parkinson's disease; Creutzfeldt-Jakob disease;
KW   meningitis; cerebral palsy; muscular dystrophy; mood disorder; anxiety;
KW   schizophrenic disorder; infection; autoimmune disorder;
KW   inflammatory disorder; acquired immunodeficiency syndrome; AIDS; asthma;
KW   allergy; Crohn's disease; atopic dermatitis; gout; multiple sclerosis;
KW   rheumatoid arthritis; ulcerative colitis; drug screening;
KW   toxicity screening; transgenic animal; SNP detection; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200144448-A2.
XX
PD   21-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-US033158.
XX
PR   16-DEC-1999; 99US-0172367P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Lal P, Tang YT, Hillman JL, Baughn MR, Azimzai Y, Lu DAM;
XX
DR   WPI; 2001-390245/41.
DR   N-PSDB; AAH24246.
XX
PT   Novel human oxidoreductase protein (ORP) useful for diagnosing, treating
PT   and preventing cell proliferative, neurological, viral, reproductive and
PT   autoimmune/inflammatory disorders associated with abnormal expression of
PT   ORP.
XX
PS   Claim 1; Page 117-119; 136pp; English.
XX
CC   Sequences AAB73668-AAB73694 represent 27 novel human oxidoreductase
CC   proteins, designated ORP-1 to ORP-27 respectively, and sequences AAH24223
CC   -AAH24249 represent cDNAs encoding ORP-1 to ORP-27. Human ORP proteins
CC   and nucleic acids are useful for diagnosing, treating or preventing cell
CC   proliferative disorders (e.g. arteriosclerosis, cirrhosis, psoriasis,
CC   cancers); endocrine disorders (e.g., type I or II diabetes mellitus,
CC   diabetes insipidus, dwarfism, hirsutism, amenorrhoea, osteoporosis);
CC   metabolic disorders (e.g., obesity, phenylketonuria,
CC   hypercholesterolaemia); reproductive disorders (e.g., infertility,
CC   ovulatory and menstrual cycle defects, endometriosis, polycystic ovary
CC   disease, disruption of spermatogenesis, impotence); neurological

Qy   706   ATTACTAATGAGGACTGGCCAATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGAT 765
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221   IleThrAsnGlyGlyLeuAlaAsnIlePheThrValPheAlaLysThrGluValValAsp 240

Qy   766   TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGTGGA 825
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241   SerAspGlySerValLysAspLysIleThrAlaPheIleValGluArgAspPheGlyGly 260

Qy   826   GTCACTAATGGGAAACCCGAAGATAAATAGGCATTCGGGGCTCCAACACTTGTGAAGTC 885
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261   ValThrAsnGlyLysProGluAspLysLysLeuGlyIleArgGlySerArgAsnThrCysGluVal 280

Qy   886   CATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGAGAGTCGGAGATGGGTTT 945
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281   HisPheGluAsnThrLysIleProValGluAsnIleLeuGluGlyValGlyAspGlyPhe 300

Qy   946   AAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTGTCGCTGGG 1005
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301   LysValAlaMetAsnIleLeuAsnSerGlyArgPheSerMetGlySerValAlaAlaGly 320

Qy   1006 CTGCTCCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAAC 1065
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321   LeuLeuLysArgLeuIleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsn 340

Qy   1066 AAGAGGCTCAGTGAATTGGATTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCT 1125
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341   LysArgLeuSerGluPheGluGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaAla 360

Qy   1126 TACGTCATGGAGAGTATGACCTACCTCACAGCAGGGATGCTGACCAACCTGGCTTCCC 1185
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361   TyrValMetGluSerMetThrTyrLeuThrAlaGlyMetLeuAspLeuAlaGlyProPhePro 380

Qy   1186 GACTGCTCCATCGAGGCAGCCATGTGTTCAGCTGGTTCAGCTCCGAGGCCGCCTGGCAGTGT 1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381   AspCysSerIleGluGluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCys 400

Qy   1246 GTGAGTGAGGCGCTGCAGATCCTCGGGGGCTGGGCTACACAAGGACTATCCGTACGAG 1305
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401   ValSerGluAlaLeuGlnIleLeuGlyGlyTrpThrArgAspTyrProTyrGlu 420

Qy   1306 CGCATATCTGCTGACACCCGCATCCTCCATCTTCGAGGGAACCAATGAGATTCTCCGG 1365
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421   ArgIleLeuArgAspThrArgIleLeuHisLeuGluPheGluGluAsnGlnIleLeuArg 440

Qy   1366 ATGTACATCGCCCTGACGGGTCTGCCAGCATGCCGGCCCATCCTGACTACCAGGATCCAT 1425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441   MetTyrIleAlaLeuThrGlyLeuProAlaCysArgProIleLeuThrThrArgIleHis 460

Qy   1426 GAGCTTAAACAGGCCAAAGTGAGCAAAGTCATGAGAACCCTGGCCGGAGGCTTCGGGAC 1485
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461   GluLeuLysGlnAlaLysValSerGlnValMetArgThrValGlyArgArgLeuArgAsp 480

Qy   1486 TCCCTGGGCCGAACTGTGACCTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGT 1545
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481   SerLeuGlyArgThrValThrTrpGlyGlnThrGlyLeuLeuThrGlyAsnHisGlyValValHisProSer 500

Qy   1546 CTTGCGGACAGTGCCAACAAGTTTGAGGAGAACACCTACTGCTTCGGCCGGACCGTGGAG 1605
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501   LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu 520

Qy   1606 ACACTGCTGCTCCGCTTTGGCAAGACCATCATGAGGAGGAGCAGCTGGTACTGAAGCGGGTG 1665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521   ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGlnLeuValLeuLysValArgVal 540

Qy   1666 GCCAACATCCTCATCAACCTGTATGCGATGACGGCCGTGCTGCGGGGCCAGCCGCTCC 1725
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541   AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 560

Qy   1726 ATCCGCATTGGGCTCCCAACCACGACCCACGAGGTTCTCTTGGCCAACACCTTCTGCGTG 1785
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561   IleArgIleGlyLeuProThrThrThrHisGluValLeuLeuAlaAsnThrPheCysVal 580

```
CC   disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
CC   disease, Parkinson's disease, meningitis, Creutzfeldt-Jakob disease,
CC   cerebral palsy, muscular dystrophy, mood, anxiety and schizophrenic
CC   disorders); viral, bacterial, fungal and parasitic infections; and
CC   autoimmune/inflammatory disorders such as acquired immunodeficiency
CC   syndrome (AIDS), allergies, asthma, Crohn's disease, atopic dermatitis,
CC   gout, multiple sclerosis, rheumatoid arthritis or ulcerative colitis.
CC   Human ORP proteins and nucleotides can be used to identify compounds
CC   which modulate their activity or expression. ORP nucleic acid sequences
CC   may also be used for assessing the toxicity of a test compound, to detect
CC   upstream sequences such as promoters and regulatory elements, and to
CC   create knock out or knock in animals or transgenic animals to model human
CC   disease. Oligonucleotide primers derived from ORP gene sequences may be
CC   used to detect single nucleotide polymorphisms (SNPs) and for mapping the
CC   naturally occurring genomic sequences. Antibodies specific for ORP
CC   proteins may be used in the diagnosis of disorders associated with
CC   aberrant ORP expression, in assays to monitor patients being treated with
CC   ORP or modulators thereof, and for assessing toxicity of potential drugs
XX
SQ   Sequence 621 AA;
```

```
Alignment Scores:
Pred. No.:
Score:                 3153.00
Percent Similarity:    100.00%          Length:          621
Best Local Similarity: 100.00%          Matches:         621
Query Match:           70.00%           Conservative:    0
DB:                    4                Mismatches:      0
                                        Indels:          0
                                        Gaps:            0

US-09-945-326-1 (1-2452) x AAB73691 (1-621)
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```
Qy   67 ATGAGCGGCTGCGGGCTCTTCCTGCGCACCACGGCTGCGGCCTGCGCTCGTTGCCGGGGTCTG 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaArgGlyLeu  20

Qy  127 GTGGTCTCTACCGCCAACCGGCGGCTGCGCACTGCGCACCACGCCGCCTACGAGCTTTCGCC 186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuArgThrSerProProValArgAlaPheAla  40

Qy  187 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAGAAGTTTCCCATTCCAGAAGTAGC 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysLysPheProPheProGluValSer  60

Qy  247 CAAGATGAACTTAATGAACAATCAGTTCTTGGGACCCGTGGAAAAATCTTCACTGAA 306
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGluIleLeuAsnGlnPheLeuGlyProValGluLysSerPheThrGlu  80

Qy  307 GAGGTGGACTCCGAAAAATGACCAGGAAGGGAAAATCCCAGATGAAAATCCCAGAAA 366
         ||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100

Qy  367 TTGAAGAGCCTAGGCTTTTTGGGCTGCAAGTCCCAGAAGAAGAATATGGTGCCTGGGCTTC 426
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluGluTyrGlyValGlyLeuGlyPhe 120

Qy  427 TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGGTCCATCACTGTG 486
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SerAsnThrMetTyrSerArgLeuGlyLeuGluIleIleSerMetAspGlySerIleThrVal 140

Qy  487 ACCCTGGCAGCGCACCCAGGCTATTGGCCTCAAGGGACTATCCTTGGCTGGCACTGAGGAG 546
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyLeuLeuLeuAlaGlyLyThrGluGluLys 160

Qy  547 CAGAAAGCCAAATACTTGCCTAAACTGGCGCCGGGAGCACATTGCAGCCTTCTGCCTC 606
         ||||||||||||||||||||||||||||||||||||||||||||
Db  161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyAluHisIleAlaAlaPheCysLeu 180

Qy  607 ACGGAGCCAGTGGAGCCGATGCAACTAGGGAGCAGCTCAATCCGGAGCAGAGCCACTAAGTGAA 666
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy  667 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC 726
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy  727 AATATTTTACTGTTTGCTCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGAC 786
         ||||||||||||||||||||||||||||||||||||||||||||
Db  221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240

Qy  787 AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAACCCGAA 846
         ||||||||||||||||||||||||||||||||||||||||||||
Db  241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260

Qy  847 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA 906
         ||||||||||||||||||||||||||||||||||||||||||||
Db  261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisProGluAsnThrLysIle 280

Qy  907 CCTGTGGAAAACATCCTTGGAGAGTCGGAGATGGGTTAAGGTGCCATGAACATCCTC 966
         ||||||||||||||||||||||||||||||||||||||||||||
Db  281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy  967 AACAGCGGCCGGTCACTGAGTGCCAGCGTCGTGGCTGGCTTGCTCAAGAGATTGATTGAA 1026
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320

Qy 1027 ATGACTGCTGAGTACGCCTGCACAAGAGAAACAGTTAACAGAGGCTCAGTGAATTTGGA 1086
         ||||||||||||||||||||||||||||||||||||||||||||
Db  321 MetThrAlaGluTyrAlaCysThrArgGluThrValAsnArgGlySerGluPheGly 340

Qy 1087 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACC 1146
         ||||||||||||||||||||||||||||||||||||||||||||
Db  341 LeuIleGlnGluGluLysPheHisAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360

Qy 1147 TACCTCACAGCAGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCC 1206
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380

Qy 1207 ATGGTGAAGGTGTTCAGCTCCGGAGGCTTTGAGTGTGAGGCCTGAGATC 1266
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Db  381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy 1267 CTCGGGGGCTTGGGCTACACAAGGACTATCCGTACGGCGCCATACTGCGTGACACCCGC 1326
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Db  401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy 1327 ATCCCTCATCTTGGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1386
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Db  421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440

Qy 1387 CTGCAGCATGCCGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy 1447 AGCACAGTCATGGATACCGTTGGCCGAGGCTTCGGAGCTTCGGAGAACTGTGGAC 1506
         ||||||||||||||||||||||||||||||||||||||||||||
Db  461 SerThrValMetAspThrValGlyArgGlyArgLeuArgLeuArgArgArgArgValAsp 480

Qy 1507 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAG 1566
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Db  481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy 1567 TTTGAGGAGAACACCTACTGTGCTTCGGCGACGACACCTGCTCCGCTTTGGC 1626
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Db  501 PheGluGluAsnThrTyrCysPheGlyTyrThrValGluThrLeuLeuLeuArgPheGly 520

Qy 1627 AAGACCATCATGGAGGAGCAGCTGGTACTGGAGCGGTGGCCAACATCCTCATCAACCTG 1686
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Db  521 LysThrIleMetGluGluGlnLeuValLeuGluArgValAlaAsnIleLeuIleAsnLeu 540

Qy 1687 TATGGCATGACGGCCGTGCTGCGCGGGCCATCCGCATTGGGCTTCCGCAAC 1746
         ||||||||||||||||||||||||||||||||||||||||
Db  541 TyrGlyMetThrAlaValLeuArgSerArgAlaSerArgIleGlyLeuArgLeuArgAsn 560

Qy 1747 CACGACCACGAGGTTCCTTGCCAACCACCTTCTGCGTGGAGAATCTC 1806
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Db  561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
```

```
Qy 1807 TTCAGCCTCTCAGCTGGACAAGTATGCTCCAGAAAAACCTAGATGAGCAGATTAAGAAA 1866
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Db  581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600

Qy 1867 GTGTCCCAGCAGATCCTTGAGAAGGCAGCCTATATCTGTGCCACCCCTCTGACAGAGACA 1926
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 ValSerGlnGlnIleLeuGluLysAlaAlaTyrIleCysAlaThrProLeuThrGluThr 620

Qy 1927 TGC 1929
         |||
Db  621 Cys 621
```

RESULT 4
AAB94839
ID AAB94839 standard; protein; 621 AA.
XX
AC AAB94839;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:16010.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 16010; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAB92446 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
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CC  oligonucleotides, all of which are used in the exemplification of the
CC  present invention
XX
SQ  Sequence 621 AA;

Alignment Scores:
Pred. No.:              1.98e-283           Length:           621
Score:                  3153.00             Matches:          621
Percent Similarity:     100.00%             Conservative:     0
Best Local Similarity:  100.00%             Mismatches:       0
Query Match:            70.00%              Indels:           0
DB:                     4                   Gaps:             0

US-09-945-326-1 (1-2452) x AAB94839 (1-621)
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Qy   67 ATGAGCCGGCTGCGGGGCTCTTCCTGCGCACCAGGCTGCGGCTCGTGCTCGGCGGGGTCTG 126
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Db    1 MetSerGlyCysGlyLeuPheLeuArgThrArgAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy  127 GTGGTCTCTACCGGCAACCGGCGGCTACTGCGCACCAGCCGCCGCCTGTACGAGCTTCGCC 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40

Qy  187 AAAGAGCTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTCCCATTCCAGAAGTTAGC 246
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Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60

Qy  247 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80

Qy  307 GAGGTGGACTCCCGAAAAATTGACACCAGGAAGGGAGAAAATCCCAGATGAAACTTGGAGAAA 366
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Db   81 GluValAspSerArgLysIleAspProGlnGluGlyGluIleProAspGluThrLeuGluLys 100

Qy  367 TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAAATATGGTGGCCTGGGCTTC 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGlyGluTyrGlyGlyLeuGlyPhe 120

Qy  427 TCCAACACCATGTACTCCAAGACTAGGGGAGATCATCAGCATGATGGTCCATCACTGTG 486
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Db  121 SerAsnThrMetTyrSerArgLeuGlyGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy  487 ACCCTGGCAGCCCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160

Qy  547 CAGAAAGCCAAATACTTGCCTAAACTGCGTCCGGGAGCACATTGCAGCCTTCTGCCTC 606
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Db  161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180

Qy  607 ACGGAGCCAGCCAGTGGAGCGATGCGAGCCGGCATGCAGAGCCCAATCCGGAGCAGAGCCACACTAAGTGAA 666
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Db  181 ThrGluProAlaSerGlySerAspAlaSerArgAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy  667 GACAAGAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC 726
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Db  201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy  727 AATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATTCTGATTCAGTGAAAGAC 786
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Qy  787 AAAATCACAGCATTCATAGTAGAAAGACTTTGGTGGAGTCACTAATGGAAACCCGAA 846
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Db  241 LysIleThrAlaPheIleValGluArgLeuTrpTrpSerHisThrArgGlyGlyProGlu 260

Qy  847 GATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA 906
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Db  261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy  907 CCTGTGAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACACCCTC 966
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Db  281 ProValGluAsnIleLeuGlyGluValGlyValGlyPheLysValAlaMetAsnIleLeu 300
Qy  967 AACAGCGGCCGGTTCAGCATGGCCAGCGTCCTGCTGGCTGGCCTGCTCAAGAGATTGATTGAA 1026
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Db  301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320

Qy 1027 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTAACAGAGGCTCAGTGAATTTGGA 1086
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Db  321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340

Qy 1087 TTGATTCAGGAGAAATTGCACTCGATGGCTCAGAGAGGCTACGTCATGAGAGTATGACC 1146
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Qy 1147 TACCTCCACAGCAGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTTCCCATCGAGCCAGCC 1206
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Qy 1207 ATGGTGAAGGTGTTCAGCTCCGAGGCGCCCTGGCAGTGTGTGAGTGAGGGCCTGCAGATC 1266
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Db  381 MetValLysValPheSerSerGluGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIleIle 400

Qy 1267 CTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCCTGACACCCGC 1326
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  401 LeuGlyLeuGlyTyrLeuGlyTyrThrArgAspPheTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy 1327 ATCCCCTCATCTTCGAGGGAACCAATGAGATTCCGGATGTACATCGCCCTGACGGGT 1386
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 IleLeuLeuIlePheGluGluThrAsnGluIleProAspValMetTyrIleAlaLeuThrArgGly 440

Qy 1387 CTGCAGCATGCGGCGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 LeuGlnHisAlaAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy 1447 AGCACAGTCGATGGATACCGGTTGGCCGGAGGCTTGGGACTCCCTGGGCCGCAACTGTGGAC 1506
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Db  461 SerThrValAspMetThrValGlyArgArgLeuGlyArgGlyLeuArgThrValAspAsp 480

Qy 1507 CTGGGGCTGACAGGCCAACCAATGAGAGTGTGCACCCCAGTCTTGCCGCAGTAGTGCCAACAAG 1566
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Db  481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerSerLeuAsnLys 500

Qy 1567 TTTGAGGAGAACACCTACTGCTTCGGCGACCGTGGAGACACTGCTGCTGCTTCCGGCTTTGGC 1626
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Qy 1627 AAGACCATCATGGAGGAGCAGCTGTACTGGTACTGGCGGTGGCCCAACATCCTCATCAACCTG 1686
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Qy 1687 TATGGCATGGCAGCGGCCCGTGCTGCGCCGCCCAGCCGCTCCATCCGCATTGGGCTCCGCAAC 1746
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Qy 1807 TTCAGCCTCTCCAGCTGGACAAGTATGCGCCAGAAAAACCTAGATGAGCAGATTAAGAAA 1866
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Qy 1867 GTGTCCGCAGAGATCCTTGAGAAGCCAGAGCCTATATATGTGTCCCACCCTCTGTCGGACGACA 1926
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Db  601 ValSerGlnIleLeuGluGluLysGluArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy 1927 TGC 1929
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Db  621 Cys 621
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XX	
AC	AAE21680;
XX	
DT	16-JUL-2002 (first entry)
XX	
DE	Human acyl dehydrogenase DHDR-7 (62112 protein).
XX	
KW	Human; dehydrogenase-7; DHDR-7; 62112 protein; CNS disorder; epilepsy;
KW	Alzheimer's disease; AS; Pick's disease; differentiation disorder;
KW	Huntington's disease; autonomic function disorder; hyperthyroidism;
KW	depression; schizophrenia; panic migraine; cardiac related disorder;
KW	anxiety; obesity; arteriosclerosis; restenosis; Parkinson's disease;
KW	angina; hypertension; cardiomyopathy; arrhythmia; muscle weakness;
KW	arterial inflammation; cell proliferation disorder; growth disorder;
KW	diabetes mellitus; hypertension; migration disorder; gene therapy;
KW	fertility disorder; autoimmune disorder; metabolic disorder; ataxia;
KW	cancer; hepatic disease; acyl-CoA dehydrogenase; beta-oxidation; enzyme.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Domain 1..36
FT	/note= "Dehydrogenase domain"
FT	Domain 23..123
FT	/note= "Dehydrogenase precursor domain"
FT	Domain 37..426
FT	/note= "Acyl-coA very long chain dehydrogenase domain"
FT	Domain 70..432
FT	/note= "Dehydrogenase-related long acyl-coA chain oxidoreductase domain"
FT	Domain 74..448
FT	/note= "Short chain related acyl-coA dehydrogenase specific domain"
FT	Domain 85..438
FT	/note= "Acyl CoA dehydrogenase domain"
FT	Domain 85..177
FT	/note= "Acyl CoA dehydrogenase middle domain"
FT	Domain 147..431
FT	/note= "ACD-3 acyl-coA dehydrogenase domain"
FT	Domain 172..549
FT	/note= "Oxidoreductase acyl-coA dehydrogenase family domain"
FT	Domain 179..286
FT	/note= "Acyl CoA dehydrogenase C-terminal domain"
FT	Region 179..191
FT	/note= "Acyl CoA dehydrogenase signature 1"
FT	Domain 207..604
FT	/note= "Acyl-coA oxidase dehydrogenase oxidoreductase flavoprotein domain"
FT	Domain 290..441
FT	/note= "Acyl CoA dehydrogenase N-terminal domain"
FT	Region 399..418
FT	/note= "Acyl CoA dehydrogenase signature 2"
FT	Domain 408..611
FT	/note= "Dehydrogenase butryl domain"
FT	Domain 432..580
FT	/note= "Polysaccharide deacetylase domain"
FT	Domain 438..621
FT	/note= "Very long chain dehydrogenase domain"
FT	Region 460..476
FT	/note= "Sugar transport protein signature"
XX	
PN	WO200218582-A2.
XX	
PD	07-MAR-2002.
XX	
PF	31-AUG-2001; 2001WO-US027186.
XX	
PR	31-AUG-2000; 2000US-0229831P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Meyers R, Hunter JJ;

RESULT 5
AAE21680
ID   AAE21680 standard; protein; 621 AA.

```
XX
DR   WPI; 2002-329775/36.
DR   N-PSDB; AAD34006.
XX
PT   New human dehydrogenase polypeptide for diagnosing and treating
PT   dehydrogenase-7 associated diseases and disorders e.g. Alzheimer's
PT   disease, and to identify modulators of therapeutic use.
XX
PS   Claim 13; Fig 1; 124pp; English.
XX
CC   The invention relates to human dehydrogenase (DHDR)-7 polypeptides
CC   referred to as 62112 and nucleic acid molecules encoding such
CC   polypeptides. DHDR-7 is an acyl-CoA dehydrogenase, a mitochondrial
CC   flavoprotein which catalyses the first step of fatty acid beta-
CC   oxidation. Sequences of the invention and their antibodies are useful for
CC   treating a disorder, disease or condition which is caused by
CC   misregulation (e.g. downregulation or upregulation) of DHDR activity.
CC   Examples of disorders include central nervous system (CNS) disorders e.g.
CC   Alzheimer's disease (AS), Pick's disease, Parkinson's, Huntington's
CC   disease, Gilles de la Tourette's syndrome, multiple sclerosis, epilepsy,
CC   amyotrophic lateral sclerosis and Creutzfeld-Jakob disease; autonomic
CC   function disorders e.g. hypertension, depression, schizophrenia, panic
CC   migraine, anxiety, obsessive-compulsive disorder and obesity; cardiac
CC   related disorder e.g. arteriosclerosis, ischaemia reperfusion injury,
CC   restenosis, arterial inflammation, angina, hypertension, cardiomyopathy
CC   and arrhythmia; disorders of musculus skeletal system paralysis, muscle
CC   weakness e.g. ataxia; cell proliferation, growth, differentiation or
CC   migration disorders e.g. cancer, diabetes mellitus, hypothyroidism or
CC   hyperthyroidism; reproductive or fertility disorders; autoimmune or or
CC   immune deficiency disorders; hepatic disease or dysfunction and metabolic
CC   disorders. They are used for screening assays, predictive medicine e.g.
CC   diagnostic assays, prognostic assays, monitoring clinical trails, and
CC   pharmacogenetics. Polypeptides of the invention are used to identify
CC   modulators that modulate their activity. Polynucleotides of the invention
CC   are used in gene therapy. The present sequence is human DHDR-7
XX
SQ   Sequence 621 AA;
```

```
Alignment Scores:
Pred. No.:
Score:                 1.98e-283         Length:        621
Percent Similarity:    3153.00           Matches:       621
Best Local Similarity: 100.00%           Conservative:  0
Query Match:           100.00%           Mismatches:    0
DB:                    70.00%            Indels:        0
                       5                 Gaps:          0

US-09-945-326-1 (1-2452) x AAE21680 (1-621)

Qy   67 ATGAGCGGCTGCGGGCTCTTCCTGCGCCACCAGGCTCGGGCTGCCTCGTTGCTGGGGTCTG 126
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Qy  127 GTGGTCTCTACCGGCGACCGGCGGCTACTGGCGCCACCAGCCCGCCTGTACGGAGCTTCGCC 186
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Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgArgHisGlnProProValProGluAlaPheAla 40

Qy  187 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGGAGAGTTTTCCATTTCCAGGAGGTAGC 246
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Db   41 LysGluLeuPheLeuGlyLysLysIleLeuLysLysGlyGluValPhePheProPheProGluValSer 60

Qy  247 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 306
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Db   61 GlnAspGluLeuAsnGluIleLeuAsnGlnPheLeuGlyProValGlyIleProPheGluGluThrGlu 80

Qy  307 GAGGTGGACTCCCGAAAAATTGACCAGGAAGGAGAAAATCCCAGATGAAACTTTGGAGAAA 366
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  367 TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGCCTGGGCTTC 426
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Db  101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyLeuPhe 120

Qy  427 TCCAACACCATGTACTCAAGACTAGGGGAGGAGATCATCAGACTAGGCGATCGGATGGTGTG 486
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Top alignment block (page 9 continuation):

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Db  121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
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Qy  487 ACCCTGCAGGGACCACCAGGCTATTGGCCTAACTGGCTCCTGGCACTGAGGAG 546

Db  141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyLeuLysLeuGlyLeuIleLeuGluLeuLeuLysGlyLeuTyrLeuGluGlu 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  547 CAGAAAGCCAAATACTTGCTAAACTGGCTCGGGGAGGAGCACATTGCAGCCTTCTGCCTC 606

Db  161 GlnLysAlaLysTyrLeuProLysGluGlyGluHisIleAlaAlaPheCysLeu 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  607 ACGGAGCCAGCCAGTGGAGGGATGCAGCCTCAATCCGGAGCAGCAGCCACACTAAGTGAA 666

Db  181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  667 GACAAGAAGCACTACATCCTCCAAGGTCGGATTACTAATGGAGGACTGGCC 726

Db  201 AspLysLysHisTyrIleLeuLysGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  727 AATATTTTACTGTGTTCAAGACTGAGGTCGTTGATTCGATGGATCAGTGAAAGAC 786

Db  221 AsnIlePheThrValPheAlaLysThrGluValLysAspSerGlySerValLysAspAsp 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  787 AAAATACAGACATTCATAGTAGAAAGAGACTTGGTGGAGTCCATTTGAAAAACACCAAGATA 846

Db  241 LysIleThrAlaPheIleValGluArgAspAspPheGlyValThrAsnGlyLysProGlu 260
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  847 GATAAATTAGGCATTCGGGGTCCACACTTGTGAGTCCATTTGAAAACACCAAGATA 906

Db  261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  907 CCTGTGGAAAAACATCCTTGGAGAGTTCGGAGATGGGTTAAGGTGGCCATGAACATCCTC 966

Db  281 ProValGluAsnIleLeuGlyGluHisGlyLysGlyValIleAlaMetAsnIleLeu 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  967 AACAGGCGCCGGTTCAGCATGGCAGCGTTGCGTGGCTGGGCTTGCTCAAGAGATTGATTGAA 1026

Db  301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1027 ATGACTGCTGAGTACGCCTGCACAACGAAAACAGTTTAACAGAGAGCTCAGTGAATTTGGA 1086

Db  321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1087 TTGATTCAGGAGAAATTGACACTGAGGCTACAAGGCTTACGTCATGGAGAGTATGACC 1146

Db  341 LeuIleGlnGluLysLeuThrLeuArgTyrAlaTyrValMetGluSerMetThr 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1147 TACCTCCAGCAGGGATGCTGAGTGACCAACCTGCTTTCCCGACTGCTCCATCGAGGCAGCC 1206

Db  361 TyrLeuThrAlaGlyMetLeuAspGlnMetLeuGlyValPheProAspCysSerSerIleGluAlaAla 380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1207 ATGGTGAAGGTGTTCAGCTCGGAGGCCCGGCCAGTGTGTGAGTGAGGCCGTCGAGATC 1266

Db  381 MetValLysValPheSerGluValAlaAlaTrpGlnCysValSerGluValAlaLeuGlnIle 400
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1267 CTCGGGGGCTTGGGCTACACAAGGACTATCCGTACGGATGCTGCTGACACCCGC 1326

Db  401 LeuGlyGlyLeuGlyTyrLeuGlyArgAspTyrProValArgIleLeuArgAspThrArg 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1327 ATCCTCCTCATCTTCGAGGGAACCAATGAATTCTTCACTGAA 1386

Db  421 IleLeuLeuIlePheGluGlyValThrAsnGluIleLeuLeuArgMetTyrIleAlaGly 440
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1387 CTGCAGCATGCCGGCCGCCATCCTGACTACCATGAGCTTAAACAGGCCAAGTG 1446

Db  441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1447 AGCACAGTCATGGATACCGTTGGCCGGAGCTTCGGGACTCCCTGGCCGAACTGTGAC 1506

Db  461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1507 CTGGGGGCTGACGACGAACCATGGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG 1566
```

Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy 1567 TTTGAGAGAACACCTACTGCTTCGGCCGGACCGTTGAGACACTGGCTCCGGCTTTGGC 1626
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520

Qy 1627 AAGACCATCATGGAGAGGAGCAGCTGGTACTGGAGCGGGGTGGCCAACATCCTCATCAACCTG 1686
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 521 LysThrIleMetGluGluGlnGlnLeuValLeuValLysArgValAlaAsnIleLeuIleAsnLeu 540

Qy 1687 TATGGGATGACGGCCGGTCGTGTCGCGGGGCCAGCCGCCGTCCATCCGCATTGGGCTCCGCAAC 1746
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuLeuArgAsn 560

Qy 1747 CACGACCAGAGGTTCTCTTGCCAACACCTTCTGCTGGAAGCTTACTTGCAGAATCTC 1806
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy 1807 TTCAGCCTCTCTCAGCTGGACAAGATGTCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1866
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 581 PheSerLeuSerGlnLeuAspLysMetSerProGluAsnLeuAspGluGlnIleLysLys 600

Qy 1867 GTGTCCCAGCAGATCCTTGAGAAGGCAGGCCTATATCTGTGCCCACCCTCTGGACAGGACA 1926
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 ValSerGlnGlnIleLeuGluLysAlaGlyLeuTyrLeuCysProProSerGlyGlnAspThr 620

Qy 1927 TGC 1929
         |||
Db 621 Cys 621

RESULT 6
ADJ69253
ID   ADJ69253 standard; protein; 621 AA.
XX
AC   ADJ69253;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID1059.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
.XX

PS   Claim 1; SEQ ID NO 1059; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. According, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 621 AA;

Alignment Scores:
Pred. No.:
Score: 1.98e-283   Length: 621
                       3153.00   Matches: 621
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 70.00%   Indels: 0
DB: Gaps: 0

US-09-945-326-1 (1-2452) x ADJ69253 (1-621)

Qy 67 ATGAGCGGCTGCGGGCTCTTCCTGCGCCACCACGGCTGCGGCTCGGCTGCCGGGGGCTG 126
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy 127 GTGGTCTCTACCGGCCGAACCGGCGGCTACTGCGCCACCAGCCCGGCCGTGTACAGAGCTTTCGCC 186
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValProValArgAlaPheAla 40

Qy 187 AAAGAGCTTTTCCTAGGACAAAATCAAGAGAAGAAAGAAGTTTCCCATTCCAGAAGTTAGC 246
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 41 LysGluLeuPheLeuGlyGlnAsnGlnGluLysLysGluValSerHisSerArgSerTyrSer 60

Qy 247 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGACACCGTGGAAAAATTCTTCACTGAA 306
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuAspThrValGluLysPhePheThrGlu 80

Qy 307 GAGGTGGACTCCCGAAAAATTGACCAGGAGGAAAATCCCAGATGAAAACTTTGAGAAA 366
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81 GluValAspSerArgLysIleAspGlnGluGluAsnProArgAspGluAsnProGluGluAsnLysLeuLys 100

Qy 367 TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAAAATATGTGGCCTGGGCTTC 426
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluAsnMetTrpProGlyLeuPhe 120

Qy 427 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTG 486
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy 487 ACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG 546
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160

Qy 547 CAGAAAGCCAAATACTTGCCTAAACTGGGCTCCGGGGAGCACATTGCCAGCCTTCTGCCTC 606
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 161 GlnLysAlaLysTyrLeuProLysLeuGlyLeuGluHisIleLeuAlaAlaPheCysLeu 180

Qy 607 ACGGAGCCAGCCAGTGGAGCGGATGCAGCGGCAGGAGCAGCCACACTAAGTGAA 666
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgArgLeuSerGlu 200

Qy 667 GACAAGAAGCACTACATCCTCAAGGTCTGGATTACTAATGGAGGACTGGCC 726
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 AspLysLysHisTyrIleLeuAsnGlySerValTrpIleThrAsnGlyGlyLeuAla 220

```
Qy   727 AATATTTTACTGTGTTGCAAGACTTGAGGTCGTTGATCTGATGATCAGTGAAAGAC 786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePheThrValPheAlaLysThrGluValAspSerAspGlySerValLysAsp 240

Qy   787 AAAATCACAGCATTCATAGTAGAAAAGAGACTTGGTGAGTCACTAATGGAAACCCGAA 846
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAlaPheIleValGluArgAspPheGlyGluSerLeuMetGluThrArg 260

Qy   847 GATAAATTAGGCATTCGGGGTCCAACACTTGTGAAGTCCATTTGAAAACCAAGATA 906
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   907 CCTGTGGAAAACATCCTTGGAGAGGTCCGAGATGGGTTTAAGGTGGCCATGAACATCCTC 966
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy   967 AACAGCGGCCGTTCAGCATGGCAGCGGTCGCAGCGGTCTGGGCGTGGCTGG...     1026
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlySerValAlaValAlaGlyLeuLeuLeuLysArgLeuIleGlu 320

Qy  1027 ATGACTGCTGAGTACCGCCTGACACAGGAAACAGTTAACAAGAGGCTCAGTGAATTTGGA 1086
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrAlaGluTyrArgLeuThrGlnGluThrValAsnLysArgLeuSerGluPheGly 340

Qy  1087 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACC 1146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysPheAlaAlaLeuMetAlaGlnAsnLysAlaTyrValMetGluSerMetThr 360

Qy  1147 TACCTCACAGGGATGCTGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCC 1206
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrLeuAlaGlyMetLeuAspSerGlnIleProGlyPheProProAspCysSerIleGluAlaAla 380

Qy  1207 ATGGTGAAGGTGTTCAGCTCCGAGCCGCCTGGCAGTGTGTGAGTGAGGGCCTGCAGATC 1266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 MetValLysValPheSerSerGluSerGluValSerValSerGluGluAlaAlaLeuGlnIleIle 400

Qy  1267 CTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGC 1326
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgArgThrArg 420

Qy  1327 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1386
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440

Qy  1387 CTGCAGCATGCCGCGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuGlnHisAlaAlaArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy  1447 AGCACAGTCATGGATACCGTGGCCGAGGCTTCGGGGACTCCCTGGGCCGAACTGTGGAC 1506
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrValAlaGluAlaSerGlyLeuProGlyProAsnCysGly 480

Qy  1507 CTGGGGCTGACAGGCAACCATGAGTTGTGACCCCCAGTCTTCTGCCGACAGTGCCAACAAG 1566
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy  1567 TTTGAGGAGAACACCTACTGCTTCGGCCGACCGTGGAGACACTGCTTCCGCCTTTGGC 1626
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGluAsnThrTyrCysPheGlyArgLeuGluThrValGluThrLeuArgPheGly 520

Qy  1627 AAGACCATGCATGGAGGAGCAGCTGGTACTGGAGGCGGTGGCCAACATCCTCATCAACCTG 1686
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrMetHisGlyGluGluGlnLeuValLeuGluAlaValAlaAsnIleLeuIleAsnLeu 540

Qy  1687 TATGGCATGACGGCGCGTGCTGCGCGGGGGCCAGCCGCTCCATCCGGCCATTGGGCTCCCAAC 1746
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgIleArgSerIleArgGlyLeuArgAsn 560

Qy  1747 CACGACCACGAGGTTCTTCTTGGCCAACACCTTCTGCGTGAAGCTTACTTGCAGAATCTC 1806
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 HisAspHisGluValLeuLeuLeuAlaAsnThrPheCysValLysLeuTyrLeuGlnAsnLeu 580
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Qy  1807 TTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1866
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600

Qy  1867 GTGTCCCAGCAGATCCTTGAGAAGGCAGCCTATATCGTGCCCACCCTCTGGACAGGACA 1926
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnIleLeuGluLysAlaAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy  1927 TGC 1929
         |||
Db   621 Cys 621
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RESULT 7
ADJ70247

ID   ADJ70247   standard; protein; 621 AA.
XX
AC   ADJ70247;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID2053.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200308768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 2053; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX

SQ   Sequence 621 AA;

Alignment Scores:
Pred. No.:
Score: 1.98e-283
Percent Similarity: 3153.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 70.00%

Length: 621
Matches: 621
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-945-326-1 (1-2452) x ADJ70247 (1-621)

```
Qy    67 ATGAGCGGCTGCGGGGCTCTTCCTGCGCACCACGGCTCGCGCTGCGCGGGCTCTG 126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy   127 GTGGTCTCTACCGGGAACCGGCGGCTACTGGGCACCAGCCCGCCTGTACGAGCTTTCGCC 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40

Qy   187 AAAGAGCTTTTCTAGGCAAAATCAAGAAGAAGAGAGTTTTCCAATTCCAGAAGTTAGC 246
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60

Qy   247 CAAGATGAACTTAATGAAACAATCAGTTCTTGGGACCCGTGAAAAATCTTCACTGAA 306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80

Qy   307 GAGGTGACTCCCGAAAAATTGACCAGGAAGGAGAAATCCCAGATGAAACTTTGGAGAAA 366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 GluValAspSerArgLysIleAspGlnGluGlyLysIleLysIleProAspGluThrLeuGluLysLys 100

Qy   367 TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGCTCCAGAAGAATATGTGGCCTGGCTTC 426
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuLysSerLeuGlyLeuLeuGlyLeuGlnValProGluTyrGlyTyrGlyLeuGlyPhe 120

Qy   427 TCCAACACCATGTACTCCAAGACTAGGGGAGGATCATCAGCATGGATGGGTCCATCACTGTG 486
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy   487 ACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG 546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160

Qy   547 CAGAAAGCCAAATACTTGCCTAAACTGGCCGGGGGAGCACATTGCAGCCTTCTGCGCCTC 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 GlnLysLysAlaLysTyrLeuProLysLeuAlaSerGlyGlyGluHisIleAlaAlaPheCysLeu 180

Qy   607 ACGGAGGCCAGTGGGAGCGATGGAGCGATCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy   667 GACAAGAAGCACTACATCCTCAAGTGCTCCAAGGTTCTGATTACTAATGGAGGACTGGCC 726
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 AspLysLysHisTyrIleLeuLysCysSerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy   727 AATATTTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATCAGTGAAAGAC 786
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePheThrValPheAlaLysThrGluValValAspGlnSerGlyValLysAspAsp 240

Qy   787 AAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGAGTCACTAATGGGAAACCCGAA 846
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAlaPheIleValGluArgAspLeuValThrAsnGlyLysProGlu 260

Qy   847 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA 906
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   907 CCTGTGGAAAACATCCTTGAGAGGTCGAGAGATGGGTTTAAGGTGGCCATGAACATCCTC 966
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ProValGluAsnIleLeuGluGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy   967 AACAGCGGCCGGTTCAGCATGGGCACGCGTCGTGGCTGGCTGCTCAAGAGATTGATTGAA 1026
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlySerValArgAlaGlyLeuLeuLysArgLeuIleGlu 320

Qy  1027 ATGACTGCTGCACGCCTGCACAAGAAACAGTTAACAAGAGGCTCAGTGAATTTGA 1086
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrAlaAlaArgLeuHisLysLysGlnLeuThrArgGlySerValAsnLeuSerGluPheGly 340

Qy  1087 TTGATTCAGGAGAAATTGCACTGAGCCTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACC 1146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysLeuHisAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360

Qy  1147 TACCTCACAGCAGCAGGATGCTGACCAACCTGCTTTCCCGACTGCTTCCATCGAGGCAGCC 1206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrAlaGlyMetLeuAspGlnProAlaPheProAspCysSerIleGluAlaAla 380

Qy  1207 ATGGTGGAGGTGTTCAGCTCCGAGGGCGCTGGCAGTGTGTGAGTGGAGGCGGCTGCAGATC 1266
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 MetValLysValPheSerSerGluValAlaGlyAlaAlaTrpGlnCysValSerGlyAlaLeuGlnIle 400

Qy  1267 CTCGGGGGCTTGGCTACACAAGGACTATCCGTACCAGCCCATACTGCGTGACACCCGC 1326
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy  1327 ATCCTCCTCATCTTCGAGGGACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1386
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440

Qy  1387 CTGCAGCATGCGCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACACGGCCAAGTG 1446
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuGlnHisAlaArgProHisProAspTyrGlnAspProMetSerLeuLysHisGlyGlnValLeuLeuLysGlnAlaLysVal 460

Qy  1447 AGCACAGTCATGGAATACCGTTGGCCGGAGTTGCACCCAGTCTTGCGAGCAGTGCCAACAAG 1506
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrValGlyArgGluLeuArgAspSerLeuGlyArgThrValAsp 480

Qy  1507 CTGGGGGCTGACAGGCAACCATGAGTTCGCACCCAGTCTTGCGAGCAGTGCCAACAAG 1566
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrGlyAsnHisGlyValHisProSerLeuAlaSerSerAlaAsnLys 500

Qy  1567 TTTGAGGAGAACACCTACTGCTTCGGCCGGTGGAGACCGTGACTGCTGCTCCGCTTTGGC 1626
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrValThrAlaAlaGluArgPheGly 520

Qy  1627 AAGACCATCATGGAGGAGCAGCTGGTACTGGAAGCCGGTGGCCAACATCCTCATCAACCTG 1686
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540

Qy  1687 TATGGCATGACGGCCGTGCTGTCCGGGGCCGCTCCATCCGCATTGGGCTCCGCAAC 1746
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560

Qy  1747 CACGACCACGAGGTCTCTTGCCAACACCCTTCGCGTGGGAAGCTTACTTGCAGAATCTC 1806
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy  1807 TTCAGCCTCTCAGCTGACAAGTATGCTCCAGAAAACTAGATGAGCAGATTAAGAAA 1866
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGlnIleLysLysLys 600

Qy  1867 GTGTCCCAGAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCCTCGGACAGGACA 1926
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnArgSerLeuArgSerGluProTyrIleCysAlaHisProLeuAspArgThr 620

Qy  1927 TGC 1929
          |||
Db   621 Cys 621
```

RESULT 8
ADM87327
ID   ADM87327 standard; protein; 621 AA.
XX
AC   ADM87327;
XX

DT   03-JUN-2004 (first entry)
XX
DE   Human protein SEQ ID NO:420.
XX
KW   respiratory; cytostatic; antiarthritic; antiinflammatory;
KW   gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW   antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW   chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW   inflammatory condition; arthritis; inflammatory bowel disease;
KW   Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW   graft versus host disease; human.
XX
OS   Homo sapiens.
XX
PN   WO200409834-A2.
XX
PD   29-JAN-2004.
XX
PF   19-JUL-2002; 2002WO-US022858.
XX
PR   21-JUL-2001; 2001US-0306971P.
PR   28-MAR-2002; 2002US-00112944.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI   Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
DR   WPI; 2004-143291/14.
DR   N-PSDB; ADM87083.
XX
PT   New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT   cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT   Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT   versus host disease.
XX
PS   Claim 20; SEQ ID NO 420; 591pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I): (a)
CC   comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC   which encodes a polypeptide with biological activity, where the
CC   polynucleotide hybridises to (I) under stringent hybridisation conditions
CC   or has greater than 99% sequence identity with (I). (II) has respiratory,
CC   cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
CC   antibacterial, immunosuppressive, antidiabetic and antirheumatic
CC   activities, and can be used in gene therapy. (I) can be used for
CC   generating polynucleotides encoding chimeric or fusion proteins and
CC   heterologous protein sequences. The polynucleotides can be used to
CC   express recombinant protein for analysis, characterisation or therapeutic
CC   use; as markers for tissues in which the corresponding protein is
CC   preferentially expressed; as molecular weight markers on gels; as
CC   chromosome markers or tags to identify chromosomes or to map related gene
CC   positions; to compare with endogenous DNA sequences in patients to
CC   identify potential genetic disorders; as probes to hybridise and discover
CC   genes, related DNA sequences; as a source of information to derive PCR
CC   primers for genetic fingerprinting; as a probe to subtract-out known
CC   sequences in the process of discovering other novel polynucleotides; for
CC   selecting and making oligomers for attachment to a gene chip or other
CC   support, including for examination of expression patterns; to raise anti-
CC   protein antibodies using DNA immunisation techniques; and as an antigen
CC   to raise anti-DNA antibodies or elicit another immune response. The
CC   polynucleotides and polypeptides can be used as nutritional sources
CC   or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC   source, as a nitrogen source or as a a source of carbohydrates. The
CC   polynucleotides and polypeptides can also be used treat cancer. The
CC   compositions are useful for promoting better or faster closure of non-
CC   healing wounds, for the generation and regeneration of tissues, for gut
CC   protection and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues, and conditions resulting from
CC   systemic cytokine damage. The compositions can also be used to treat
CC   inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC   Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC   or graft versus host disease. The present sequence represents a novel
CC   human polypeptide sequence from the present invention. N.B. The sequences
CC   for this patent were obtained from the USPTO web site from an equivalent
CC   US patent US2004048249A1.
XX
SQ   Sequence 621 AA;

Alignment Scores:
Pred. No.:   1.98e-283   Length: 621
Score: 3153.00   Matches: 621
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 70.00%   Indels: 0
DB: 8   Gaps: 0

US-09-945-326-1 (1-2452) x ADM87327 (1-621)

Qy   67 ATGAGCGGCTGCGGGTCTTCCTGCCACCACGGCTGCGGCTCGTCGCTGCCGGGGTCTG 126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy   127 GTGGTCTCTACCGGCAACCGGCGCTACTGGCCGGACCAGCCCGCTGTACGAGCTTTCGCC 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40

Qy   187 AAAGAGCTTTTCCTAGGCAAATCAAGAAGAAGAAGAAGTTTCCATTTCCAGAAGTTAGC 246
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysGluLeuPheLeuGlyLysLeuLysLysLysLysLysGluValPheProPheProGluValSer 60

Qy   247 CAAGATGAACTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysAsnPhePheThrGlu 80

Qy   307 GAGGTGACTCCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAA 366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100

Qy   367 TTGAAGAGCCTAGGGCTTTTGGGCTGCCAAGTCCCAGAAGAATATGTGGCCTGGGCTTC 426
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe 120

Qy   427 TCCAACACCAGTACTCAAGACTAGGGGAGATCATCAGCATGGGGTCCATCACTGTG 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SerAsnThrMetTyrSerArgLeuGlyLeuIleIleSerMetAspGlySerIleThrVal 140

Qy   487 ACCCTGCAGGCCACCAGGCTATTGGCCTCAAGGGGATCATCTGGCTGGCACTGAGGAG 546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLeuGlyLysGlyIleIleLeuAlaGlyThrGluGlu 160

Qy   547 CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGACACATTGCAGCCTCTGCCTC 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysSerLeu 180

Qy   607 ACGGAGCCAGCCAGTGGGAGCGGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA 666
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy   667 GACAAGAGCCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGACTGAGC 726
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 AspLysSerHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyLeuAla 220

Qy   727 AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATGATCAGTGAAAGAC 786
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePheThrValPheAlaLysThrGluValValAlaAspSerAspSerValLysAsp 240

Qy   787 AAAATCACAGACATTCATAGTAGAAAGAGACTTTGGTGAGTGCACTAATGGAAACCCGAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAspIleHisArgArgLysArgLeuGlyGluCysValHisGluGlyValProGlu 260

Qy   847 GATAAATTAGGACTGGGCTCCAACACTTGTGAAGTCCATTTGAAACACCAAGATA 906
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyLeuGlyArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   907 CCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGCCATGAACATCCTC 966

```
Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
     281    ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy   967    AACAGCGGCCGGTTCAGCATGGGCAGCGTCGTGGCTGGCTGCTCAAGAGATTGATTGAA 1026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301    AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320

Qy   1027   ATGACTGCTGAGTACGCCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGGA 1086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321    MetThrAlaGluTyrAlaCysThrArgLysThrArgLysAsnLysArgLeuSerGluPheGly 340

Qy   1087   TTGATTCAGGAGAAATTGCACTGATGGCTCAGAGAGGCTTACGTCATGGAGAGTATGACC 1146
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341    LeuIleGlnGluLysPheAlaLeuMetAlaGlnArgGlyLeuArgValMetGluSerMetThr 360

Qy   1147   TACCTCCACAGCAGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCC 1206
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361    TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380

Qy   1207   ATGGTGAAGGTGTTCAGCTCCGAGGCCGGCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC 1266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381    MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy   1267   CTCGGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGC 1326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401    LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy   1327   ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCCGGATGTACATCGCCCTGACGCGGGT 1386
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421    IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrArgGly 440

Qy   1387   CTGCAGCATGCCGGCCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441    LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluHisArgIleAlaLysVal 460

Qy   1447   AGCACAGTCCATGGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGGCCCGAACTGTGGAC 1506
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461    SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480

Qy   1507   CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCCGGACAGTGCCAACAAG 1566
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481    LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy   1567   TTTGAGGAGACAACACCTACTGCTTCGGCCGACCGTGGAGACACTGCTGTCTCCGTTTGGC 1626
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501    PheGluGluAsnThrProThrAlaSerGlyArgGlyArgThrValGlyAspThrLeuLeuLeuArgPheGly 520

Qy   1627   AAGACCATCATGGAGGAGGCAGCTGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTG 1686
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521    LysThrIleMetGluGluAlaAlaValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540

Qy   1687   TATGGCATGACGGCCCGTGCTGCGCGGGCCAGCCCGTCCATCCGGCATTGGCTCCGCAAC 1746
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541    TyrGlyMetThrAlaArgAlaAlaArgAlaSerProSerIleArgIleGlyLeuArgAsn 560

Qy   1747   CACGACCAGAGGTTCTCTTGGCCAACAACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC 1806
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561    HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy   1807   TTCAGCCTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1866
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581    PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600

Qy   1867   GTGTCCCAGCAGATCCTTGAAGAGGCAGCCTATATCTGTGCCCACCCTCTGGACAGGACA 1926
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601    ValSerGlnGlnIleLeuGluGluAlaAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy   1927   TGC 1929
            |||
Db   621    Cys 621
```

ID   AAB41800 standard; protein; 565 AA.
XX
AC   AAB41800;
XX
DT   08-FEB-2001 (first entry)
XX
DE   Human ORFX ORF1564 polypeptide sequence SEQ ID NO:3128.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection; asthma;
KW   severe combined immunodeficiency; malaria, autoimmune disorder; burn; wound;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US008621.
XX
PR   31-MAR-1999;   99US-0127607P.
PR   02-APR-1999;   99US-0127636P.
PR   05-APR-1999;   99US-0127728P.
PR   30-MAR-2000;   2000US-00540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,   Leach M;
XX
DR   WPI; 2000-602362/57.
DR   N-PSDB; AAC76009.
XX
PT   Novel nucleic acids and peptides derived from open reading frame X,
PT   useful for treating e.g. cancers, proliferative disorders,
PT   neurodegenerative disorders and cardiovascular disease.
XX
PS   Claim 11; Page 2345-2346; 5507pp; English.
XX
CC   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC   which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC   sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC   antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC   anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC   cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC   dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC   antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC   sequences can be used for determining the presence of or predisposition
CC   to, or preventing or treating pathological conditions associated with an
CC   ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC   proteins in gene therapy vectors. The proteins and nucleic acids may be
CC   used to treat cancers, proliferative disorders, neurodegenerative
CC   disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC   diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC   storage, systemic lupus erythematosus, severe combined immunodeficiency
CC   (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC   disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC   cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC   enhance coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ   Sequence 565 AA;

Alignment Scores:

Pred. No.:
Score: 1.42e-256
Percent Similarity: 2864.00
Best Local Similarity: 100.00%
DB: 63.59%

Length: 565
Matches: 564
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 3

US-09-945-326-1 (1-2452) x AAB41800 (1-565)

```
Qy   238  GAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTC  297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2  GluValSerGlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhe  21

Qy   298  TTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGAAGGGAAAATCCCAGATGAAACT  357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    22  PheThrGluGluValAspSerArgLysIleAspGlnGluGlyLysSerProGluAspGluThr  41

Qy   358  TTGGGAGAAATTGAAGAGCCTAGGGCTTTTTGGCTGCAAGTCCCAAGAAGAATATGTGGC  417
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    42  LeuGluLysLeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGly  61

Qy   418  CTGGGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCC  477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    62  LeuGlyPheSerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySer  81

Qy   478  ATCACTGTGACCCTGGCAGCCCACCAGGCTATTGGCCTAAGGGGATCATCTTGGCTGGC  537
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    82  IleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuLeuAlaGly  101

Qy   538  ACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGACACATTGCAGCC  597
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   102  ThrGluGluGlnLysLysAlaLysTyrLeuProLysLeuAlaSerGlyGlyHisIleAlaAla  121

Qy   598  TTCTGCCTCACGGAGCCAGCCAGTCTGGGAGGCGATGAGCCCAATCCGGAGCAGAGCCCA  657
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122  PheCysLeuThrGluProAlaSerLeuGlyGlyAspGluProAsnProGluGlnSerArgAlaIle  141

Qy   658  CTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGA  717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   142  LeuSerGluAspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGly  161

Qy   718  GGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGCTCGTTGATTCTGATGATCA  777
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   162  GlyLeuAlaAsnIlePheThrValPheAlaLysThrGluAlaValAspSerAspAspSer  181

Qy   778  GTGAAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGG  837
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182  ValLysAspLysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGly  201

Qy   838  AAACCCGAAGATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAAAAC  897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202  LysProGluAspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsn  221

Qy   898  ACCAAGATACCTGTGAAAAATCCTTGGAGAGTTCGGAGATGGGTTTAAGGTGGCCATG  957
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Db   222  ThrLysIleProValLysAsnProValGluAsnGluLeuLeuGlyValGlyValAlaMet  241

Qy   958  AACATCCTCAACACGCGGCCCGGTTCAGCATGGGCAGCGTTGCGGCTGGCCTGCTCAAGAGA  1017
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Db   242  AsnIleLeuAsnSerGlyArgPheSerMetGlySerValValAlaLeuAlaGlyLeuLeuLysArg  261

Qy  1018  TTGATTGAAATGACTGCTGAGTACGGCCTGCACAAGGAAACAGTTAACAGAGAGGCTCAGT  1077
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   262  LeuIleGluMetThrAlaGluTyrGlyLeuHisLysGluThrArgLysGlnPheGlnAsnLysArgSer  281

Qy  1078  GAATTTGGATTGATTCAGGAGAAATTGCACTGATGGCTTACGTCATGGAG  1137
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Db   282  GluPheGlyLeuIleGlnGluLysLeuHisAlaLeuMetAlaGlnLysAlaTyrValMetGlu  301

Qy  1138  AGTATGACCTACCTCACAGCAGGGATGCTGACCAACCTGGCTTTCCCGACTGCTCCATC  1197
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302  SerMetThrTyrLeuThrAlaGlyMetLeuAspAspGlyProGlyProAspCysSerIle  321
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Qy  1198  GAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCGCCCTGCCAGTGTGTGACTGAGCG  1257
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Db   322  GluAlaAlaMetValLysValPheSerSerGluAlaAlaLeuTrpGlnCysValSerGluAla  341

Qy  1258  CTGCAGATCCTCGGGGGCTTGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCGT  1317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   342  LeuGlnIleLeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArg  361

Qy  1318  GACACCCGCCATCCTCCATCTTCGAGGAGAACCAATAGATTCCGGATGTACATCGGCC  1377
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Db   362  AspThrArgHisProProSerSerArgArgAsnGlnIleLeuLeuArgMetTyrIleAla  381

Qy  1378  CTGACGGGTCTGCAGCATGCCGGCCGATCCTGACTACCAGGATCCATGAGCTTAAACAG  1437
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Db   382  LeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGln  401

Qy  1438  GCCAAAGTGAGCACAGTCATGGATACCGTTGGCCGGAGGCTTCCGGGACTCCCTGGGCCGA  1497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   402  AlaLysValSerThrValMetAspThrValGlyArgArgLeuProGlyLeuProGlyArg  421

Qy  1498  ACTGTGACCTGGGGCTGACAGGCAACAGGAGTTGTGCACCCAGTCTTGCGGACAGT  1557
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Db   422  ThrValAspLeuGlyLeuThrGlyThrGlyAsnHisGlyValValHisProSerLeuAlaAspSer  441

Qy  1558  GCCAACAAGTTGAGGAGAACACCTACTGCTTCGGCCGGACCCTGAGACACTGCTGCTC  1617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   442  AlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeu  461

Qy  1618  CGCTTTGGCAAGACCATCATGAGAGGACTGGTACTGAACGGCGGTGGCCAACATCCTC  1677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   462  ArgPheGlyLysThrIleMetGluGluLeuGlyGlnLeuValLeuAsnGlyAlaAsnIleLeu  481

Qy  1678  ATCAACCTGTATGGACATGACGCGCCGTCTGTCGTCGCGGGCGCTCCATCCGCATTGGG  1737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482  IleAsnLeuTyrGlyMetThrArgAlaValLeuSerSerArgAlaSerIleArgIleGly  501

Qy  1738  CTCCCGCAACCACGACCACGAGGTTCTTCTTGGCCAACACCTTCTGCTGGAAGCTTACTTG  1797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   502  LeuArgAsnHisAspHisGluValLeuLeuAlaLeuAsnThrPheCysTrpValGluAlaTyrLeu  521

Qy  1798  CAGAATCTCTTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAG  1857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   522  GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln  541

Qy  1858  ATTAAGAAGTGTCCCAGCAGAATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCCTG  1917
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542  IleLysLysValSerGlnGlnIleLeuGluLeuGluLysArgAlaTyrIleCysAlaHisProLeu  561

Qy  1918  GACAGGACATGC  1929
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Db   562  AspArgThrCys  565
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RESULT 10
AAB94077
ID   AAB94077   standard; protein; 498 AA.
XX
AC   AAB94077;
XX
DT   26-JUN-2001   (first entry)
XX
DE   Human protein sequence SEQ ID NO:14271.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000;   2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.

PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000;   2000JP-00118776.
PR   02-MAY-2000;   2000JP-00183767.
PR   09-JUN-2000;   2000JP-00241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT   length cDNAs defined in the specification, and for the detection and/or
PT   diagnosis of the abnormality of the proteins encoded by the full-length
PT   cDNAs.
XX
PS   Claim 8; SEQ ID NO 14271; 2537pp + Sequence Listing; English.
XX
CC   The present invention describes primer sets for synthesising 5602 full-
CC   length cDNAs defined in the specification. Where a primer set comprises:
CC   (a) an oligo-dT primer and an oligonucleotide complementary to the
CC   complementary strand of a polynucleotide which comprises one of the 5602
CC   nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in the
CC   specification. The primer sets can be used in antisense therapy and in
CC   gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC   represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC   oligonucleotides, all of which are used in the exemplification of the
CC   present invention
XX
SQ   Sequence 498 AA;

Alignment Scores:
Pred. No.:
Score: 3.62e-225   Length: 498
                       2526.00   Matches: 498
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 56.08%   Indels: 0
DB: 4   Gaps: 0

US-09-945-326-1 (1-2452) x AAB94077 (1-498)

Qy   436 ATGTACTCAAGACTAGGGAGATCATCAGCATGATGGTTCCATCACTGTGACCCTGCA 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetTyrSerArgLeuGlyGluIleIleSerMetMetGlySerIleThrValThrLeuAla   20

Qy   496 GCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCCACTGAGGAGCAGAAAGCC 555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 AlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGluGlnLysAla   40

Qy   556 AAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCA 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysTyrLeuProLysLeuAlaSerGlyHisIleAlaAlaPheCysLeuThrGluPro   60

Qy   616 GCCAGTGGGAGCGATGCAGCCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAAG 675
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Db   61 AlaSerGlySerAspAlaAlaSerIleArgAlaGluProAlaThrLeuSerGluGluAsp 80

Qy   676 CACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGACAATAATAATATTTTT 735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 HisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAlaAsnIlePhe 100

Qy   736 ACTGTGTTTGCAAAGACTGAGTCGTTGATCTGATCAGTGAAAGACAAAATACA 795
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Db   101 ThrValPheAlaLysThrGluValValAspSerAspLysLysAspLysIleThr 120

Qy   796 GCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAGATAAATTA 855
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Db   121 AlaPheIleValGlyArgAspPheGlyGlyValThrAsnGlyLysProGluAspLysLeu 140

Qy   856 GGCATTCGGGGCTCCACACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAA 915
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Db   141 GlyIleArgGlySerAsnThrCysGluValHisPheGluLysThrLysIleProValGlu 160

Qy   916 AACATCCTTGGAGAGTGCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGGC 975
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 AsnIleLeuGlyGluGlyAspGlyPheLysGlyProMetAsnIleLeuAsnSerGly 180

Qy   976 CGGTTCAGCATGGGCAGCGCTGCTGGCTGGCTGCTCAAGAGATTGATTGAAATGACTGCT 1035
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Db   181 ArgPheSerMetGlySerValAlaGlyLeuLeuLysArgLeuIleGluMetThrAla 200

Qy   1036 GAGTACGCCTGCACAAGGAAACAGTTAACAGAGGCTCAGTGAATTTGATTGATTCAG 1095
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GluTyrAlaCysThrArgLysGlnPheAsnArgLeuSerGluPheGlyLeuIleGln 220

Qy   1096 GAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACTACCTCACA 1155
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Db   221 GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrTyrLeuThr 240

Qy   1156 GCAGGGATGCTGGACCAACCTGGCTTCCCACTGCTCATCGAGGCAGCCATGGTGAAG 1215
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Db   241 AlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAlaMetValLys 260

Qy   1216 GTGTTCAGTCCGAGGCCGCCTGGCAGTGTGTGAGTGGAGGGCTGCAGATCCTCCGGGGC 1275
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Qy   1276 TTGGGCTACAACAAGGGACTATCCGTACGAGGCCATACTGCGTGACACCCGCATCCTCCTC 1335
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Db   281 LeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArgIleLeuLeu 300

Qy   1336 ATCTTCGAGGGAACCAATGAGATTCCGGATGTACATCGCCCTCGACGGGTCTGCAGCAT 1395
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Db   301 IlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyLeuGlnHis 320

Qy   1396 GCCGGCCGCCATCCTGCTACCAGGATCCATGAGCTTAAACAGGGCCAAAGTGAGCACAGTC 1455
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Db   321 AlaGlyArgHisProCysTyrThrArgIleHisGluLeuLysGlnGlyGlnSerGluHisSerGlnThrVal 340

Qy   1456 ATGGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGGGGCTG 1515
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Db   341 MetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAspGlyLeuLeu 360

Qy   1516 ACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGCAGTGCCAACAAGTTTGAGGAG 1575
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu 380

Qy   1576 AACACCTACTGCTTCGGCCGCACCGTCGAGACACTGCTCTCCGTTGGCAAGACCATC 1635
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Db   381 AsnThrTyrCysPheGlyArgThrValGluThrLeuLeuSerValGlyLysThrIle 400

Qy   1636 ATGGAGGAGCAGAGTGGTACTGGAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATG 1695
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Db   401 MetGluGluGlnSerGlyThrGlyAlaGlyGlyAlaAsnIleLeuIleAsnLeuTyrGlyMet 420

Qy   1696 ACGGCCGTGCTGTCGCGGGCCAGCCGCTCCATCCGCATTGGCCTCCGCAACCACGACCAC 1755
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Db   421 ThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsnHisAspHis 440

Qy   1756 GAGGTTCTCTTGGCCAACACCTTCGCGTGGAAGCTTACTTGCAGAATCTTCAGCCTC 1815
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Db   441 GluValLeuLeuAlaAsnThrPheCysValGlnAlaTyrLeuGlnAsnLeuPheSerLeu 460

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Qy    1816 TCTCAGCTGGACAAGTATGCTCCAGAAAAACCTAGATGAGCAGATTAAGAAAGTGTCCCAG 1875
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Db     461 SerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLysValSerGln 480

Qy    1876 CAGATCCTTGAGAAGGGAGCCTATATCTGTGCCCACCCTCTGGACAGGACATGC 1929
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Db     481 GlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThrCys 498

RESULT 11
AAU23012
ID   AAU23012 standard; protein; 306 AA.
XX
AC   AAU23012;
XX
DT   18-DEC-2001 (first entry)
XX
DE   Novel human enzyme polypeptide #98.
XX
KW   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW   nephrotropic; anticoagulant.
XX
OS   Homo sapiens.
XX
PN   WO20155301-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001239.
XX
PR   31-JAN-2000;  2000US-0179065P.
PR   04-FEB-2000;  2000US-0180628P.
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PR   02-MAR-2000;  2000US-0186350P.
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PR   17-MAR-2000;  2000US-0190076P.
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PR   27-SEP-2000;  2000US-0235834P.
PR   27-SEP-2000;  2000US-0235836P.
PR   29-SEP-2000;  2000US-0236327P.
PR   29-SEP-2000;  2000US-0236367P.
PR   29-SEP-2000;  2000US-0236368P.
PR   29-SEP-2000;  2000US-0236369P.
PR   29-SEP-2000;  2000US-0236370P.
PR   02-OCT-2000;  2000US-0236802P.
PR   02-OCT-2000;  2000US-0237037P.
PR   02-OCT-2000;  2000US-0237038P.
PR   02-OCT-2000;  2000US-0237039P.
PR   02-OCT-2000;  2000US-0237040P.
PR   13-OCT-2000;  2000US-0239935P.
PR   13-OCT-2000;  2000US-0239937P.
PR   20-OCT-2000;  2000US-0240960P.
PR   20-OCT-2000;  2000US-0241221P.
PR   20-OCT-2000;  2000US-0241785P.
PR   20-OCT-2000;  2000US-0241786P.
PR   20-OCT-2000;  2000US-0241787P.
PR   20-OCT-2000;  2000US-0241808P.
PR   20-OCT-2000;  2000US-0241809P.
PR   20-OCT-2000;  2000US-0241826P.
PR   01-NOV-2000;  2000US-0244617P.
PR   08-NOV-2000;  2000US-0246474P.
PR   08-NOV-2000;  2000US-0246475P.
PR   08-NOV-2000;  2000US-0246476P.
PR   08-NOV-2000;  2000US-0246477P.
PR   08-NOV-2000;  2000US-0246478P.
PR   08-NOV-2000;  2000US-0246523P.
PR   08-NOV-2000;  2000US-0246524P.
PR   08-NOV-2000;  2000US-0246525P.
PR   08-NOV-2000;  2000US-0246526P.
PR   08-NOV-2000;  2000US-0246527P.
PR   08-NOV-2000;  2000US-0246528P.
PR   08-NOV-2000;  2000US-0246532P.
PR   08-NOV-2000;  2000US-0246609P.
PR   08-NOV-2000;  2000US-0246610P.
PR   08-NOV-2000;  2000US-0246611P.
PR   08-NOV-2000;  2000US-0246613P.
PR   17-NOV-2000;  2000US-0249207P.
PR   17-NOV-2000;  2000US-0249208P.
PR   17-NOV-2000;  2000US-0249209P.
PR   17-NOV-2000;  2000US-0249210P.
PR   17-NOV-2000;  2000US-0249211P.
PR   17-NOV-2000;  2000US-0249212P.
PR   17-NOV-2000;  2000US-0249213P.
PR   17-NOV-2000;  2000US-0249214P.
PR   17-NOV-2000;  2000US-0249215P.
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PR   17-NOV-2000;  2000US-0249216P.
PR   17-NOV-2000;  2000US-0249217P.
PR   17-NOV-2000;  2000US-0249218P.
PR   17-NOV-2000;  2000US-0249244P.
PR   17-NOV-2000;  2000US-0249245P.
PR   17-NOV-2000;  2000US-0249264P.
PR   17-NOV-2000;  2000US-0249265P.
PR   17-NOV-2000;  2000US-0249297P.
PR   17-NOV-2000;  2000US-0249299P.
PR   17-NOV-2000;  2000US-0249300P.
PR   01-DEC-2000;  2000US-0250160P.
PR   01-DEC-2000;  2000US-0250391P.
PR   05-DEC-2000;  2000US-0251030P.
PR   05-DEC-2000;  2000US-0251988P.
PR   05-DEC-2000;  2000US-0256719P.
PR   06-DEC-2000;  2000US-0251479P.
PR   08-DEC-2000;  2000US-0251856P.
PR   08-DEC-2000;  2000US-0251868P.
PR   08-DEC-2000;  2000US-0251869P.
PR   08-DEC-2000;  2000US-0251989P.
PR   08-DEC-2000;  2000US-0251990P.
PR   11-DEC-2000;  2000US-0254097P.
PR   05-JAN-2001;  2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465566/50.
DR   N-PSDB; AAS40882.
XX
PT   Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT   treating neural, immune system, muscular, reproductive, pulmonary,
PT   cardiovascular, renal, proliferative disorders and cancerous diseases.
PS   Claim 11; SEQ ID NO 1008; 1180pp; English.
XX
CC   The present invention relates to the isolation of novel human enzyme
CC   polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC   encoding them. The enzyme polypeptides of the invention may comprise the
CC   functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC   isomerases or ligases. The sequences of the invention are useful in the
CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC   the novel human enzyme polypeptides of the invention. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 306 AA;

Alignment Scores:
Pred. No.:
Score:               2.61e-133      Length:           306
Percent Similarity:  1537.00        Matches:          302
Best Local Similarity: 99.34%       Conservative:     0
Query Match:         99.34%         Mismatches:       2
DB:                  34.13%         Indels:           0
                     4              Gaps:             0

US-09-945-326-1 (1-2452) x AAU23012 (1-306)

Qy   1018 TTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGT 1077
              |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 Leu***GluMetThrAlaGluTyrAlaCysThrArgLysThrValGlnPheAsnLysArgLeuSer 22

Qy   1078 GAATTTGGATTGATTCAGGAGAAATTTGCACTGACTGGCTCAGAAGGCTTACGTCATGGAG 1137
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```
Db     23 |||||||||||||||||||||||||||||||||||||||||||||||||||||
                GluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGlu  42

Qy   1138 AGTATGACTACCTCACAGCAGGATGCTGACCAACCTGGCTTCCCGACTGCTCCATC 1197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     43 SerMetThrTyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIle  62

Qy   1198 GAGGCAGCCATGGTGAAGGTGTTCAGTCCGAGGCGCCCTGCAGTGTGAGTGAGGCG 1257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 GluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnGlnCysValSerGluAla  82

Qy   1258 CTGCAGATCCTCGGGGGCTTGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCGT 1317
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     83 LeuGlnIleLeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArg 102

Qy   1318 GACACCCGCCATCCTCCATCTTCGAGGGAACCAATGAGATTCTCCGGGATGTACATCGCC 1377
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    103 AspThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAla 122

Qy   1378 CTGACGGGTCTGCAGCATGCGGCCCATCCTGACTACCAGGATCCATGAGCTTAAACAG 1437
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 LeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluHisLysGln 142

Qy   1438 GCCAAAGTGAGCACAGTCATGGATACCGTTGCCGGAGGCTTCGGACTCCCTGGGCCGA 1497
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    143 AlaLysValSerThrValMetAspThrValGlyArgArg***ArgAspSerLeuGlyArg 162

Qy   1498 ACTGTTGGACCTGGGGTGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTCGGACAGT 1557
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    163 ThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSer 182

Qy   1558 GCCAACAAGTTGAGGAGAACCACTTACTGCTTCGGCCGGACCGTGGAGACACTGCTGCTC 1617
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 AlaAsnLysPheGluGluAsnHisTyrCysPheGlyArgThrValGluThrLeuLeuLeu 202

Qy   1618 CGGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGGAGCGGGTGGCCAACATCCTC 1677
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    203 ArgPheGlyLysThrIleMetGluGluGlnLeuValLeuGluArgValAlaAsnIleLeu 222

Qy   1678 ATCAACCTGTATGGCATGACGCCCGTGCTGTCGCGGCCGCTCCATCCGCATTGGG 1737
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    223 IleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGly 242

Qy   1738 CTCCGCAACCACCAGGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTG 1797
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 LeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeu 262

Qy   1798 CAGAATCTCTTCAGCCTCTTCAGCTGACAAGTATGCTCCAGAAAACCTAGATGAGCAG 1857
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln 282

Qy   1858 ATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGGCAGGCCTATATCTGTGCCCACCCTG 1917
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 IleLysLysValSerGlnGlnIleLeuGluLysAlaGlyLeuTyrLeuCysAlaHisProLeu 302

Qy   1918 GACAGGACATGC 1929
              ||||||||||
Db    303 AspArgThrCys 306

RESULT 12
ABB06991
ID   ABB06991 standard; protein; 653 AA.
XX
AC   ABB06991;
XX
DT   20-JUN-2002  (first entry)
XX
DE   Rat very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID NO:9.
XX
KW   Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
KW   insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
KW   antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW   glucose transport; hyperglycaemic disorder.
```

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XX
OS   Rattus sp.
XX
PN   WO20021642B-A1.
XX
PD   28-FEB-2002.
XX
PF   20-AUG-2001; 2001WO-JP007117.
XX
PR   21-AUG-2000; 2000JP-00254263.
PR   07-SEP-2000; 2000JP-00276633.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Tojo H, Katayama N, Kakimoto S;
XX
DR   WPI; 2002-269344/31.
XX
PT   Protein binding to insulin-responsive aminopeptidase and glucose
PT   transporter 4, useful for prevention and treatment of diseases associated
PT   with blood sugar level disturbance.
XX
PS   Disclosure; Page 90-92; 103pp; Japanese.
XX
CC   The present invention describes human MD25 (very long chain acyl-CoA
CC   dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
CC   (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
CC   activity. IRAP and GLUT4 are involved in the intracellular regulation of
CC   glucose metabolism and glucose transport across the cell membrane.
CC   Expression of MD25 (whose ligands are these proteins) is also involved in
CC   this regulatory process. MD25 can be used in the prevention, treatment
CC   and diagnosis of diseases involving disturbances of glucose metabolism,
CC   such as diabetes and other hyperglycaemic disorders. The present sequence
CC   represents rat VLCAD which is given in the exemplification of the present
CC   invention
XX
SQ   Sequence 653 AA;
```

```
Alignment Scores:
Pred. No.:                         Length:        653
Score: 4.35e-117                   Matches:       303
Percent Similarity: 1365.00        Conservative:  110
Best Local Similarity: 62.77%      Mismatches:    202
Query Match: 46.05%                Indels:        43
DB: 30.31%                         Gaps:          13
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US-09-945-326-1 (1-2452) x ABB06991 (1-653)

Qy    30 GGGAGACTGAGGCTGAGGCTGGGG---AACATCGGCAGCATGAGCGGCTGCGGGCTCTT    86
         |||||| ||||||||||||||||      :::
Db    11 GlyArgGlnLeuLeuGlyAlaArgSerSerArgSerAlaLeuGlnGlyGln            30

Qy    87 CCTGGCGCCACCAGGCTGCGGCTGGGGCTGCCGGGGGTCGTGGTGTCTCTACCGGCGAACCG   146
         |||||| ||:::|||  ||| ||:::|||    ||
Db    31 Pro-ArgProThrSerAlaGlnArg------------LeuTyrAlaSerGluAlaThrGl     46

Qy   147 GCGGCTACTCGGC----------------------ACCAGCCGCCTGT                173
         ||:::|||
Db    46 nAlaValLeuGluLysGluProGluThrLeuSerSerAspAlaSerThrArgGluAspProAl  66

Qy   174 ACGAGCT----------TTCGCCAAAGAGCTTTTCCTAGGCAAATCAAGAAGAAAGA      221
         ||||||           :::||| |||:::||||
Db    66 aArgAlaGluSerLysLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGl   86

Qy   222 AGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTAATGAA-----------AT       266
         ||:::||| |||:::|||   ||
Db    86 nValPheProTyrProSerVal----------LeuAsnGluGlnThrGlnPheLe          102

Qy   267 CAATCAGTTCTTGGGACCCGTCGGAAAAATTCTTCACTGAAGAGGTGGACTTCCCGAAAAAT  326
         : :::|||||||:::|||  ||:::|||
Db   102 uLysGluValGlyProValAlaArgPheGluGlyValAlaAsnAspProAlaLysAs       122

Qy   327 TGACCAGGAAGGGAAAAATCCAGATGAAACTTTGGAGAAATTTGAGAAATGAAGAGACCAGT  386
         :: :::|||||  |||||
Db   ...
```

```
Db   122 nAspSerLeuLysGluGluValGluGluAspThrLeuGlnGlyLeuLeuLysGluGlyGlyAlaPh 142
         |||     ::::||||||:::
Qy   387 TGGGCTGCAAGTCCCAGAAGAATATGTGGCGCCTTCTCCAACACCATGTACTACTCAAG      446
         |||||||||||||:::
Db   142 eGlyLeuGlnValProSerGluLeuLeuGlyLeuGlyLeuSerAsnThrGlnTyrAlaAr     162

Qy   447 ACTAGGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGCAGCGCACCA    503
         |||| |||||||||:::||||||
Db   162 gLeuLeuAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuValAlaHisGl  182

Qy   504 GGCTATTGGCCTCAAGGGGATCATCTTGGCTGCACTGAGGAGCAGAGAAAGCCAAATACTT   563
         |:::|||||   ||||||||:::||||
Db   182 nSerIleGlyPheLysGlyIleLeuLeuTyrGlyIleGlyThrLysAlaGlnLysGluLysTyrLe 202

Qy   564 GCCTAAACTGGCGTCCGGGAGCCACATTGCAGCCTTCTGCCTCACGAGCCAGCCAGTGG    623
         |||||||||:::   :::||||||
Db   202 uProArgValAlaSerGlyGlnAlaLeuAlaAlaPheCysLeuThrGluProSerSerGl    222

Qy   624 GAGCGATGCAGCCTCAATCCGAGCAGCAGCCACACTAAGTAGACAAGAAGCACTACAT     683
         |||||||| |||||||||||:::|||
Db   222 ySerAspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyrTyrTh    242

Qy   684 CCTCAATGGCTCCAAGTCTGGATTACTAATGAGGACTGGCCAATATTTTTACTGTGT     743
         |||||||||||:::||||||
Db   242 rLeuAsnGlySerLysSerTrpIleSerSerAsnGlyGlyLeuAlaAspIlePheThrValPh   262

Qy   744 TGCAAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTAGAAGACAAAATACACAGACATT 800
         ||||||| :::  |||   :::||||
Db   262 eAlaLysThrProIleLysAspAlaAlaThrGlyAlaValLysLysIleThrAlaPh       282

Qy   801 CATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAAATTAGGCAT  860
         |:::||||   ::::||||||
Db   282 eValValGluArgSerPheGlyValThrHisGlyLysLysMetGlyIl               302

Qy   861 TCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACAACCAAGATACCTGTGGAAAAACAT  920
         :||::   |||   :::||||
Db   302 eLysAlaSerAsnThrSerGluValTyrPheAspValLysValLysProAlaGluAsnVa    322

Qy   921 CCTTGAGAGTCGAGATGGGTTAAGGTGCCATGAACATCCTCAACAGCGGCCGGTT        980
         :|||||||||:::|||   ::::||||
Db   322 lLeuGlyValGlyLysGlyPheLysValAlaValAlaAsnIleLeuAsnGlyArgPh       342

Qy   981 CAGCATGGGCAGCGTCGTGGCTGGGCTGGGGCTCAAGAGATTGATTGAAATGACTGCTGAGTA 1040
         | |||||||:::||||
Db   342 eGlyMetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleAlaLysValAlaAspHi    362

Qy  1041 CGCCTCGCACAGGAAACAGTTAACAAGAGGCTCAGTGAATTGATTGAGGAGAA         1100
         ::||   ::::::  |||||||
Db   362 sAlaThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLuY    382

Qy  1101 ATTTGCACTGATGGCTCAGAGAGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGG   1160
         :::||||||||||:::|||
Db   382 sLeuAlaArgMetAlaIleLeuGlnIleTyrValMetGluSerMetAlaTyrMetLeuSerAl  402

Qy  1161 GATGCTGGACCAACCTGGCTTTCCCGACTGCTTCCATGGAGCAGCCATGGTGAAGGTGTT   1220
         ::: ::::: |||||||
Db   402 aAsnMetAspGln---GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePh    421

Qy  1221 CAGCTCCGAGGGCCGCCTGCGCAGTGTGTGAGTGAGGGCCGTCGAGATCCTCGGGGGCTTGGG 1280
         :::||||||||||:::|||
Db   421 eGlySerGluAlaAlaThrTrpLysValThrArgAspGluCysIleGluGlnIleMetGlyMetGl 441

Qy  1281 CTACACAAGGGACTATCCGTACGAGGGCCATACTGCGTGACACCGGCATCCTCCTCATCTT  1340
         ::: |||||||||:::|||  ::
Db   441 yPheMetLysGluProGlyValGlyArgValLeuArgAspIleArgIlePheArgIlePheGlu  461

Qy  1341 CGAGGGGACCAATGAAGATTCTCCGGATGTACATCGCCTGACGGGTCTGCAGCCATGCCGG  1400
         |:::   ::::: |||||:::
Db   461 eGluGlyThrAsnAspIleLeuArgLeuPheLeuValAlaLeuAlaLeuGlnGlyCysMetLysGl 481

Qy  1401 CCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAGTGAGCACAGT   1454
         |:::   ::: |||||
Db   ...
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Db      481 yLysGluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLe 501

Qy     1455 CATGGATACCGGTTGGCGGAGGCTTCGGGACTTCCCTGGCCGAACTGTGGACCTGGGGCT 1514
                 ::::::||||||     ||||||    ::
Db      501 ulleGlyGluAlaSerLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLe 521

Qy     1515 GACAGGCAACCATGGAGTTGTGACCCAGTCTGCGACAGTGCCAACAAGTTTGAGGA 1574
                 |::|||||||:||:::  ||
Db      521 uSer---------GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGl 538

Qy     1575 GAACACCTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGCGTTTGGCCAAGACCAT 1634
                 |||||||     ||:::::   |||
Db      538 nAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuMetLysHisLysLysGlyIl 558

Qy     1635 CATGGAGGAGCAGCTGGTACTGAAGGCGGTGCCAACATCCTCAACCTGTATGGCAT 1694
                 |::  |||||||   :::||||||::||
Db      558 eValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMe 578

Qy     1695 GACGGGCCGTGCTGTCGCGGGGCCAGCCGTCCATCCGCATTGGGCTCCGCAACCACGACCA 1754
                 |||||||||||||||:::  ||
Db      578 tValValLeuSerArgArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHi 598

Qy     1755 CGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCT-------TACTTGCAGAATCT 1805
                 |||||      :::||||:::||||
Db      598 sGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMe 618

Qy     1806 CTTCAGCTCTCTCAGCTGGACAAGTAGTGCTCCAGAAAAACCTAGATGAGCAGATTAAGAA 1865
                 |||||     ::     |||   |||
Db      618 tAlaSerLeuGlnSerAsnProGln-----GlnGlnGluLeuPheArgAsnPheArgSe 636

Qy     1866 AGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTG 1917
                 :::||||||::   :::::||||      |:    |||||
Db      636 rIleSerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu 653
```

```
RESULT 13
ADE56093
ID   ADE56093 standard; protein; 655 AA.
XX
AC   ADE56093;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Rat Protein P45953, SEQ ID NO 1934.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO200301675-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-03121147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P45953.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
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CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 655 AA;
```

```
Alignment Scores:
Pred. No.:              4.35e-117        Length:              655
Score:                  1365.00          Matches:             303
Percent Similarity:     62.77%           Conservative:        110
Best Local Similarity:  46.05%           Mismatches:          202
Query Match:            30.31%           Indels:               43
DB:                     7                Gaps:                 13
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US-09-945-326-1 (1-2452) x ADE56093 (1-655)

Qy      30 GGGAGACTGAGCTGAGGCTGGGG--AACATCGGCAGCATGAGCGGCTGCGGCGGCTCTT 86
            ||||||   ||||||||||||||     :::     ||||||||||||||||:::
Db      11 GlyArgGlnLeuLeuArgLeuGlyAlaArgSerArgSerAlaAlaLeuGlnGlyGln 30

Qy      87 CCTGCGCACCACGGCTGCGCGGCTGCGCGGGTCTGGTGGTTCTACCGCGAACCG 146
            ||| |||||||:|:||:|||     :::   ||:|||||||:::
Db      31 Pro-ArgProThrSerAlaGlnArg---------LeuTyrAlaSerGluAlaThrGl 46

Qy     147 GCGGCTACTGCGC-------------------------ACCAGCCGCCCTGT 173
            ||::||||     :::|||     ||
Db      46 nAlaValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl 66

Qy     174 ACGAGCT--------------TTCGCCAAAGAGCTTTCCTAGGCAAATCAAGAGAAGAAGA 221
            |||||||     ||::|||     ::|||     |||||::::
Db      66 aArgAlaGlaSerLysSerArgValAlaValGlyMetPheLysGlyLeuThrThrAspGl 86

Qy     222 AGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTAATGAA----------------AT 266
            ||||||||     |||||:::||||||||||||     ::
Db      86 nValPheProTyrProSerVal----------------LeuAsnGluGlyGlnThrGlnPheIle 102

Qy     267 CAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGAGTGGACTCCCGAAAAAT 326
            :     :::||||||||     ::|||     |||||     :::
Db     102 uLysGluLeuValGlyProValAlaArgPhePheGluGluAlaAsnAspProAlaLysAs 122

Qy     327 TGACCAGGAAGGAGAAATCCCAGATGAAACTTTGGAGAAATTCAAGAGCCTAGGGCTTT 386
            |||||     ||::||     |||||::||     ||||||     ||||||
Db     122 nAspSerLeuGlyLysValGluAspThrArgLeuGlnGlyLeuLysGlyLeuGlyAlaPh 142

Qy     387 TGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGCTTCCCAACACCATGTACTCAAG 446
            |||||     ||:|||||     |||||||     :::
Db     142 eGlyLeuGlnValProSerGlyLeuGlyLeuGlyLeuSerAsnThrGlnTyrAlaAr 162

Qy     447 ACTAGGGAGGAGATCATCAGCATG--GATGGGTCCATCACTGTGACCCTGCCAGCCACCA 503
            |||||||||||||||     |||     :::::|||||||
```

```
Qy    162  gLeuAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGl  182
                ||||| ||  ||| :: ||||||| || ::||||||||||||||| :|||||
Db    504  GGCTATTGGCTCAAGGGGATCATCTTGGCTGGCCACTGAGGAGCAGAAAGCCAAATACTT  563

Qy    182  nSerIleGlyPheLysGlyIleLeuTyrGlyThrLysAlaGlnLysGlyLysTyrLe    202
                ||||| ||||||| || ||||| ||  ||| ||||| || ||||||||
Db    564  GCCTAAACTGGCTCCGGGGAGCACATTGAGCCTTCTGCCTCAGGGAGCCAGCCAGTGG   623

Qy    202  uProArgValAlaSerGlyValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrPheGluProSerSerGl  222
                |||||| :: ||| ||||||| :: ||||||:::||||| ||  ||||
Db    624  GAGGCGATGCAGCCCAATCCGAGCAGAGCGACCTAAGTGAAGACAAGAAGCACTACAT  683

Qy    222  ySerAspValAlaSerIleArgSerSerAlaValProSerProCysGlyTyrLysTyrTh  242
                ||||| ||||| || ::||||  ||||||| ||||||  |||| :|:||
Db    684  CCTCAATGGCTCCAAGGTCTGATTACTAATGGAGACTGCCAATATTTTACTGTGTT    743

Qy    242  rLeuAsnGlySerLysSerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPh  262
                |||||||||| :||| |||||| ||| ||| ||||||| ||||| ::|||
Db    744  TGCAAAGACTGAGGTCGTTGAT---TCTGATGATCAGTGAAAAGACAAAATCACAGCATT  800

Qy    262  eAlaLysThrProIleLysAspAlaAlaThrGlyAlaValLysGlyGluLysIleThrAlaPh  282
                ||| ||||| || :::|||:|  |||||||||||| ::|||| ||| ::||
Db    801  CATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGAAACCCGAAGATAAAATTAGGCAT  860

Qy    282  eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluGluGlyLysMetGlyIl  302
                |||| |||| :: ::||||  ||||||| :::||  |||| ::|:|||
Db    861  TCGGGGCTCCACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAAACAT  920

Qy    302  eLysAlaSerAsnThrSerGluVa1TyrProAlaAspGlyValLysValGluAlaGluAsnVa  322
                |: |||||||||| ||||  :: ||||  ||||||| ||||| ||  :::
Db    921  CCTTGGAGAGGTCGGAGATGGGTTTAAGGTGCCATGAACATCCTCAACAGCGGCCGGTT  980

Qy    322  lLeuGlyValGlyValGlyMetGlyPheLysGlyPheTyrGlyGluAsnIleLeuAsnGlyArgPh  342
                :::|||||||  ||||| ||||| :: ||||||||||||||||||| |||
Db    981  CAGCATGGGCAGCAGTGCTCGTGCTCGCTCAAGAGATGATGAAATGACTGCTGAGTA  1040

Qy    342  eGlyMetAlaAlaThrLeuAlaGlyThrMetLysMetAlaAlaIleIleAlaLysAlaValAspHi  362
                ||||||||| ::  ||||||| || ||||| |||||||||:|||||::||
Db    1041  GGCCTGCACAAGAAACAGTTAACAGAGGCTCAGTGATGATTGATTCAGGAGAA  1100

Qy    362  sAlaThrAsnArgThrGlnPheGlyAspLysAspIleAsnPheGlyValIleGluGlnGluLuy  382
                || :: :||  || :||||||:: ||||| |||||||||| ||:
Db    1101  ATTTGCACTGATGGCTCAGAAGGCTTACGTCATGAGAGTMATGACCTACCTCACGCAGG  1160

Qy    382  sLeuAlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAl  402
                | :||||||||| :|  ||||| :: :::  ||||||||| ||:
Db    1161  GATGCTGGACCAACCTGGCTTCCCGACTGCTTCCATCGAGGCAGCCATGGTGAAGGTGTT  1220

Qy    402  aAsnMetAspGln--GlyPheLysAspPheGlnIleLeuGlnIleAlaAlaIleSerLysIlePh  421
                ||||| |||| ::||| |||||||||| ::||||||||||||||| ||
Db    1221  CAGCTCCGAGGCCGCCTGGCAGTGTGTGAGGAGGCGCTCGCAGATCCTCGGGGCTTGGG  1280

Qy    421  eGlySerGluAlaAlaTrpLysValThrAspLysAspCysIleGlnIleMetGlyGlyMetGl  441
                ||  :::||| ||||  |||||| ||:||||| ::|||||| :||||::
Db    1281  CTACAGAGGGACTAGCCGTACGAGCGCATACTGCGTGACACCCGCATCCTCCATCTT  1340

Qy    441  yPheMetLysGlyGlnGluArgMetAlaArgValValLeuArgValGlyAspIleProArgIlePh  461
                || :: |:  :||||||| ||| || ||||||||||| ::  |||| |||
Db    1341  CGAGGGAACCAATGAGATTCCCGGATGTACATCGCCCTGACGGGTCTCAGCATGCCGG  1400

Qy    461  eGluGlyThrAsnAspIleLeuArgLeuArgLeuGlyAspGlnHisGlyMetAspLysLysGl  481
                || |:|  |:  ||  ||  ::|| :::||||| |||| |  ||  ||
Db    1401  CCGGATACCGTTGGCCGGAGGCTTCAGAGATCCATGAGCTTAAACAG------GCCAAAAGTGAGCACAGT  1454

Qy    481  yLysGluLeuThrGlyLeuGlnAlaLeuLysAsnAlaLeuGlyAsnValGlyLeuLe  501
                |:::|                     || |||||| ::||| || || ||||
Db    1455  CATGGATACCGGTTGGCCGGAGGCTTCGGGACTCCCGTGGCCCGAACTGTGGACCCTGGGGGCT  1514

Qy    501  uIleGlyGluAlaSerLysGlnLeuArgArgArgThrGlyIleGlySerGlyLeuSerLe  521
                :: ||  ||  ||||||||  :::::|||| ||||||||| ||  ||||||
Db    1515  GACAGGCAACCATGAGTTGTGCACCCCAGTTCTGCGACAGTGCCAACAAGTTTGAGGA  1574

Qy    521  uSer------GlyIleValHisProGluLeuSerArgSerArgGlyGluLeuGluAlaValGl  538
                ||             ||||| ||||| ||||| ||||| ::|||
Db    521  GACAGGCAACCATGAGTTGTG...
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Qy    1575  GAACACCTACTGCTTCCGCCGACCGTGGAGACACTGCTGCGCTTCCAAGAGACCAT  1634
                 :        ||| :::||||:||||||||||||||| ||   ||||||||||||
Db     538  nAlaLeuGluGlnPheAlaThrValGluAlaLysLeuMetLysHisLysGlyIl    558

Qy    1635  CATGGAGGAGCAGCTGTACTGAAGCGGTGGCCAACATCCTCATCAACCTGTATGGCAT  1694
                 :::    |||||| :: ||||||||||:|  ||||||||||||||||||||||||||||
Db     558  eValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMe    578

Qy    1695  GACGGGCCGTGCTGTCGCGGGCAGCCGGCTCCATCCCGCCATTGGGCTCCGCAACCACGACCA  1754
                 ||||:||  ||||| |||||| ||||  ::|||| ||||| |||||  ||||||||||||
Db     578  tValValLeuSerArgAlaSerArgLeuSerGluSerGluGlyTyrProThrAlaGlnHi    598

Qy    1755  CGAGGTTCTCTTGGCCAACACCTTCGGTGGAAGCT------TACTTGCCAGAATCT  1805
                 ||||| :||  ||||| ||||  ||||| :::|||||               :::||||||||
Db     598  sGlyLysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMe    618

Qy    1806  CTTCAGCCTCCTCAGCTGGCACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAA  1865
                 :     |||||||||| ||    |                 |||    :::
Db     618  tAlaSerLeuGlnSerAsnProGln-------GlnGlnGluLeuPheAsnPheArgSe    636

Qy    1866  AGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCTCTG  1917
                 ::::|:::   :::|||||                       :: :::||||||:|||||
Db     636  rIleSerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu   653
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RESULT 14
ABB06992
ID   ABB06992 standard; protein; 655 AA.
XX
AC   ABB06992;
XX
DT   20-JUN-2002  (first entry)
XX
DE   Mouse very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID:10.
XX
KW   Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
KW   insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
KW   antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW   glucose transport; hyperglycaemic disorder.
XX
OS   Mus sp.
XX
PN   WO200216428-A1.
XX
PD   28-FEB-2002.
XX
PF   20-AUG-2001; 2001WO-JP007117.
XX
PR   21-AUG-2000; 2000JP-00254263.
PR   07-SEP-2000; 2000JP-00276633.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Tojo H,  Katayama N,  Kakimoto S;
XX
DR   WPI; 2002-269344/31.
XX
PT   Protein binding to insulin-responsive aminopeptidase and glucose
PT   transporter 4, useful for prevention and treatment of diseases associated
PT   with blood sugar level disturbance.
XX
PS   Disclosure; Page 92-95; 103pp; Japanese.
XX
CC   The present invention describes human MD25 (very long chain acyl-CoA
CC   dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
CC   (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
CC   activity. IRAP and GLUT4 are involved in the intracellular regulation of
CC   glucose metabolism and glucose transport across the cell membrane.
CC   Expression of MD25 (whose ligands are these proteins) is also involved in
CC   this regulatory process. MD25 can be used in the prevention, treatment
CC   and diagnosis of diseases involving disturbances of glucose metabolism,
CC   such as diabetes and other hyperglycaemic disorders. The present sequence
CC   represents mouse VLCAD which is given in the exemplification of the
```

```
CC   present invention
XX
SQ   Sequence 655 AA;

Alignment Scores:
Pred. No.:
Score:                 1.27e-116        Length:              655
Percent Similarity:    1360.00          Matches:             287
Best Local Similarity: 66.05%           Conservative:        106
Query Match:           48.24%           Mismatches:          184
DB:                    30.20%           Indels:              18
                       5                Gaps:                9

US-09-945-326-1 (1-2452) x ABB06992 (1-655)
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Qy    169  CCTGTACGAGCT--------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAG  216
                 |||||          ||||||    :::|||    ||||||:::::
Db     66  ProAlaArgAlaSerLysSerPheAlaValGlyMetPheLysGlnLeuThrIle     85

Qy    217  AAAGAAGTTTTCCCATTTCCAGAAGTT---AGCCAAGATGAACTTAATGAAATCAATCAG  273
                 ::||||||||:::|||  |||        ||:::::::     ||    :::
Db     86  AspGlnValPheProTyrProSerValLeuSerGluGluGlnAlaGlnLnPheLeuLysGlu  105

Qy    274  TTCTTGGGACCCGTGAAAAATTCTTCACTGAAGAGGTGACTCCCGAAAAATTGACCAG   333
                 |||||||||    |||    ||||||||||||:::|||  |||||||||||
Db    106  LeuValGlyProValAlaArgPheGluGlnValAlaArgPheGluLeuValLysGluGlu    125

Qy    334  GAAGGGAAAATCCCAGATGAAAACTTTGGAGAGAAAATTGAAGAGCCTAGGGCTTTTGGGCTG  393
                 ||||:::          ||||||||||:::|||  |||||||  ||||||||||||
Db    126  LeuGluLysValGluAlaAspThrPheLeuGlyLeuLysGlyLeuGlyAlaPheGlyLeu   145

Qy    394  CAAGTCCCAGAAGAATATGTGGCCTGGGCTTCTCCAACACCATGTACTCAAGACTAGGG  453
                 |||||||||||    |||  |||||||||:::|||  |||||||:::|||||||||
Db    146  GlnValProSerGluGluTyrValGlyLeuGlyLeuSerAsnThrGlnThrLysArgLeuAla  165

Qy    454  GAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGCAGCGCACCAGGCTATT   510
                 |||||||  |||||  ||||||    :::|||  ||||||||||:::||
Db    166  GluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyValAlaHisGlnSerIle  185

Qy    511  GGGCCTCAAGGGATCATCTTGGCTGCGCACTGCCTGAGGACGCAGAAAGCCAAATACTTGCCTAAA  570
                 |||  |||||||||||:::|||||||||:::    ||||||:::|||||||:::
Db    186  GlyPheLysGlyGlyIleLeuLeuThrGlyTyrGlyTyrArgGlnLysGluLysTyrLeuProArg  205

Qy    571  CTGTAGGGTCCGGGGAGCACATTGCCAGCCTTCTGCCTCACGGAGCCAGTGGGAGCGAT   630
                 |||:::  ||||||||||||||||:::||||||||||:::|||||||||||
Db    206  ValAlaSerGlyGlnAlaLeuAlaAlaPheCysLeuThrGluProSerGlySerAsp     225

Qy    631  GCAGCCCAATCCGGAGCAGCAGCCACCAGTAGAGAAGAAGAGCCACTACATCTTCAAT   690
                 |||  ||||||||:::|||||||||||||  |||||||||||||:::|||
Db    226  ValAlaSerIleArgSerSerAlaIleProSerProCysGlyLysTyrProThrLeuAsn   245

Qy    691  GGCTCCAAGGTCTGGATTACTAATGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAG  750
                 |||||||||||:::|||  |||||||||:::|||||||:::    ||||||||||||
Db    246  GlySerLysIleTrpIleSerAsnGluAspTrpProLysLeuLeuAlaLysPhePheThrValPheAlaLys  265

Qy    751  ACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGAACAAAATCACAGCCATTCATAGTA  807
                 ||  :::  ||||||  ||  |||  :::|||  |||||||  :::|||||||
Db    266  ThrProIleLysAspAlaAlaThrGlyValThrAlaValLysGlyValIleThrAlaPheValVal  285

Qy    808  GAAAGAGAGACTTTGGTGGAGTCCGAGAGCAAGAAAACCCGAGAGATAAAATTAGGCATTCGGGGC  867
                 |||||  |||||||||||||||||||:::|||||||||:::||  :::|||||||||||||
Db    286  GluArgSerPheGlyValThrGlyValGlyLeuProGluLysLysMetGlyIleLysLeuAla     305

Qy    868  TCCAACACTTGTGAAGTCCATTTGAAAACACCAGTACCTGTGAAAAACATCCTTGGA  927
                 :::  ||||||||  :::|||||    ||:::|||||:::|||||||:::||
Db    306  SerAsnThrSerGluValTyrPheGluAspGlyValLysValProSerGluAsnValLeuGly   325

Qy    928  GAGGTCGGAGATGGGTTAAGGTGCCATGAAGATCCTCAACAGCGCCGGTTCAGCATG  987
                 |||||||:::|||||||:::|||  ||||||:::||||  :::|||||||||||
Db    326  GluValGlyIleGlyAspGlyPheLysValAlaValAlaAsnIleLeuAsnGlyArgPheGlyMet  345

Qy    988  GGCAGCCGTCGTGGCTGGGCTGCCTCCAAGAGATTGATTGAAATGACTGCTGAGTACGCCCTGC  1047
                 :::  |||:::|||||||||  :::|||||||||||||:::|||||||||||:::
Db    346  AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysLeuAlaAlaValAspHisAlaThr  365
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KW   antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW   glucose transport; hyperglycaemic disorder.
XX
OS   Bos taurus.
XX
PN   WO20216428-A1.
XX
PD   28-FEB-2002.
XX
PF   20-AUG-2001; 2001WO-JP007117.
XX
PR   21-AUG-2000; 2000JP-00254263.
PR   07-SEP-2000; 2000JP-00276633.
XX
PA   (TAKE) TAKEDA CHEM IND LTD.
XX
PI   Tojo H, Katayama N, Kakimoto S;
XX
DR   WPI; 2002-269344/31.
XX
PT   Protein binding to insulin-responsive aminopeptidase and glucose
PT   transporter 4, useful for prevention and treatment of diseases associated
PT   with blood sugar level disturbance.
XX
PS   Disclosure; Page 95-97; 103pp; Japanese.
XX
CC   The present invention describes human MD25 (very long chain acyl-CoA
CC   dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
CC   (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
CC   activity. IRAP and GLUT4 are involved in the intracellular regulation of
CC   glucose metabolism and glucose transport across the cell membrane.
CC   Expression of MD25 (whose ligands are these proteins) is also involved in
CC   this regulatory process. MD25 can be used in the prevention, treatment
CC   and diagnosis of diseases involving disturbances of glucose metabolism,
CC   such as diabetes and other hyperglycaemic disorders. The present sequence
CC   represents bovine VLCAD which is given in the exemplification of the
CC   present invention
XX
SQ   Sequence 655 AA;

Alignment Scores:
Pred. No.:   Length: 655
Score: 3.16e-115   Matches: 285
                    1345.00   Conservative: 110
Percent Similarity: 65.51%   Mismatches: 194
Best Local Similarity: 47.26%   Indels: 14
Query Match: 29.86%   Gaps: 9
DB: 5

US-09-945-326-1 (1-2452) x ABB06993 (1-655)

Qy   133 TCTACCGGACCGGCGGCTACTGCGCACCAGCCCGCCTGTACGAGCTTTCGCCCAAAGAG   192
           |||:::: |||| |||| || ||| ||||||| :::|||||
Db   57 SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly   76

Qy   193 CTTTTCCTAGGCAAAATCAACAGAGAAGAAGAAGTTTCCCATTTCCAGAAGTT--AGCCAA   249
           :::||||||||| ||||||:::||| || ::: |||
Db   77 ThrPheLysGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGlu   96

Qy   250 GATGAGACTTAATGAAATCAACAGTTCTTGGGACCCGTGGAAAATTCTTCACTGAAGAG   309
           |||||| :: :: :||||||| ||||:|||||| ||||||||
Db   97 AspGlnThrGlyPheGlnPheLeuLysGluLeuValGlyProValThrArgPheArgGluGluVal 116

Qy   310 GTGGACTCCCAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAAATTG   369
           ||||::: |||| ||| || ::: :: |||||:::
Db   117 AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluGluThrMetGlnLeuGlyLeu 136

Qy   370 AAGAGCCTAGGGCTTTTGGCTGCCAAGAAGAAGAATATGGTGGCCTTCTCC   429
           ||| ||||| ||||||||:::||||| ||| |||||
Db   137 LysGluLeuGlyAlaPheGlyLeuLeuGlnValProAsnGluLeuGlyValGlyLeuCys   156

Qy   430 AACACCATGTACTCAAGACTAGGGGAGATCATCAGCATG--GATGGTCCATCACTGTG   486
           ||| |||||||::: |||||:::::|||| ||| ||: :::
Db   157 AsnThrGlnTyrAlaArgLeuValGluValIleValGlyMetTyrAspLeuLeuValGlyIle 176

Qy   487 ACCCTGGCAGCCACCAGGCTATTGGCCTCCAAGGGGATCATCTTGGCTGCCACTGAGGAG   546
           |||:: ||||||||||||| |||:||| ||||||||||||| :::|||
Db   177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlnSerIleGlyIleLeuLeuPheLysLysGlyThrLysAla 196

Qy   547 CAGAAAGCCAAATACTTGCCTAAACTGCGTCCGGGAGCACATTGCAGCCTTCTGCCCTC   606
           |||||||| ||| ||||||||||| |||:|||||||||||:|||||||||:||||
Db   197 GlnLysGluLysTyrLeuProLysLeuAlaSerGlyAlaHisCysSerLeuLeuProLeu 216

Qy   607 ACGGAGCCAGCCAGTGGGAGCGATGCAGCGTCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA   666
           ||| ||||||||||||||||| |||| |:||| |||||||:||||| ||| :|||:::|||
Db   217 ThrGluProSerGlySerGlySerAspAlaAlaSerIleArgSerArgAlaValProSerPro   236

Qy   667 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAAGGACTGGCC   726
           ||||| |||||| ||| :||||:::||| |||| :|||||||:||| |||||
Db   237 CysGlyLysTyrTyrThrLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAla   256

Qy   727 AATATTTTTACTGTGTTGCAAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAA   783
           :::|||::::::|||||||| |||||| ||| ||| :::
Db   257 AspIlePheThrValPheAlaLysThrGluValThrAspThrAlaThrGlyAlaValLys   276

Qy   784 GACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCC   843
           ||| |||||:::::|||| ||:::||| |||::::|||:::|| |||||:::|||
Db   277 GluLysIleThrAlaPheAlaValGluArgSerPheGlyGlyValThrHisGlyProPro   296

Qy   844 GAAGATAAATTAGGCATTCGGGGCTCAACACTTGTGAAGTCCATTTGAAAACACCAAG   903
           ||| ||| ||||| |||:::::|||| |||||:::|||:::||||| :::
Db   297 GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg   316

Qy   904 ATACCTGTGGAAAACATCCTTGGAGAGTCGGAGATGGCCATGAATCC   963
           :::||| |||| ||||:::|||| |||| |||:::||||||||:::
Db   317 ValProAlaGluAsnValLeuGlyGluValGlyGlyGlyPheLysValAlaMetHisIle   336

Qy   964 CTCAACAGCGGCCGGTTCAGCATGGGCAGCGTCGTGGCTGCTCAAGAGATTGATT   1023
           |||||::: |||:||||:::||| ||| :: |||||| |:::||
Db   337 LeuAsnGlyArgPheGlyMetAlaAlaAlaAlaAlaLeuAlaGlyThrMetLysGlyIleIle   356

Qy   1024 GAAATGAGCTGTGCGTACGCCTGCACAAGAAACAGTTAACAGAGGCTCAGTGAATTT   1083
           |||:: |||:: :||| || :||||||||||| |||:::|||||
Db   357 AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsnPhe   376

Qy   1084 GGATTGATTCAGGAGAAATTGCACTGATGGGCTCAGGAGGCTTACGTCATGGAGAGTATG   1143
           |||||||::::::||||||||:::|| |||| |||| |::: :||||
Db   377 GlyLeuIleGlnGluLysLeuGluAlaLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet 396

Qy   1144 ACCTACCTCACAGCAGCAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCCGAGGCA   1203
           ||||:::: |:: :: :||| ||:||:|| --GlySerThrAspPheGlnIleIleGluAla   415
Db   397 AlaTyrMetValSerAlaAsnMetAspGln-----

Qy   1204 GCCATGGTGAAGGTGTTCAGCTCGAGCCGCCTGGACGTGTCAGTGGTGAGCGGCCTGCAG   1263
           |||:::: |||||||||| ||||||||:::|||||
Db   416 AlaIleSerLysIlePheGlySerGluValAlaLeuAlaTrpLysValThrArgAspGluCysIleGln   435

Qy   1264 ATCCTCGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGGCCATACTGCGTGACACC   1323
           :::||||||||||:::: :: |||||
Db   436 IleMetGlyValPheMetLysGlyMetLysProGlyValGlnGluArgValLeuArgValAspLeuArg   455

Qy   1324 CGCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACG   1383
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Db   456 ArgIlePheArgIlePheAspGluGlyThrAsnAspIleLeuArgMetTyrIleAlaLeuGln   475

Qy   1384 GGTCCGGACTCCCGGCCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG------   1437
           ||| ||||||| :: ||||||||
Db   476 GlyCysMetAspLysGlyLysGluLeuSerGlyLeuArgGlyLeuAsnAlaLeuAsnProPhe   495

Qy   1438 GCCAAGTGAGCAGCAGTCATGATCACCGTTGGCCGAGGCTTCGGAGGTTCCCTGGGACCGA   1497
           :::::|||||||| ||||| ||:::|||:::|||
Db   496 GlyAsnAlaGlyLeuLeuLeuGlyLeuGluAlaGlyLysLysGlnLeuLysLeuArgArgAlaGlyLeu   515

Qy   1498 ACTGTGGACCTGGGGCTGCGACAGGCAACCATGAGTTGTGCACCCCAGTTCTTGCGGACAGT   1557
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Db   516 GlySerGlyLeuSerLeuSer--------GlyIleValHisGluLeuGluLeuSerArgSer   532

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Qy   1738 CTCCGCAACCACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCT------ 1791
                 |||||    :::|||     :::::::::||:::||||||
Db    593 HisProThrAlaGlnHisGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaAla  612

Qy   1792 ---TACTTGCAGAATCTCTTCAGCCTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTA 1848
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Db    613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlu---Leu  630

Qy   1849 GATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC 1908
                    |||        :::|||    :::::::|||:::         :::    :::
Db    631 PheArgAsnPheLysSerIleSerAlaLeuValGluValGlyArgGlyValValThrSer  650

Qy   1909 CACCCTCTG 1917
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Search completed: May 2, 2005, 15:08:55
Job time : 385.879 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     May  2, 2005, 14:33:24 ; Search time 63.9282 Seconds
                                      (without alignments)
                                5726.413 Million cell updates/sec

Title:       US-09-945-326-1
Perfect score: 4504
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           Delop    6.0 , Delext    7.0

Searched:    513545 seqs, 7464064 residues

Total number of hits satisfying chosen parameters:    1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US09945326/runat_02052005_135411_22376/app_query.fasta_1.4686
-Db=Issued Patents AA -QFMT=fastan -SUFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :   Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	824	18.3	164	4	US-09-621-976-5565	Sequence 5565, Ap
2	816	18.1	601	4	US-09-902-540-11184	Sequence 11184, A
3	783	17.4	336	4	US-09-270-767-44314	Sequence 44314, A
4	691.5	15.4	390	4	US-09-252-991A-26058	Sequence 26058, A
5	666	14.8	389	4	US-09-328-352-6380	Sequence 6380, Ap
6	650	14.4	384	4	US-09-648-004-6	Sequence 6, Appli
7	650	14.4	384	4	US-10-272-419-6	Sequence 6, Appli
8	623	13.8	387	4	US-09-328-352-6442	Sequence 6442, Ap
9	618.5	13.7	403	4	US-09-252-991A-27960	Sequence 27960, A
10	608	13.5	382	4	US-09-328-352-4850	Sequence 4850, Ap
11	604	13.4	432	4	US-09-949-016-6098	Sequence 6098, Ap
12	603.5	13.4	419	4	US-09-252-991A-31097	Sequence 31097, A
13	596	13.2	394	4	US-09-328-352-6801	Sequence 6801, Ap
14	595.5	13.2	409	3	US-09-364-230-30	Sequence 30, Appl
15	592	13.1	459	4	US-09-949-016-10443	Sequence 10443, A
16	588.5	13.1	427	3	US-09-364-230-32	Sequence 32, Appl
17	559.5	12.4	383	4	US-09-328-352-7081	Sequence 7081, Ap
18	549.5	12.2	610	4	US-09-949-016-7708	Sequence 7708, Ap
19	546.5	12.1	421	4	US-09-949-016-5872	Sequence 5872, Ap
20	538.5	12.0	331	4	US-09-902-540-15531	Sequence 15531, A
21	514.5	11.4	402	4	US-09-328-352-4281	Sequence 4281, Ap
22	501	11.1	424	4	US-09-252-991A-24653	Sequence 24653, A
23	500	11.1	464	4	US-09-252-991A-33108	Sequence 33108, A
24	499	11.1	399	4	US-09-328-352-4360	Sequence 4360, Ap
25	481	10.7	444	4	US-09-949-016-10163	Sequence 10163, A
26	479	10.6	415	4	US-09-806-536A-13	Sequence 13, Appl
27	472	10.5	282	4	US-09-252-991A-29144	Sequence 29144, A
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39	399	8.9	683	4	US-09-252-991A-26189	Sequence 26189, A
40	399	8.9	826	4	US-09-543-681A-5053	Sequence 5053, Ap
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42	391	8.7	227	4	US-09-270-767-32675	Sequence 32675, A
43	391	8.7	384	4	US-09-543-681A-6433	Sequence 6433, Ap
44	390.5	8.7	998	4	US-09-252-991A-21058	Sequence 21058, A
45	383.5	8.5	440	4	US-09-949-016-8372	Sequence 8372, Ap

ALIGNMENTS

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RESULT 1
US-09-621-976-5565
; Sequence 5565, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Jobert, S.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 5565
;  LENGTH: 164
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SIGNAL
;  LOCATION: -16..-1
US-09-621-976-5565

Alignment Scores:
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Score:                     824.00         Matches:          164
Percent Similarity:        100.00%        Conservative:       0
Best Local Similarity:     100.00%        Mismatches:         0
Query Match:               18.29%         Indels:             0
DB:                        4              Gaps:               0

US-09-945-326-1 (1-2452) x US-09-621-976-5565 (1-164)

Qy       67 ATGAGCGGCTGCGGGTCTTCTTCCTGCGCCACCACGGCGTGGGCTGCCGGGGTCTG 126
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Db        1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgGlyArgGlyLeu 20
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Qy    127 GTGGTCTCTACCGGCGAACCGGCGGCTACTGCGCACCAGCGCCGCTGTACGAGCTTCGCC 186
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Db     61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80

Qy    307 GAGGTGGACTCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAAA 366
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Qy    427 TCCAACACCATGACTACTCAAGACTAGGGGAGATCATCAGCATGCATGGGTCCATCACTGTG 486
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RESULT 2
US-09-902-540-11184

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; Sequence 11184, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT:  Goldman, Barry S.
; APPLICANT:  Hinkle, Gregory J.
; APPLICANT:  Slater, Steven C.
; APPLICANT:  Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-1015849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE:  2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11184
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(601)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-902-540-11184
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Best Local Similarity:	36.09%	Indels:	90
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US-09-945-326-1 (1-2452) x US-09-902-540-11184 (1-601)

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Qy    856 GGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAA 915
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Db    371 SerGluSerPheGlyHisLeuValAspAspAlaValGlnLeuHisGlyGlyValAlaGlyTyr 390

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Db     43 GlyProProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheGlu  62

Qy    895 AACACCAAGATACCTGTGAAAACATCCTTGGAGAGTCGGAGGATGGGTTAAGGTGGCC  954
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Db     63 AspValLysIleProIleGluAsnValLeuGlyLysGluGlyPheGlyLysValAla  82

Qy    955 ATGAACATCCTCAACAGCGGCCGGTTCAACAGGGCAGCGTCGTCGTCGTGCTCAAG 1014
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Qy   1015 AGATTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACACAGAGGCTC 1074
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Db    143 GluSerMetAlaPheThrIleSerGlnAsnMetAsp--AlaGlySerLysAspTyrHis 161

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Db    162 LeuGluAlaIleSerLysLysIleTyrAlaSerGluSerAlaTrpTyrValCysAspGlu 181

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          ||| ||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db    274 ValGlyGluProTyrArgLeuArgThrAlaLysThrAlaHisCysIleAspLeuPheIle 293

Qy   1597 ACCGGTGGAGACACTGCTGCTCCGCTTTGGCCAAGACCATCATGGAAGACGGCAGCTGGTACTG 1656
          |||||||:||||||||||  |||:||||||||||||||||||||||||:||| ||||||
Db    294 SerValGluGluLeuLeuArgTyrAsnLysAsnIleValAlaAsnGluGlnIleLeuLeuLeu 313

Qy   1657 AAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGAGCGGCCGTCGTGCGGGGCC 1716
          |||:::::|||||||||||||:|:||||||||||||||||||||||
Db    314 ThrArgLeuAlaAsnAlaAlaIleAspIlePheTyrAlaMetValThrGlnSerArgSer 333

Qy   1717 AGCCGCTCC 1725
          |||:::
Db    334 SerArgAla 336
```

```
Alignment Scores:
Pred. No.:                            Length:            336
Score:              3.25e-64          Matches:           169
                    783.00            Conservative:       54
Percent Similarity: 65.01%            Mismatches:        104
Best Local Similarity: 49.27%         Indels:             16
Query Match:        17.38%            Gaps:                5
DB:                336
```

```
US-09-945-326-1 (1-2452) x US-09-270-767-44314 (1-336)

Qy    718 GGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGAT---TCTGATGGA 774
          ||:::|||  ||  |||||||||||||:::|||||||||||||  |||
```

```
Db      3 GlyIleAlaGluIleMetThrValPheAlaGlnThrGluGlnValAspProLysThrGly 22
```

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26058
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26058

Alignment Scores:
Pred. No.:   Length: 390
Score: 1.29e-55   Matches: 147
Percent Similarity: 691.50   Conservative: 82
Best Local Similarity: 58.87%   Mismatches: 121
Query Match: 37.79%   Indels: 39
DB: 15.35%   Gaps: 8

US-09-945-326-1 (1-2452) x US-09-252-991A-26058 (1-390)

Qy   265 ATCAAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTG-----GACTCC 318
                 ||:|| ||| ::||| ||| ::
Db   14   LeuAsnLeuLeuLeuAspSerIleArgGlnPheValArgGluSerLeuValProHisGlu 33

Qy   319 CGAAAAATTGACCAGGAGGAGGATCATCAGCATGGATGGTCCATCACTGTGACC------ 378
                       ::|| ||||||||:::
Db   34   GlnGluValAlaGluThrAspArgIleProGluAlaIleIleAlaArgMetArgGluMet 53

Qy   379 GGGCTTTTTGGGCTGCGAAGTCCAGAAGAGATATGGTGGCCTGGCTTCTCCAACACCATG 438
           ||||||||| |||| |||||||||| ||||||||||
Db   54   GlyLeuPheGlyLeuSerIleProGluAlaTyrGlyValGlyLeuGly------------ 68

Qy   439 TACTCAAGACTAGGGGGAGATCATCAGCATGGATGGTCCATCACTGTGACC--------- 489
                    :::|||||| :::::::::
Db   69   -----ValThrMetGluGluGluValSerIleAlaPheGluLeu 81

Qy   490 ----------------------CTGGCAGCGCACCAGGCTATTGGCCTCAAG 519
                                  ||| :|| |||||||||||| :::
Db   82   GlyArgThrSerProAlaPheSerLeuLeuGlyThrAsnGlyIleGlySerGln 101

Qy   520 GGGATCATCTTGGCTGGCCACTGAGGACGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCC 579
           ||||||:::||| ||||||||| |||||| :::
Db   102 GlyIleValIleAspGlyThrGluGlnLysArgArgTyrLeuProArgLeuAlaSer 121

Qy   580 GGGGAGCACATTGCAGCCCTTCGCCTCACGGAGCCAGTGGGAGCGATGCAGCCTCA 639
                   :::|||||| |||| ||||||||||||||
Db   122 GlyGluLeuLeuSerSerPheCysLeuThrGluProAspSerGlySerAspAlaAlaSer 141

Qy   640 ATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAGACCACTACATCCTCAATGGCTCCAAG 699
                  ::|||||| ::: ||||||:::::||
Db   142 LeuLysThrThrAlaVal-----ArgAspGlyGluHisTyrValLeuAsnGlyThrLys 159

Qy   700 GTCTGGATTACTAATGCAATGCTGCCAATATTTTACTGTGTTTGCAAAGACTGAGGTC 759
           ::||||||||||| ||:::| ||| |||||
Db   160 ArgPheThrAsnAlaProGlnAlaGlyIleTyrThrValMetAlaArgThr------ 177

Qy   760 GTTGATTCTGATGGATCAGTAGTGAAAGACAAA-----ATCACAGGATTCATAGTAGAAAGA 813
                 :::||||| ::|||||||| :::||||| ||:::||
Db   178 -------AspProAlaIleArgGlyAlaAlaGlyAlaGlyIleSerAlaPheValValGluArg 194

Qy   814 GACTTTGGTGGAGTCACTAATGGACAAACCCGAGATAAATTAGGCATTCGGGGCTCCAAC 873
           |||:::|||||| ||||||||||||| :::::
Db   195 GlyThrProGlyLeuSerLeuLysGlyLysProAspArgGluAsnGluValAlaValHis 214

Qy   874 ACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGAGAGGTC 933
           ||||||:::|||:::|| :::::|||
Db   215 ThrCysAspValIlePheAspAspCysArgValProAlaSerGlnLeuIleGlyGlyVal 234

Qy   934 ---GGAGATGGGTTAAGTGCCATGAACATCCTCAACAGCGCCGGTTCAGCATGGGC 990
                 :::||||| ||||| :::
Db   235 GluGlyValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgLeuHisIleAla 254

Qy   991 AGCGTCGTGGCTGGCCTGCTCAAGAGATTGAAATGACTGAGTACGCCTGCACA 1050
           :::|| |||||| ||||||||||||||| |||||||||
Db   255 AlaValCysValGlyValAlaGluMetLeuGlnAspAlaLeuArgTyrAlaLeuGlu 274

Qy   1051 AGGAAACAGTTAACAAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTG 1110
           ||||||||||| :::::|||||| |||
Db   275 ArgLysGlnPheGlnProIleAlaGluProGlnLeuLeuLeuGlnAlaMetLeuAlaAsp 294

Qy   1111 ATGGCTCAGAGGCTTACGTCATGGAGAGTATGAGCTACCTCACAGCAGCAGGGATGCTGGAC 1170
                 :::||||||||||| :::
Db   295 SerLysAlaGluAlaTyrAlaAlaAlaArgCysMetValIleAspAlaAlaArgGlnArgAsp 314

Qy   1171 CAACCTGGCTTCCGACTGCTCCATCGAGCGCAGCCATGGTGAAGGTGTTCAGCTCCGAG 1230
           ::: |||||||| :::||:||||||||||||
Db   315 GluGly------ArgAspValGlyThrGluAlaSerCysAlaLysLeuPheAlaSerGlu 332

Qy   1231 GCCGCCTGGCAGTGTGTGAGTGAGGGCGGCTGCAGATCCTCGGGGGCTTCGGGCGGCTACACCAAGG 1290
                             |||||||||||||| :::
Db   333 MetCysLysGlyArgValAlaAlaAspArgAlaValGlnIlePheGlyGlyAlaGlyTyrIleGluGly 352

Qy   1291 GACTATCCGTACGAGCCGCATACTGCTGACACCCGCATCCTCCTCATCTTCGAGGGAACC 1350
           |||||||| |||||||||||| :::||||||:::
Db   353 AspTyrGlyIleGluArgPheTyrArgAspValArgLeuPheArgIleTyrGluGlyThr 372

Qy   1351 AATGAGATTCCCGGATGTACATCGCC 1377
                 :::||:::
Db   373 ThrGlnIleGlnLeuLeuIleAla 381

RESULT 5
US-09-328-352-6380
; Sequence 6380, Application US/0932832
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6380
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6380

Alignment Scores:
Pred. No.:   Length: 389
Score: 3.12e-53   Matches: 150
Percent Similarity: 666.00   Conservative: 79
Best Local Similarity: 58.27%   Mismatches: 148
Query Match: 38.17%   Indels: 16
DB: 14.79%   Gaps: 8

US-09-945-326-1 (1-2452) x US-09-328-352-6380 (1-389)

Qy   238 GAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTC 297
               :::::   ::|||||
Db   5   GlnMetIleArgAspGlu---GlyMetLeuGlnLeuLeuSerThrIleArgAspPhe 23

Qy   298 TTCACTGAAGAGGTGGACTTCCCGA------AAAATTGACCAGGAGGAGAAATCCCAGAT 351
           ||||||||||||| :::::
Db   24   ValLysAsnGluLeuIleProArgGluAsnGluValAlaValGluIleProAsp 43

Qy   352 GAAACTTTGGAGAAATTGAAGAGCCTAGGCGGCTTTTGGGCTGCGAAGTCCCAGAAGAATAT 411

```
; Sequence 6, Application US/0964004
; Patent No. 6498242
; GENERAL INFORMATION:
;   APPLICANT: CHEN, QIONG
;   APPLICANT: THOMAS, STUART
;   APPLICANT: NAGARAJAN, VASANTHA
;   TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
;   TITLE OF INVENTION: INTERMEDIATES
;   FILE REFERENCE: CL-1341-A
;   CURRENT APPLICATION NUMBER: US/09/648,004
;   CURRENT FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 09/252,553
;   PRIOR FILING DATE: 1999-02-19
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Acinetobacter sp.
US-09-648-004-6

Alignment Scores:
Pred. No.:                  9.69e-52        Length:         384
Score:                       650.00         Matches:        154
Percent Similarity:          57.89%         Conservative:    77
Best Local Similarity:       38.60%         Mismatches:     132
Query Match:                 14.43%         Indels:          36
DB:                              4          Gaps:            11

US-09-945-326-1 (1-2452) x US-09-648-004-6  (1-384)
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Qy    247  CAAGATGAACTTAATGAA-------------ATCAATCAGTTCTTGGACCCCTGTGAAAAA  294
                 ||   ||| ::                 ::||||::: ::|||||||
Db      5  GlnAspThrLeuGlnLeuValAspMetIleArgGlnPheValAspGlyVal--Leu   23

Qy    295  TTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAGGAAAATCCCAGATGAA  354
                 ||||||:                ::: :::  ::||||||||::::||||||
Db     24  IleProAsnGluGlyIle------------ValAlaGluThrAspGluIleProAlaGlu   39

Qy    355  ACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCCAAGTCCCAGAGAAATATGGT  414
                 ::::::||||||||:::||||||||||||   :||:::||||||||||||:::||
Db     40  IleValGlnGlnMetLysGluLeuGlyLeuPheGlyLeuThrIleProGluGlyTyrGlu   59

Qy    415  GGGCTCGGGCTTCTCCAACACCATGTACTCAAGACTA-------GGGGAGGATCATCAGC  465
                 |||||||:::||||    |||| :||||||||||           |||||||:||||||
Db     60  GlyLeuGlyLeu------ThrMetGluGluValTyrIleAlaPheGluLeuGlyArg   77

Qy    466  ATGGATGGGTCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATC  525
                 |||||            :::  ::::||||||||:::||||
Db     78  ThrSerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleIleSerSerGlyLeu   97

Qy    526  ATCTTGGCTGGCACTGAGGAGCCAGGAGAAGCCAAATATTTTACTGTGTTTGCAAAG---  585
                 :|||: ||||:::||||||||||||||||||:::||||||||||:::||||||||
Db     98  IleIleAspGlySerGluGlnLysGlnLysTyrPheGluValPheAlaArgLeuAlaSerGlyGlu  117

Qy    586  CACATTGCAGCCTTCTGCCTCACGAGCCAGTGGAGCTGGAGGATGGAGCCTCAATCCGG  645
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118  IleIleGlySerThrGluValPheCysLeuThrGluGlnProAspSerGlySerAspAlaAlaSerLeuLys  137

Qy    646  AGCAGAGCCACACTAAGTGAAGACAAGAGCACTACATCCTCAATGGCTCCAAGGTCTGG  705
                 :::        ::|||           ::||||||||||:::||||||||
Db    138  ThrThrAlaVal-----LysAspGlyAspHisTyrIleLeuLeuAsnGlyThrLysArgTyr  155

Qy    706  ATTACTAATGAGGACTGGCCAATATTTTTTACTGTGTTTGCAAAG-------ACTGAGGTC  759
                 ::::||||||||||||:||||||::: ::||||||||||||||        ||||||
Db    156  IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrGlnValTyrSerThrGlnVal  175

Qy    760  GTTGATTCTGATGGATCAGTGAAAGACAAAATCACGACATTCATAGTAGAAAGAGACTTT  819
                 |||                        :::       ::||||||||||||:::||||
Db    176  LysGlyThrGlyGly-------------IleSerAlaPheIleValAspSerLysThr  190

Qy    820  GGTGGAGTCACTAATGGAAACCCGAAGATAAATTAGGCATTCGGGGTCCAACACTTGT  879
                 ||:::|||      |||||| :::          :::||||||::::||||||:::|||||
```

```
Db      44  AspIleValGlnGlnMetArgGluArgLeuGlyLeuPheGlyLeuThrIleProGluGlyTyr   63

Qy    412  GGTGGCCTGGGCTTCTCCAACACCATGTACTCAAGACTAGGG---GAGATCATCAGCATG  468
                 ||||||||                  :::              :::
Db      64  GlyLeuGlyLeuIleThrMetGluGluValAlaPheGluLeuGlyGlnThr   83

Qy    469  GATGGGTCCATCACTGTGACCCTGGCAGCGCCACCAGGCTATTGGCCTCAAGGGGATCATC  528
                 ||||||||||        :::  ::||||||||||||||||||||||
Db      84  SerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleIleSerSerGlyAlaIleLeu  103

Qy    529  TTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCTAAACTGGGTCCGGGAGCAC  588
                 |||||||||||||||||||        ::: :|||||:||
Db    104  IleAspGlyThrGluGluGluGlnLysGlnLysLysTyrArgAlaSerGlyGlyIle  123

Qy    589  ATTGCAGCCTTCTGCCTCACGGAGCCAGTGGGAGGCAGCGATGCAGCCTCAATCCGGAGC  648
                 |||   ::|||||||||||||||||||||||||||||:::||||:::||||||||||
Db    124  IleGlySerPheCysLeuThrGluProGluSerGlySerAspAlaAlaSerLeuLysThr  143

Qy    649  AGAGCCACACTAAGTGAAGACAAGAGCACTACATCCTCAATGGCTCCAAGGTCTCGATT  708
                 |::          ::|||           ::|||||::||||
Db    144  SerAlaVal-----LysAspGlyTyrValLeuAsnGlyThrLysArgPheIle  161

Qy    709  ACTAATGGAGACTGCCAATATTTTTACTGTGTTTGCAAAGACT-----GAGGTCGTT  762
                 |||||||:::||||||      ::: ::::||||||||||||         ::::
Db    162  ThrAsnAlaProHisAlaAlaThrPheThrValMetAlaArgThrArgAsnProGluIleLys  181

Qy    763  GATTCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGT  822
                 ||||               :::||||||:::
Db    182  GlySerGlyGly------------IleSerAlaPheLeuValAlaIleAlaAsnThrPro  196

Qy    823  GGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCCGGGGTCCAACACTTGTGAA  882
                 ||:::|||      ||||| :::          ::||||||||||||||||||||:::|||
Db    197  GlyIleThrLeuGlyLysIleAspGlnLysMetGlyGlnLysGlySerHisThrCysAspAsp  216

Qy    883  GTCCATTTGAAAACACCAAGATACCTGTGAAAACATCCTTGAGAGGTC--GGAGAT  939
                 |||||||||||||||||||::::||||:||||||||||||||||||    |||||
Db    217  ValIlePheGluAsnCysArgValAlaSerValLeuIleGlyGlyValGlyGluGlyVal  236

Qy    940  GGGTTAAGGTGGCCATGAACAGCATCCGCCGGTTCAGCATGGGCAGCGTCGTG  999
                 ||||||:::||||||||||||||||||||||:::||:||||||||||||||||
Db    237  GlyPheLysThrAlaMetLysGlyValArgGlyLeuHisIleGlyAlaTyrSer  256

Qy   1000  GCTGGGCTGCTCAAGAGATTGATTGAAATGACTGCTGCTCGAGTACGCCACAAGGAAACAG 1059
                 |||||||||||||||||||||||||||||||||||    ::|:|||||||||||||
Db    257  ValGlyValAlaGluArgMetLeuAsnAspAlaAlaLeuAsnTyrAlaIleGluGlyLysGln  276

Qy   1060  TTTAACAAGAGGCTCAGTGAGTTGAATTGCAGGAGAAATTGCACTGATGGTCAG 1119
                 |||       ::::::||||||||||||||||||||||||||||:||||||||
Db    277  PheGlyGlnProIleAlaAsnPheGlnLeuIleLeuGlyAsnAlaMetLeuAlaMetLeuAlaAsnSerLysAla  296

Qy   1120  AAGGCTTACGTCATGGAGGAGTATGACCTACCTCCACAGCAGGGATGCTGGACCAACCTGGC 1179
                 :::||||| ||||:: ||||||||||||||||||||:|||:::||||||||||||||
Db    297  GlyIleTyrArgAlaAlaLysCysValMetValLeuAspProAlaAlaArgArgAspArgAspArgAspGlyAsnGly--  315

Qy   1180  TTTCCCGACTGCTCCATCGAGCTGAAATGTCGTGAAGGTGTTCAGCTCCGAGCAGCCGCCTGG 1239
                 |||   :::||||:: ||||||||||||||||||||||||||||||||||||||||||||||
Db    316  --GluAsnIleSerThrGlyValAlaSerCysAlaSerMetThrGluMetCysGlyGly  334

Qy   1240  CAGTGTGTGAGTGAGGCGCTGCAGATCCTGGGGCTGGACCACAAGGGGACTATCCG 1299
                 :::     ::||||||||||||||||||||||||:::||||||||:::||||||||||
Db    335  ArgValAlaAlaAspArgCysArgValGlnIleHisGluHisTyrIleSerGlyGluTyrArgAla  354

Qy   1300  TACGAGCGCCATACTGCGTGACACTGCGTGCTACCTTCGAGGGAACCAATGAGAGATT 1359
                 |||:::||||||||||||||||||||||||::::|||||||||||||:::|||||||||
Db    355  IleGluArgPheTyrArgAspValArgLeuPheArgLeuTyrGluGlyThrGlnVal  374

Qy   1360  CTCCGGATGTACATCGCCCTGTACGGGTCTCGCAGCATGCC 1398
                 :::|||||||||||||||||||||||||||||
Db    375  GlnGlnLeuLeuIleIleAlaLysAsnMetIleArgGluAla  387

Qy   1820  GGTGGAGTCACTAATGGAAACCCGAAGATAAATTAGGCATTCGGGGTCCAACACTTGT  879

RESULT 6
US-09-648-004-6
```

```
Db    5  GlnAspThrLeuAsnGlnLeuValAspLysArgArgGlnPheValAspGlyVal---Leu  23

Qy  295  TTCTTCACTGAGAGGTGGACTCCCGAAAATTGACCAGGAGGAAATCCCAGATGAA  354
          |||||||  :::        |||  |||  |||||  |||
Db   24  IleProAsnGluGluIle------------ValAlaGluThrAspGluIleProAlaGlu  39

Qy  355  ACTTTGGAGAAATTGAAGAGCTAGGGCTTTTGGGTGCAAGTCCAGAAGAATATGGT  414
          :::::::|||  ||||||||||  ||||||  ::::||
Db   40  IleValGlnGlnMetLysGluLeuGlyLeuPheGlyLeuThrIleProGluGluTyrGlu  59

Qy  415  GGCCTGGGCTTCTCAACACCATGCTCAGACTA----------GGGGAGATCATCAGC  465
          |||||||        :::        ||||||
Db   60  GlyLeuGlyLeu------ThrMetGluGluValTyrIleAlaPheGluGluGlyArg  77

Qy  466  ATGGATGGGTCCATCACTGTGACCCTGGCAGCGCCTATTGGCCTCAAGGGGATC  525
          |||||||        :::        ||||||
Db   78  ThrSerProAlaPheArgSerLeuIleGlyThrAsnGlyIleGlySerGlyLeu  97

Qy  526  ATCTTGGCTGCACTGAGGACGAGAAGCCAAATACTGCTAAACTGGCTCCGGGGAG  585
          :::::::|||  ||||||||||  ||||||
Db   98  IleIleAspGlySerGluGlnLysGlnTyrPheLeuProArgLeuAlaSerGlyGlu  117

Qy  586  CACAATTGCAGCCTTCTGCCTCACGGAGCCAGCCGATGGGAGCGATGCAGCCTCAATCCGG  645
          |||||||        :::        ||||||
Db  118  IleIleGlySerPheCysLeuThrGluProAspGlySerAspAlaAlaSerLeuLys  137

Qy  646  AGCAGAGCCACACTAGTGAAGACAAGAAGCACTACATCCTCAAGGTCTGG  705
          ::  |||        :::        ||||||
Db  138  ThrThrAlaVal------LysAspGlyAspHisTyrIleLeuAsnGlyThrLysArgTyr  155

Qy  706  ATTACTAATGAGGACTGGCCAATATTTTACTGTGTTTGCAAAG------ACTGAGGTC  759
          ||||||||        :::        ||||||
Db  156  IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrSerThrIle  175

Qy  760  GTTGATTCTGATGGATCAGTGAAAGACAAAATCACAGATTCATAGTAGAAAAGAGACTTT  819
          ||||||        :::        ||||||
Db  176  IleSerAlaPheIleValAspSerLysLysThr  190

Qy  820  GGTGGAGTCACTAATGCAATGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGT  879
          ||||||        :::        ||||||
Db  191  ProGlyIleSerLeuGlyLysArgAspLysMetGlyGlnLysMetGlyAlaHisThrCys  210

Qy  880  GAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTC---GGA  936
          ::::||||  :::        ||||||
Db  211  AspValIlePheGluAsnThrLysIleProAlaSerArgAlaLeuLeuGlyGlyValGluGlyGly  230

Qy  937  GATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTC  996
          ||||||        :::        ||||||
Db  231  ValGlyPheLysThrAlaMetLysAsnIleLeuAsnSerGlyArgIleHisIleAlaAlaLeu  250

Qy  997  GTGGCTGGGCGTGCTCAAGATGTTGATTGAAATGAAATGACTCGCTGAGTACGCCTGCACAAGGAA  1056
          ||||||        :::        ||||||
Db  251  SerValGlyAlaAlaThrArgMetLeuGluAsnGlnTyrArgLeuAspSerArgLys  270

Qy 1057  CAGTTTAACAAGAGGCTCAGTGAATTGGATTGATTCAG----------GAGAAA  1101
          ||||||        :::        ||||||
Db  271  GlnPheGlyGlnAlaIleAlaAsnPheGlnLeuIleGluGlnGlyMetLeuAlaAspSerLys  290

Qy 1102  TTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGG  1161
          ::  |||        :::        ||||||
Db  291  AlaGluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgLeuAspAlaGly  310

Qy 1162  ATGCTGGACCAACCTGGCTTCCCGACTGCTTCCATCAGAGGCAGCCATGGTGAAGGTGTTC  1221
          :::  |||        :::        ||||||
Db  311  Gln------AsnValSerThrGluAlaSerCysAlaLysMetPhe  323

Qy 1222  AGCTCCGAGGCCGCCTGCAGTGTGAGTGAGGCGCTGCAGAATCCTCGAGGGGCTTGGGC  1281
          ||||||        :::        ||||||
Db  324  AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyValAlaGly  343

Qy 1282  TACACAAGGGACTATCCTACGAGCGCATACTGCGTGACACCCGTGTGGAAAAA  1341
          ||  |||        :::        ||||||
Db  344  TyrIleSerGluTyrArgIleGluArgPheTyrArgAspValArgPheLeuTyr  363
```

RESULT 7
US-10-272-419-6
; Sequence 6, Application US/10272419
; Patent No. 6794165
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-10-272-419-6

Alignment Scores:
Pred. No.:
Score: 9.69e-52
Percent Similarity: 650.00
Best Local Similarity: 57.89%
Query Match: 38.60%
DB: 14.43%
                          4

Length: 384
Matches: 154
Conservative: 77
Mismatches: 132
Indels: 36
Gaps: 11

US-09-945-326-1 (1-2452) x US-10-272-419-6 (1-384)

```
Qy  247  CAAGATGAACTTAATGAA----------ATCAATCAGTTCTTGGGACCCGTGGAAAAA  294
          ||||||        |||  ||||||:::        |||
```

Qy 1342 GAGGGAACCAATGAGATTCTCCGGATGGTACATCGCCCTGCGACGGGTCTGCAGCATGCC 1398
          |||||||||||| :: |||||||||| ||||||
Db 364 GluGlyThrThrGlnIleGlnIleGlnValIleIleAlaArgAsnMetIleArgGluAla 382

RESULT 8
US-09-328-352-6442
; Sequence 6442, Application US/0928352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6442
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6442

Alignment Scores:
Pred. No.:   3.2e-49
Score: 623.00
Percent Similarity: 56.85%
Best Local Similarity: 36.80%
Query Match: 13.83%
DB: 4
                        Length: 387
                        Matches: 145
                        Conservative: 79
                        Mismatches: 130
                        Indels: 40
                        Gaps: 10

US-09-945-326-1 (1-2452) x US-09-328-352-6442 (1-387)

Qy 247 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGGAAAAATTCTTCACTGAA 306
         ||||||| ||||||:::: ::: ||| ||| |||
Db 9 GlnGluThrLeuAsnGlnLeuValAspMetIle--------ArgGlnPheValGlu 24

Qy 307 GAGGTG-------GACTCCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACT 357
         ||||| :::: || : :||:: ||
Db 25 GlyValLeuIleProHisGluAsnGluValAlaGluThrAspGluProProAspIle 44

Qy 358 TTGGGAGAAAATTGAAGAGCTTAGGGGCTTTTTGGGCTGTCAAGTCCCAGAAGAATATGTGGC 417
         :::||||:::::||||||| |||||||||||||||| ::||||||
Db 45 ValGluGlnMetLysAlaLeuGlyLeuPheGlyLeuThrIleProGluGluTyrGluGly 64

Qy 418 CTGGGCTTCTCCAACACCATGTACTCCAAGACTAGGGGAGATCATCAGCATGGATGGGTCC 477
         ::::: :: :||:||||||
Db 65 LeuGly-------------------------------------LeuThrMetGluGluGlu 72

Qy 478 ATCACTGTGACC----------------------------------CTGGCAGCG 498
         :: ||||||
Db 73 ValTyrValAlaPheGluLeuGlyArgThrProAlaPheSerLeuIleGlyThr 92

Qy 499 CACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGCCACTGAGGAGCAGAAAGCCAAA 558
         |||||||||||:::
Db 93 AsnAsnGlyIleGlySerSerGlyLeuIleIleAspGlyThrGluAlaGlnLysSerPhe 112

Qy 559 TACTTGCCTAAACTGGCGGTCCGGGGAGCACATTGCAGCCTTGCCTGCTCACCGAGCCAGCC 618
         :::::||||:::|||: |||| ||||||::||||||||||
Db 113 PheLeuProArgLeuAlaArgGlyLeuValAlaIleSerSerPheCysLeuThrGluProAsp 132

Qy 619 AGTGGGAGCGATGCAGCGCTCAATCCGGAGCAGAGCCCACACTAAGTGAAGACAAGAAGCAC 678
         ::::||||:||||::::||||||:||| :::
Db 133 AlaGlySerAspAlaAlaLeuAsnProGluGlnSerProHisLysSerGluAspLysLysHis 150

Qy 679 TACATCCTCAATGGCTCCCAAGGTCTCGGATTACTAATTGGAGGACTGGCCAATATTTTTACT 738
         ::::||||:|||||||| ||||||
Db 151 TyrIleLeuAsnGlyThrArgPheIleThrAsnAlaProHisAlaGlyValPheThr 170

Qy 739 GTGTTTGCAAAGACTGAGGTCGTTGATTCTGATGATCAGTGAAAGACAAAATCACAGCA 798
         ||| ||||:||:||
Db 171 ValMetAlaArgThrAsn--PheAspIleLysGlyAla------SerGlyIleSerSerAla 187

Qy 799 TTCATATGTAGAAAGAGACTTTCGGTGAGTCACTAATGGAACCCGAGATAAATTAGGC 858
         |||||||::: ||||| ||:::||
Db 188 PheIleValAspSerGlnThrProGlyIleSerLeuGlyLysArgAspLysLysMetGly 207

Qy 859 ATTCGGGGCTCCAACACTTGTGAGTCCATTTGAAAACACCAAGATACCTGTGGAAAAC 918
         ||| ::: |||||||||||||||||||||||
Db 208 GlnLysGlyValHisThrCysAspValIlePheGluAsnCysArgIleProAlaSerAla 227

Qy 919 ATCCTTCGAGAGTC---GGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGGC 975
         :::||||||| ||| ||||||||||||
Db 228 LeuIleGlyIleValGlyValGlyPheLysThrAlaMetLysValLeuAspLysLysGly 247

Qy 976 CGGTTCAGCATGGGCAGCGGTCGTGGCTGGCTCGGCGTCGTGCTCAAGAGATTGATTGAAATGACTGCT 1035
         ||| ::: : ||| ||||||||||||
Db 248 ArgLeuHisIleAlaAlaLeuSerValGlyAlaAlaThrArgMetLeuAspAspSerLeu 267

Qy 1036 GAGTACGCCCTGACAAGGAAACAGTTTAACAAGAGCTCAGTGAATTTGGATTGATTCAG 1095
         ||| ::: ||| |||||||||||||
Db 268 AsnTyrAlaIleGluArgLysAspGlnPheGlyLysGlnProIleAlaGlnPheGlnLeuIleGln 287

Qy 1096 GAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACA 1155
         ::: ||| ::: ||||||
Db 288 AlaMetLeuAlaAspSerLysAlaGluIleTyrAlaALysCysMetVal---LeuAsp 306

Qy 1156 GCAGGGATGGTGGACCAACCTGGCTTCCCGACTGCTCCATGCAGCCATGGTGAAG 1215
         ||| ::: || |||||||||||||||
Db 307 AlaAlaArgLeuArgAspAlaGly--GlnAsnValSerThrGluAlaSerCysAlaLys 325

Qy 1216 GTGTTCAGCTCCGAGGCCGCCTGCCAGTGTGAGTGAGGCGGCTGCAGATCCTCGGGGGC 1275
         ::||||||||| :::
Db 326 MetPheAlaThrGluMetCysGlyArgValAlaAspArgCysValGlnIleHisGlyGly 345

Qy 1276 TTGGGCTACACAAGGGACTATCCGTACGAGCGGCCCATACTGCGTGACACCCGCATCCTCTC 1335
         |||||||||:::||||||| |||||
Db 346 AlaGlyTyrIleSerGlyTyrAlaIleGluArgGlyPheTyrArgAspValArgLeuPheArg 365

Qy 1336 ATCTTCGAGGAACCAATGAGATTCTCCGGATGTACATCGCC 1377
         ::::::||||||||| :::||
Db 366 LeuTyrGluGlyThrGlnIleGlnIleGlnValIleIleIleAla 379

RESULT 9
US-09-252-991A-27960
; Sequence 27960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27960
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27960

Alignment Scores:
Pred. No.:   8.83e-49
Score: 618.50
Percent Similarity: 55.42%
Best Local Similarity: 37.53%
Query Match: 13.73%
DB: 4
                        Length: 403
                        Matches: 149
                        Conservative: 71
                        Mismatches: 148
                        Indels: 29
                        Gaps: 8

US-09-945-326-1 (1-2452) x US-09-252-991A-27960 (1-403)

Qy 220 GAAGTTTTCCCATTTCCAGAGAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTG 279

```
Db           |||           :::::
        15 GluSerMetThrTyrProSerLeuAsnPheAlaLeuGlyThrIleAspMetLeuArg  34

Qy     280 GGACCCGTGGAAAAATTCTTCACTGAGAGGTGGACTCCCGA-----AAAATTGACCAG  333
               |||       |||::          |||   |||||||
Db      35 AspGlnValArgGlyPheValAlaAlaGluLeuGlnProArgAlaAlaGlnIleAspGln  54

Qy     334 GAAGGGAAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGCGTTTTGGGCTG  393
               :::||||||         |||        :::::
Db      55 AspAsnGlnPheProMetAspMetTrpArgLysPheGlyMetGlyLeuLeuGlyIle  74

Qy     394 CAAGTCCCAGAAGAGAATATGTGGCCTGGGCTTCTCCAACACCATGTACTCAAGACTAGGG  453
               ||||||||||          :::    ::
Db      75 ThrValAspGluGluTyrGlyGlyTyrGlySerAlaLeuGlyLeuTyrLeuAlaHisAlaValValMet  94

Qy     454 GAGATCATCAGC---ATGGATGGGTCCATCACTGTGCACCCTGCAGCGCACCAGGCTATT  510
               ||| |||||            :::::
Db      95 GluGluIleSerArgAlaSerValAlaLeuSerValAlaHisSerAsnLeu  114

Qy     511 GGCCTCAAGGGGATCATCTTGGCTGCACTGAGGACGCAGAAAGCCAAATACTTGCCTAAA  570
               ||||||||||||||||
Db     115 CysValAsnGlnIleLysArgAsnGlyAsnGluGluGlnIleLysAlaArgTyrLeuProAla  134

Qy     571 CTGGGCGTCCCGGGAGCACAATTGCAGCCTTCTGCCTCACCGAGCCAGTGGAGGCGGAT  630
               ||||||||||||          :::::|||||
Db     135 LeuValSerGlyGluHisIleGlyHisIleAlaMetSerGluProAsnAlaGlySerAsp  154

Qy     631 GCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAGCACTACATCCTCAAT  690
               :::::: |||||         ||||||
Db     155 ValValSerMetLysArgAlaAlaSerValAlaAspArgValGlyAspArg------PheValLeuAsn  172

Qy     691 GGCTCCAAGGTCTGGATTACTAATGAGGACTGGCCAATATTTTACTGTGTTTGCAAAG  750
               |||         ::: |||    |||:::::||||
Db     173 GlySerLysMetTrpIleThrAsnGluAspTrpProAspAlaHisThrTyrValIleTyrValLys  192

Qy     751 ACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGACAAA-----ATCACAGCA  798
               ||||                          |||||||
Db     193 ThrAspAla---------------------------AspLysGlyAlaHisGlyIleThrAla  204

Qy     799 TTCATAGTAGAAAGACTTTGGTCAGTCCACTAAGTGAAGAGTAAATTAGGC  858
               :::::::: ||||         |||
Db     205 PheIleGluValAspArgTrpLysGlyPheSerArgGlyTyrLysLysLeuGlyLeuGly  224

Qy     859 ATTGGCGGCTTCCAACACTTGTGAAGCTCATTTTGAAAACACCAAGATACCTGTGAAAAC  918
               |||:::|||||||         :::      |||||
Db     225 MetArgGlySerAsnThrGlyIleLeuPheGluGlnIleAspAspValProGluGluAsn  244

Qy     919 ATCCTTGGAGAGGTCGGAGAGTGGTTTAAGGTGGCCATGAACATCCTCACAGCGGCCCG  978
               ::::|| ||||         :::::|||
Db     245 ValLeuGlyAlaValAlaAsnGlyGlyValGlyValLysMetSerGlyLeuAspMetSerGlyLeuAspArg  264

Qy     979 TTCAGCATGGCAGCGTCGTGGCTGCGTGCTCAAGAGATTGATTGAAATGACTGCTGAG  1038
               :::                          :::::::
Db     265 ValValLeuSerGlyValGlyProValGlyIleLeuMetGlnAlaCysMetAspValValValPro  284

Qy    1039 TACGGCTGCACAAGGAAACAGTTTAACAGAGGCTTAACAGTGAAGTTGGATTGATTCAGGAG  1098
               :::|||||||||||          :::  ::|||||||
Db     285 TyrIleHisAspArgArgGlnPheGlnSerIleGluGlyIleLeuGlyPheGlnLeuValGlyIleGlnGly  304

Qy    1099 AAATTT----------GCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATG  1143
               |||
Db     305 LysValAlaAspMetTyrThrAlaLeuAlaAsnAlaSerArgAlaTyrLeu------  320

Qy    1144 ACCTACCTCACAGGGGATGCTGCACCAACCTGCTTTCCCGACTGCTCCATCGAGGCA  1203
               :::::::||||||         :::
Db     321 ---TyrAlaValAlaAlaAlaCysAspArgArgGly-----GluThrThrArgLysAspAla  337

Qy    1204 GCCATGGTGAAGTGTGCGGCCGCCGCCCGCCTGGGTGTGTGAGTGAGGCCGCTGCAG  1263
               |||:::::||||||||         :::::
Db     338 AlaGlyValIleLeuLeuTyrSerArgLeuArgAlaThrGlnMetAlaLeuAspAlaIleGluGln  357

Qy    1264 ATCCTCGGGGGCGTTGGCTACACAAGGGACTATCCGTACGAGGCCCATCGCGTGACACC  1323
               |||||||||||          :::::||||||
Db       ...
```

```
Alignment Scores:
Pred. No.:
Score:                  8.17e-48      Length:        382
Percent Similarity:     608.00        Matches:       142
Best Local Similarity:  56.20%        Conservative:  71
Query Match:            37.47%        Mismatches:    154
DB:                     13.50%        Indels:        12
                                      Gaps:          6

US-09-945-326-1 (1-2452) x US-09-328-352-4850 (1-382)
```

```
Db         358 IleLeuGlyGlyAsnGlyTyrIleAsnGluPheProThrGlyArgLeuLeuArgAspAla  377

Qy        1324 CGGATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGATGTACATC  1374
                   ||| ||                   |||||||
Db         378 LysLeuTyrGluIleGlyAlaGlyThrSerGluIleLeuArgArgMetLeuIle  394

Qy         253 GAACTTAATGAAATCAATCAGTCTTGGGACCCGTGGAAAAATTCTTCACTGAGAG---  309
                   :::              :::|||         :::||
Db           9 GlnPheThrGluGluGlnLeuLeuLeuArgAspMetAlaLysSerPheAlaGlnGluGln  28

Qy         310 ------GTGGACTCCCGAAAAATTGACCAGAAGGAAAATCCCAGATGAAACTTTGGAG  363
                         |||:::            ::::::
Db          29 IleLysProAsnAlaSerAspTrpAspArgArgAspGlyThrPheProLysGluThrLeuThr  48

Qy         364 AAATTGAAGAGCCTAGGCGTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGCCTGGGC  423
                   |||:::            |||           :::
Db          49 GlnMetGlyGlnPheMetGlyMetLeuValSerGluGluTrpGlyGlySerAsp  68

Qy         424 TTCTCCAACACCATGTAC---TCAAGACTAGGGGAGATCATCAGCATGGGTCCATC  480
                   :::                        |||:::
Db          69 ThrGlyAsnLeuAlaTyrValLeuGluGluLeuGluAspAlaAlaAspGlyAlaThr  88

Qy         481 ACTGTGACCCTGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCATCTTGGCTGCACT  540
                   :::         :::||         |||:::
Db          89 SerThrIleMetSerValHisAsnSerValGlyCysValProIleLeuLysPheGlyThr  108

Qy         541 GAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGGCGTCCCGGGAGCACATTCGAGCCTTC  600
                   :::|||||||||         |||:::::|||
Db         109 AspGluGlnLysAspAlaArgPheLeuLysProAlaLeuAlaGlnLeuGlyLysAlaPhe  128

Qy         601 TGCCTCACCGAGCCAGCCAGTGGAGGCGGATGCAGCCTCAATCCGGAGCAGAGCCACACTA  660
                   |||||||         |||:::::        |||||
Db         129 AlaLeuThrGluProHisGlySerAspAlaAlaAlaIleLeuThrArgAlaVal--  147

Qy         661 AGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGA  720
                   ::::::|||         |||||:::::||
Db         148 ---LysAspAspTyrIleLeuAsnGlyAlaLysGlnPheIleThrSerGlyAsn  166

Qy         721 CTGGCCAATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTG  780
                   |||         :::::|||         |||:::
Db         167 AsnAlaGlyValIleIleValPheAlaValThrAsp---------ProSerAlaGly  182

Qy         781 AAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTCAGTCCACTAATGGGAAA  840
                   |||         :::::||         |||:::
Db         183 LysLysGlyIleSerAlaPheLeuValProArgGluThrProGlyTyrGluValIleArg  202
```

```
Qy    841  CCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAACACC  900
                ||||||||:||||||||||        |||:|:||||:||          :::
Db    203  ValGluGluLysLeuGlyLeuHisAlaSerAspThrCysGlnIleAlaLeuThrAspVal  222

Qy    901  AAGTACCTGTGGAAACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAAC  960
                :::||||||||:::   |||||||:::|||  ||||||||::::
Db    223  ArgIleHisLysSerLeuMetLeuGlyLysGlyGluGlyGluLysIleAlaLeuAla  242

Qy    961  ATCCTCAACAGCGGCCGGTTCAGCATGGCAGCGTCGTGGCGTGCTCAAGAGATTG  1020
                ||:::              ||||||||||:||||||||||||||||||
Db    243  AsnLeuGluGlyGlyTyrArgIleGlyTyrIleAlaAlaGlnAlaValGlyLeuAlaArgAlaAla  262

Qy   1021  ATTGAAATAACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAGAGAGGCTCAGTGAA  1080
                ||||||                   |||        :::  ||  |||
Db    263  LeuGluGluAlaThrArgTyrAlaLysGluArgIleThrPheGlyLysProIlePheGlu  282

Qy   1081  TTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGT  1140
                ||          ||  ||||          :::
Db    283  HisGlnThrIleAlaPheArgLeuAlaSerMetAlaThrGluIleLeuGluAlaAlaArgGln  302

Qy   1141  ATGACCTACCTCACAGCAGGGATGCTGACCAACCTGGCTTCCCGACTGCTCCATCGAG  1200
                :::                 ||        :::
Db    303  LeuValHisTyr---AlaAlaArgLeuLysGluAlaGlyAlaGlyGlnPro---CysLeuAsnGln  320

Qy   1201  GCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCGCTCCGAGGCCTGGCAGTGTGAGTGAGGGCCTG  1260
                |||||||||        |||:::|||||||||||||
Db    321  AlaSerMetAlaLysLeuPheSerAlaSerGluMetThrGluArgValCysSerSerAlaLeu  340

Qy   1261  CAGATCCTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCCCATACTGCGTGAC  1320
                ||:::  ||||||  ||||||||||||        |||||
Db    341  GlnValPheGlyGlyTyrGlyTyrArgAspPheProIleGluArgIleTyrArgArgAsp  360

Qy   1321  ACCCGGCCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCC  1377
                                      |:::|||||||||||||
Db    361  AlaArgArgLeuCysGlnIleTyrGluGlyLeuThrSerAspIleLeuThrSerAspIleLeuArgGlnArgLeuValIleAla  379
```

RESULT 11
US-09-949-016-6098
; Sequence 6098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6098
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6098

Alignment Scores:
```
Pred. No.:              432
Score:            2.1e-47         Length:            432
Percent Similarity:  604.00       Matches:           157
Best Local Similarity: 54.46%     Conservative:       81
Query Match:         35.93%       Mismatches:        155
DB:                  13.41%       Indels:             44
                        4         Gaps:               14
```

US-09-945-326-1 (1-2452) x US-09-949-016-6098 (1-432)

```
Qy    121  GGTCTGGTGGTCTCTACCGGCGAACCGGCGGCTACTGCGGCACCAGCCGCCTGTACGGAGCT  180
```

```
Db      3  GlyLeuLeuVal-------------------ArgLeuLeuArgGlySerArgLeuLeuArg---  16
                ||||||| |||                       ||||||||||| |||
Qy    181  TTCGCCAAGAGAGCTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTCCA---TTTCCA  237

Db     17  ------------ArgAsnPheLeuThrCysLeuSerSerTrpLysIleProProHisValSer  33
                           :::::::
Qy    238  GAAGTTAGCCAAGATGAA------CTTAATGAAATCAATCAG---TTCTTGGGACCC  285

Db     34  LysSerSerGlnSerGluAlaLeuLeuAsnIleThrAsnGlyIleHisPheAlaPro  53
                ::: |||||||||||||
Qy    286  GTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAA--------------  324

Db     54  LeuGlnThrPheThrAspGluGluMetIleLeuLysSerValLysLysPheAlaGln  73
                                          ||  |||     :::
Qy    325  ------------------ATTGACCAGGAAGGAGAAAATCCCAGATGAAACT  357

Db     74  GluGlnIleAlaProLeuValSerGluThrMetAspGluAsnSerLysMetGluLysSerVal  93
                                    |||||||:::
Qy    358  TTTGGAGAAATTGAAGAGCTAGGCTTTTTGGGCTGCAAGTCCGAAGAGAATATGGTGGC  417

Db     94  IleGlnIleLeuPheGlnIleGlyLeuMetGlyIleGluValAspProGluTyrGlyGly  113
                ::||||||||||       |||
Qy    418  CTGGGC-------TTCTCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGAT  471

Db    114  ThrGlyAlaSerPheLeuSerPheValLeuVal---IleGluGluAlaLysValAlaAsp  132
                :: ::||||:::
Qy    472  GGGTCCATCACTGTGACCCTGGCAGCGCCACCAGGCTATTGGCCTCAAGGGGATCATCCTG  531

Db    133  AlaSerValAlaValPheCysGlyIleIleGlnIleAsnThrLeuIleLeuAsnThrArgLys  152
                                   :::
Qy    532  GCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCCTCGGGGAGCACATT  591

Db    153  HisGlyThrGluGluGlnLysAlaLysTyrLeuProGlnLeuThrThr---GluLysVal  171
                                          :::||||||||||
Qy    592  GCAGCCTTCGCCTCACGGAGCCAGTCAGGCGGATGCAGCCTCAATCCGAGCAGA  651

Db    172  GlySerPheSerPheCysSerGlnSerGluAlaLaGlyAlaGlySerAspSerPheAlaLeuLysThrArg  191
                ||||||||||:::||||||
Qy    652  GCCACACTAAGTGAAGACAAGAAGCCACTACATCCTCAATGGCTCCAAGGTCTGGATTACT  711

Db    192  AlaAspLysGluGlyAsp------TyrTyrValLeuAsnGlySerLysMetTrpIleSer  209
                ||                ||
Qy    712  AATGGAGGACTGGCCAATATTTTACTGTGTTGCAAGACTGAGGTCGTTGATTCTGAT  771

Db    210  SerAlaGluHisAlaGlyTyrLeuPheLeuValMetAlaAsnVal------------AspAsp  224
                ::: ||||||
Qy    772  GGATCAGTGAAAGACAAA---ATCACAGCATTCATAGTAGAAAGAGAGACTTGGTGGAGTC  828

Db    225  ProThrIleGlyTyrLysGlyIleThrSerPheLeuValAspArgAspThrProGlyLeu  244
                :::||||||||||
Qy    829  ACTAATGGGAAGAGATAAATAGGCATTCGGGGCTCCAACACTTGTGAAGTCCAT  888

Db    245  HisIleGlyLysProGluAsnLysLeuGlyLeuArgAlaSerThrCysProLeuThr  264
                ||||||||||:::||||||
Qy    889  TTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTAAG  948

Db    265  PheGluAsnValLysValProGluLysLeuGlyIleLeuGlyHisGlyTyrLys  284
                ||||||    :::||||||
Qy    949  GTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTCGTGGCGTG  1008

Db    285  TyrAlaIleGlySerLeuAsnGlyArgIleGlyTyrIleAlaAlaGlnMetLeuGlyLeu  304
                ||||||||  ::: ::
Qy   1009  CTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAAG  1068

Db    305  AlaGlnGlyCysPheAspTyrThrIleProTyrIleLysLysAlaArgIleGlnPheGlyLys  324
                ||||||       |||||||||
Qy   1069  AGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTAC  1128

Db    325  ArgLeuPheAspPheGlyGlnLeuGlnHisGlnAlaHisValAlaThrGlnLeuGlu  344
                ||||||   :: |||
Qy   1129  GTCATGGAGAGTATGACCTACCTCACAGCAGGGATGCTGGACCAACCTGGCTTCCCGAC  1188
```

Db   345 AlaAlaArgLeuLeuThrTyrAsnAlaAlaArgLeuLeu--GluAlaGlyLysProPhe 363

Qy   1189 TGCTCCATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCGAGCCGCCTGGCCAGTGTGTG 1248
          ||||||| ||| || :: :: :||||||||||||||
Db   364 IleLys---GluAlaSerMetAlaLysTyrTyrAlaSerGlyIleAlaGlyGlnThrThr 382

Qy   1249 AGTGAGGCGCTCGAGATCCTCGGGGCGTTGGGCTACACAAGGGACTATCCGTACGAGCGC 1308
          ||||: ::::: :||||||||: ::||||||||::||||
Db   383 SerLysCysIleGluTrpMetGlyGlyValGlyTyrThrLysAspTyrProValGluLys 402

Qy   1309 ATACTGGGTGACACCCGCCATCCTCCTCATCTTCGAGGGACCAATGAGATT 1359
          |||| :::   : ::||||||||||::   :::
Db   403 TyrPheArgAspAlaLysIleGlyThrIleTyrGluGluGlyAlaSerAsnIle 419

RESULT 12
US-09-252-991A-31097
; Sequence 31097, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31097
;   LENGTH: 419
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31097

Alignment Scores:
Pred. No.:   419
Score: 2.29e-47   Length: 419
                    603.50   Matches: 136
Percent Similarity: 57.83%   Conservative: 67
Best Local Similarity: 38.75%   Mismatches: 139
Query Match: 13.40%   Indels: 9
DB: Gaps: 6

US-09-945-326-1 (1-2452) x US-09-252-991A-31097 (1-419)

Qy   328 GACCAGGAGGGAAAATCCCAGATGAAACTTTGAGAGAACTTGAGCAGCCTAGGGCTTTTT 387
          ||||:::||| ||| |: :::   :::   ::: ||||||
Db   74 AspArgGluHisArgPheProAlaGluAlaIleArgGluMetAlaAspLeuGlyPheLeu 93

Qy   388 GGGCTGCAAGTCCCAGAAGAATATGGTGGCCGCTGGGCTTCCAACACCATGTACTACTCA-- 444
          ||||:::||| :||||| :::||||||:: :: ||| :::
Db   94 GlyMetLeuValProGluGluThrTrpGlyGlyAlaGlnThrGlyHisLeuAlaTyrAlaMet 113

Qy   445 AGACTAGGGGAGATCATCAGCATGATGGGTCCATCCATGCTGTGACCCTGCAGCGCACCAG 504
          |||| || :: :::::|| :: ::|||||| ::||||
Db   114 AlaLeuGluGluIleAlaAlaGlyAspGlyAlaCysSerThrIleMetSerValHisAsn 133

Qy   505 GCTATTGGCTCAGGGGATCATCTTGGCTGACGAGGAGCAGAAAGCCAAATACTTG 564
          ::::||||| :: |||||:: ::||||||
Db   134 SerValGlyCysMetProIleHisLysPheGlySerAlaGluGlnLysGluArgPheLeu 153

Qy   565 CCTAAACTGGCGTCCGGGGAGCACATTGAGCCTTCGCCTCACGAGCCAGCCAGTGGG 624
          ::: ||||| ||||||: || :::||
Db   154 ArgProLeuAlaGlnGlySerMetLeuGlyTyrAlaPheAlaLeuThrGluProGlnAlaGly 173

Qy   625 AGCCATGCAGCCTCAATCCGAGCCACTAAGTGAAGACAAGAAGACTACACATC 684
          ::||||| |: :|||||: ||:::||| ::||||||
Db   174 SerAspAlaSerPheLeuLysThrArgAla------ArgArgAspGlyAspHisTyrVal 191

Qy   685 CTCAATGGCTCCAAGTCTGGATTACTAATGGAGGACTGGCCAATATTTTTACTGTGTTT 744
          ||||:::|| :||: ::|||| ::||||
Db   192 LeuAsnGlyAlaLysGlnPheIleThrSerGlySerHisAlaGlyMetValIleValPhe 211

Qy   745 GCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGACAAAAATCACAGGATTCATA 804
          ||| ||| ||||||
Db   212 Ala---------ValThrAspProAspAlaGly---LysArgGlyIleSerAlaPheIle 227

Qy   805 GTTGAAAAGAGACTTTGTGTGGAGTCACTAATGGGAACACCCGAAGATAAATAGGCATTCGG 864
          ||| |||::: |||||||||||||
Db   228 ValProThrAspThrProGlyThrGluValArgIleGluValValArgIleGlyGlnHis 247

Qy   865 GGCTCCACACTTGTGAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTT 924
          |||| || ::: ::: ||:: :::: ::: || :::
Db   248 AlaSerAspThrCysGlnLeuAlaPheAsnAspLeuArgIleProAlaThrLeuArgLeu 267

Qy   925 GGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCGGTTCAGC 984
          ||||| :::   :|||| :: :::||||||||
Db   268 GlyGluGluGlyGlyGlyTyrArgIleAlaLeuAlaAsnLeuGluGluGlyArgIleGly 287

Qy   985 ATGGGCAGGTCGCTGCTGGGCTGTCAAGAGATTGATTGAAATGACTGGTGAGTACGCC 1044
          :: :::|||||: |:|| : || :::||||
Db   288 IleAlaAlaGlnAlaValGlyMetAlaAlaArgAlaAlaPheGluAlaAlaArgAspTyrAla 307

Qy   1045 TGCACAAGGAAACAGTTAACAAGAGGCTCAGTGATTTGGATTGATTCAGGAGAAAATT 1104
          ||||||| :: ::: :||||| ||||
Db   308 HisGluGluThrPheGlyLysProIleIleGluHisGlnAlaValAlaPheArgLeu 327

Qy   1105 GCACTGATGGCTCAGAAGGCTTAGTCATGGAGAGTATGACCTACCTCCAGCAGGGATG 1164
          ||:::|||||| :: |||||| :::||||||||||
Db   328 AlaAspMetAlaThrArgIleAlaValAlaArgGlnMetValHis---HisAlaAlaSer 346

Qy   1165 CTGGACCAACCTGGCTTCCCGACTGTCTCCATCGAGCCAGCCATGTGAAGGTGTTCAGC 1224
          ||||| :: :: ::||||||||| |||||
Db   347 LeuArgGluAlaGlyLeuPro---CysLeuThrGluAlaSerMetAlaLysLeuPheAla 365

Qy   1225 TCCGAGCCGCCGCTGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGGGCTTGGGCTAC 1284
          ||| :: :::   :: :::   :::||||||
Db   366 SerGluMetAlaGluGluValCysSerAlaLeuGlnThrLeuGlyGlyTyrGlyTyrTyr 385

Qy   1285 ACAAGGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGCATCCTCCATCTTCGAG 1344
          ::|||||||||||: ||||||:: ||
Db   386 LeuLysAspPheProValGluArgIleTyrArgAspValAlaArgValCysGlnIleTyrGlu 405

Qy   1345 GGAACCAATGAGATTCTCCGGATGTACATCGCC 1377
          ||||||| |||| :||:: ||||||
Db   406 GlyThrSerAspValGlnArgLeuValIleAla 416

RESULT 13
US-09-328-352-6801
; Sequence 6801, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6801
;   LENGTH: 394
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-6801

Alignment Scores:
Pred. No.:   Length: 394
Score: 1.1e-46   Matches: 140
                        596.00   Conservative: 73
Percent Similarity: 57.10%   Mismatches: 138
Best Local Similarity: 37.53%   Indels: 22
Query Match: 13.23%   Gaps: 9
DB: 4

US-09-945-326-1 (1-2452) x US-09-328-352-6801 (1-394)

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Db        373 IleGlyAlaGlyThrSerGluIleArgArgMetLeuIle 385
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RESULT 14
US-09-364-230-30
; Sequence 30, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
;   APPLICANT: Cahoon, Rebecca E.
;   APPLICANT: Hitz, William D.
;   APPLICANT: Kinney, Anthony J.
;   APPLICANT: Rafalski, J. Antoni
;   TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
;   FILE REFERENCE: BB-1178
;   CURRENT APPLICATION NUMBER: US/09/364,230
;   CURRENT FILING DATE: 1999-07-29
;   EARLIER APPLICATION NUMBER: 60/094,990
;   EARLIER FILING DATE: July 31, 1998
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: Microsoft Office 97
;   SEQ ID NO 30
;   LENGTH: 409
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-09-364-230-30

Alignment Scores:
Pred. No.:   409
Score: 1.26e-46   Length: 409
Percent Similarity: 595.50   Matches: 150
Best Local Similarity: 54.87%   Conservative: 64
Query Match: 38.46%   Mismatches: 143
DB: 3   Indels: 33
                                              Gaps: 13

US-09-945-326-1 (1-2452) x US-09-364-230-30 (1-409)

Qy   250 GATGAACTTAATGAAATCAATCAGTTCTTGGACCCGTCGAAAAATTCTTCACTGAAGAG 309
              ||| ::::::::||||:: ||| ||||||
Db   32 AspAspThrGlnGlu------GlnPheLysGluSerValHisLysPheAlaGlnGluThr 49

Qy   310 GTG------GACTCCCAGAAAAATTGACCAGGAAGGGAAAATCCCA---GATGAAACTTG 360
              ::: |||| ::: |||: || ||||
Db   50 IleAlaProHisAlaAlaIleAlaSerAsnHisPheProLysAspValAsnLeu 69

Qy   361 GAGAAATTGAAG---AGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAGAATATGGTGGC 417
              |||||||| ||||||||||||:::|| ||::
Db   70 TrpLysLeuMetGlyAspPheAsnLeuHisGlyLeuThrAlaProGluGluTyrGlyGly 89

Qy   418 CTGGGCTTCTCCAACACCATGTACTCA------AGACTAGGGGAGATCATCAGCATGGAT 471
              :::||| |||||| ||
Db   90 MetGlyLeu--GlyTyrMetTyrHisCysIleAlaMetGluGluIleAsnArgAlaSer 108

Qy   472 GGGTCCATCATGGAAACAGTTAACAAGAGCTCAGTGAATTGATTCAGGAGAAA 531
              |||||::||::::|| ||||| |||| ::::||:::
Db   109 GlySerValGlyLeuSerTyrSerAlaHisSerAsnLeuCysIleAsnValArg 128

Qy   532 GCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCTCGGGGAGCACATT 591
              ||:::: |||| ||:::
Db   129 HisGlySerProAlaGlnLysLeuLysProLysLeuThrGlyHisHisVal 148

Qy   592 GCAGCCTTCTGCCTCACGGAGCCAGTGGAGCCGGATGCGTCCAATCCGGAGCAGA 651
              ::|||| |||| ||
Db   149 GlyAlaAlaLeuAlaMetSerGlyAsnSerGlySerMetLysCysLys 168

Qy   652 GCCACACTAAGTGAAGACAAGAAGCAC------TACATCCTCAATGGCTCCAAGGTCTGG 705
              ||| |||| ||:::
Db   169 Ala----------Ala------GluLysValTyrGlyGlyTyrValIleAsnGlyLysMetTrp 184

Qy   706 ATTACTAATGAAGGACTGGCCAATATTTTACTGTGTTTGCAAAGACTGAGTC---GTT 762
              ||||||| :::
Db   185 CysThrAsnGlyProSerAlaGlnThrLeuGlyValTyrAlaLysThrAspIleThrAla 204

Qy   763 GATTCTGATGGATCAGTGAAAGACAAAAATCATCAGCATTCATAGTAGAAAGAGACTTTGGT 822
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Query Match:    13.14%    Indels:    46
DB:             4          Gaps:     13

US-09-945-326-1 (1-2452) x US-09-949-016-10443 (1-459)

Qy    74 GCTGCGGCGGCTCTTCCTGCGCACCACGGCTGCGGCTGCGGGGTCGGCTGCGGGGTCGTCGGCTGCGGTGCGTCGGGGTCGGCTGCGGTGCGTCT 133
         |||||||||||||||||||||||||||||||:::||:||||||||||||||
Db    74 SerAlaGlySerSerCysMetAlaGluMet--AlaThrAlaThrArgLeuLeuGlyTrpA  47

Qy   134 CTACCGGCAACCGGCCGCTACTGCGCCACCAGCCGCCTGTACGAGCTTCGCCAAAGAGC 193
         ||||||:||||| ||||||
Db    47 rgValAlaSerTrpArgLeu--------ArgProProLeuAlaGlyPheValSerGln-  63

Qy   194 TTTTCCTAGGCAAATCAAGAGAAGAAAGAGTTTCCCATTTCCAGAAGTTAGCCAAGATG 253
         ::: |||     |||
Db    64 ------------ArgAlaHisSerLeuLeuProValAspAspAlaIleAsnGlyL  78

Qy   254 AACTTAATGAAATCAATCAGTTCTTGGCACCCGTGGAAAAATTCTTCACTGAAGAGGTG- 312
         :::||||
Db    78 euSerGluGluGlnArgGlnLeuArgGlnThrMetAlaLysPheLeuGlnLeuHisLeuA  98

Qy   313 ----GACTTCCGCAAAAATTGACCAGGAGGAAGGGAAAATCCCAGAT-----GAAACTTGG 361
         ::::::::::::|||||:::::
Db    98 laProLysAlaGlnGlnIleGluAspArgSerAsnGluPheLysAsnLeuArgGlnPheTrpL 118

Qy   362 AGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGG 421
         |||||||||||:::|||||||||
Db   118 ysGlnLeuGlyAsnLeuGlyValLeuGlyValLeuThrAlaProValGlnLnTyrGlyGlySerG 138

Qy   422 GCTTCTCCAACACCATGACTACTCAAGACTAGGGAGGATCATCAGC---ATGGATGGGTCCA 478
         :::::::::||:::   :|||||
Db   138 lyLeuGlyTyrLeuGluHisGluValMetGluGluIleSerArgAlaSerGlyAlaV 158

Qy   479 TCACTGTGACCCTGCAGCCGCCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCA 538
         :::    :::
Db   158 alGlyLeuSerTyrGlyAlaHisSerAsnLeuCysIleAsnGlnLeuValArgAsnGlyA 178

Qy   539 CTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGACAATTGCAGCCT 598
         |||     ::: :::
Db   178 snGluAlaGlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluTyrIleGlyAlaL 198

Qy   599 TCTGCCTCACGGAGCCCAGCCAGCCGAGGATGCGAGCCGATGCCAATCCGAGCAGCCACAC 658
         :::::::::::|||||   ::|||
Db   198 euAlaMetSerGluProAsnAlaGlySerAspValSerMetLysLeuLysAla----- 216

Qy   659 TAAGTGAAGACAAGAAG-------CACTACATCCTCAAGGTCTCCAAGGTCTGGATTACTA 712
         ::|||||||                  ||||||||:::||:::|||
Db   217 -------GluLysGlyAsnHisTyrIleLysValSerLysValTrpIleThrA 234

Qy   713 ATGGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACTGAGGTGTCGTTCGTTCTGATG 772
         ||||                     :::::::
Db   234 snGlyProAspAlaAspValLeuIleValTyrAlaLysThrAspLeuGluAlaValProA 254

Qy   773 GATCAGTGAAAGACAAAATCCATAGTAGAAGAAAGAGACTTTGGTGAGTCACTA 832
         ||||||||:::|||||||||
Db   254 laSer-----ArgGlyIleTyrLeuThrAlaPheIleValGluLysGlyMetProGlyPheSer 272

Qy   833 ATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTTG 892
         |||       :::|||||||||
Db   272 hrSerLysLeuAspLysMetArgGlySerAsnThrCysAsnLeuLeuIlePheG 292

Qy   893 AAAACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGG 952
         ||:::     |||||||||
Db   292 luAspCysLysHisIleProAlaAlaAlaAsnIleLeuGluAsnLysGlyValTyrValL 312

Qy   953 CCATGAACATCCTCAACACCGCCGGTTCAGCATGGGCAGCCTGCGGCTGCTCA 1012
         ||:::       :::
Db   312 euMetSerGlyLeuAspLeuArgLeuValLeuAlaGlyLeuProLeuGlyLeuMetG 332

Qy  1013 AGAGATTGATTGAAATGAAATGACTGCTGAGTCAAGAAAACAGTTAACAAGAGGC 1072
         |||:::       :::::::
Db   332 lnAlaValLeuAspHisThrIleProTyrLeuHisValArgGluAlaPheGlyLysI 352
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Db   205 GlySerLysGly---------IleThrAlaPheIleGluGluLysGlyMetAla 219
         |||                   ||||||||||||||:::||
Qy   823 GGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAA 882

Db   220 GlyPheSerThrAlaGlnLysLeuAspLysMetArgGlySerAspThrCysGlu 239
         ::: |||     |||:::||||||||||
Qy   883 GTCCATTTTGAAAACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGG 942

Db   240 LeuValPheGluAsnCysPheValProHisGluArgLysLeuGluGlyLyLysGly 259
         |||||||:::||||||||||
Qy   943 TTTAAGGTGGCCATGAACATCCTCAACACCGCCGGTTCAGCATGGGCAGCCTCGGTGCT 1002

Db   260 ValTyrValMetMetSerGlyLeuAsnLeuGluArgPheValLeuAlaAlaGlyProSer 279
         ||||||:::   |||   ::: :::
Qy  1003 GGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTCACGCCTGCACAAGGAAACAGTTT 1062

Db   280 AlaLeuMetGlnAlaCysLeuAspLeuAlaValAlaValLeuTyrValArgGluArgGlnPhe 299
         |||:::       :::::::
Qy  1063 AACAAGAGGCTCAGTGATTGATTCAGGAGAAATTGCACTGATGGCTCAGAAG 1122

Db   300 GlyArgProIleGlyGluPheGlnPheIleArgGlyLysLeuAlaAspMetTyrThrSer 319
         |||||||:::
Qy  1123 GCTTACGTCATGGAGAGTATGACCTACCTCACAGCA---------GGGATGCTG 1167

Db   320 LeuGlnSerSerArgPheValTyrSerValAlaArgAspCysAspAsnGlyLysVal 339
         |||:::       :::
Qy  1168 GACCAACCTGGCTTCCCGACTGCTCCATCGAGCGCAGCCATGGTGTTCAGCTCC 1227

Db   340 AspArg---------LysAspCys---------AlaGlyValIleLeuPheAlaAla 352
         ||:::       :::::::::
Qy  1228 GAGGCCCCTGCCAGTGTGAGGCGGCGTCAGATCCTTGCGGGCTTGGCTACACA 1287

Db   353 GluArgAlaThrGlnValAlaLeuGlnAlaIleLeuGlnCysLeuGlyLeuGlyAsnGlyTyrIle 372
         :::|||||||:::   :::
Qy  1288 AGGGACTATCCGTACGAGCCGCCATACTGCGTCACACCGCATCCTCCTCATCTTCGAGGGA 1347

Db   373 AsnGluTyrProThrAlaArgLeuLeuArgAspAlaLysLeuAspPheGluIleGlyProGly 392
         :::::::       |||
Qy  1348 ACCAATGAGATTCTCCGGATGTACATCGCC 1377

Db   393 ThrSerGluIleArgArgMetIleIleAla 402
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RESULT 15
US-09-949-016-10443
; Sequence 10443, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10443
;   LENGTH: 459
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10443

Alignment Scores:
Pred. No.:
Score: 2.89e-46   Length: 459
                        592.00   Matches: 161
Percent Similarity: 51.61%   Conservative: 79
Best Local Similarity: 34.62%   Mismatches: 179

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Qy   1073  TCAGTGAATTGGATTGATTCAGGAGAAATTGCA----------------CTGATGGCTC  1117
                 ::  |||||||:::||| ||| |||                       ||||||||||
Db    352  leGlyHisPheGlnLeuMetGlnGlyLysMetAlaAspMetTyrThrArgLeuMetAlaC  372

Qy   1118  AGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGGATGCTGGACCAACCTG  1177
                 :::  |||||||      |||      ||| |||          |||:::
Db    372  ysArgGlnTyrVal----------------TyrAsnValAlaLysAlaCysAspGlu----  385

Qy   1178  GCTTTCCCGACTGCTCCATC---GAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCG  1234
                 |||:::    :::  ||| |||   :::::|||:::||| |
Db    386  -----GlyHisCysThrAlaLysAspCysAlaGlyValIleLeuTyrSerAlaGluCysA  404

Qy   1235  CCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGGGCTTGGGCTACCACAAGGGACT  1294
                 ||  |||     :: :::|||      ||||||||||     |||:
Db    404  laThrGlnValAlaLeuAspGlyIleGlnCysPheGlyGlyAsnGlyTyrIleAsnAspP  424

Qy   1295  ATCCGTACGAGCCGCCATACTGCGTGACACCCGCATCCTCCTCATCTTCGAGGGAACCAATG  1354
                 ::||| |||      ||| ||||||||| ::::::  |||||||:::
Db    424  heProMetGlyArgPheLeuArgAspAlaLysTyrGluIleGlyAlaGlyThrSerG  444

Qy   1355  AGATTCTCCGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGCCGCATCCTGACTA  1414
                 ||:::  |||:::    |||
Db    444  luValArgLeuValIle----------------------GlyArgAlaPheAsnA  456

Qy   1415  CCAGGATCCAT  1425
                 |||
Db    456  laAspPheHis  459

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          GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    May 2, 2005, 14:49:52 ; Search time 272.192 Seconds
                              (without alignments)
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Title:          US-09-945-326-1
Perfect score:  4504
Sequence:       1 cgtgtgtgtgtccctgcggc.........actgtaaaaaaaaaaaaa 2452

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          Ygapop  10.0 , Ygapext  0.5
          Fgapop   6.0 , Fgapext  7.0
          Delop    6.0 , Delext   7.0

Searched:       1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters:       2852064

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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   9:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
  10:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
  11:  /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
  12:  /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
  13:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
  14:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
  15:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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  17:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
  18:  /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
  19:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
  20:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	3171	70.4	628	15	US-10-112-944-869	Sequence 869, App
2	3153	70.0	621	9	US-09-945-326-2	Sequence 2, Appli
3	3153	70.0	621	14	US-10-168-274-24	Sequence 24, Appl
4	3153	70.0	621	15	US-10-112-944-420	Sequence 420, App
5	3153	70.0	621	16	US-10-408-765A-1059	Sequence 1059, Ap
6	3153	70.0	621	16	US-10-408-765A-2053	Sequence 2053, Ap
7	1365	30.3	653	15	US-10-362-537-9	Sequence 9, Appli
8	1360	30.2	655	15	US-10-362-537-10	Sequence 10, Appl
9	1345	29.9	655	15	US-10-362-537-11	Sequence 11, Appl
10	1321	29.3	655	15	US-10-362-537-1	Sequence 1, Appli
11	1321	29.3	655	16	US-10-408-765A-534	Sequence 534, App
12	1312	29.1	655	16	US-10-408-765A-320	Sequence 320, App
13	1210.5	26.9	613	15	US-10-369-493-5444	Sequence 5444, Ap
14	954	21.2	188	16	US-10-408-765A-1442	Sequence 1442, Ap
15	954	21.2	188	16	US-10-408-765A-2052	Sequence 2052, Ap
16	844.5	18.8	594	15	US-10-369-493-16704	Sequence 16704, A
17	821	18.2	594	15	US-10-369-493-17429	Sequence 17429, A
18	816	18.1	581	15	US-10-369-493-19424	Sequence 19424, A
19	815.5	18.1	594	15	US-10-369-493-23285	Sequence 23285, A
20	799	17.7	585	15	US-10-369-493-9765	Sequence 9765, Ap
21	795.5	17.7	583	15	US-10-369-493-9771	Sequence 9771, Ap
22	765	17.0	583	15	US-10-369-493-10383	Sequence 10383, A
23	704	15.6	373	15	US-10-369-493-16614	Sequence 16614, A
24	699	15.5	382	15	US-10-369-493-16795	Sequence 16795, A
25	690	15.3	379	15	US-10-369-493-17460	Sequence 17460, A
26	686.5	15.2	377	15	US-10-369-493-9826	Sequence 9826, Ap
27	682	15.1	378	15	US-10-369-493-23196	Sequence 23196, A
28	678	15.1	381	15	US-10-369-493-16918	Sequence 16918, A
29	675.5	15.0	379	15	US-10-369-493-16613	Sequence 16613, A
30	663	14.7	646	14	US-10-156-761-10104	Sequence 10104, A
31	658	14.6	380	15	US-10-369-493-17459	Sequence 17459, A
32	652.5	14.5	379	15	US-10-369-493-23337	Sequence 23337, A
33	652	14.5	387	15	US-10-272-419-577	Sequence 577, App
34	650	14.4	384	14	US-10-272-419-6	Sequence 6, Appli
35	644.5	14.3	370	15	US-10-369-493-14087	Sequence 14087, A
36	641	14.2	375	15	US-10-369-493-8807	Sequence 8807, Ap
37	640	14.2	378	15	US-10-369-493-16449	Sequence 16449, A
38	633	14.1	375	15	US-10-369-493-17779	Sequence 17779, A
39	630.5	14.0	387	15	US-10-369-493-13698	Sequence 13698, A
40	629.5	14.0	381	15	US-10-369-493-546	Sequence 546, App
41	629	14.0	374	15	US-10-369-493-9830	Sequence 9830, Ap
42	626	13.9	373	15	US-10-369-493-11638	Sequence 11638, A
43	626	13.9	377	15	US-10-369-493-14685	Sequence 14685, A
44	625.5	13.9	379	15	US-10-369-493-10412	Sequence 10412, A
45	624	13.9	378	15	US-10-369-493-9086	Sequence 9086, Ap

ALIGNMENTS

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RESULT 1
US-10-112-944-869
; Sequence 869, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Yang, Yonghong
;  APPLICANT: Weng, Gezhi
;  APPLICANT: Zhang, Jie
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Ghosh, Malabika
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Wang, Zhiwei
;  TITLE OF INVENTION: No. US20040048249A1e1 Nucleic Acids and
;  TITLE OF INVENTION:  Secreted Polypeptides
; FILE REFERENCE: 805A
;  CURRENT APPLICATION NUMBER: US/10/112,944
;  CURRENT FILING DATE:  2002-03-28
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PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_FL_genes Version 5.0

SEQ ID NO 869
LENGTH: 628
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(628)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
OTHER INFORMATION: in Example 2
US-10-112-944-869

Alignment Scores:
Pred. No.:
Score: 8.15e-251
Percent Similarity: 3171.00
Best Local Similarity: 99.52%
Query Match: 99.20%
DB: 70.40%

Length: 628
Matches: 623
Conservative: 2
Mismatches: 3
Indels: 0
Gaps: 0

US-09-945-326-1 (1-2452) x US-10-112-944-869 (1-628)

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Qy 106 GCTCGTGCCTGCCGGGGTCTGTGGTCTCTACCGGCGAACCGGCTACTGCGCACCAGC   165
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Db   21 AlaArgAlaCysArgGlyLeuValSerThrAlaAsnArgArgLeuLeuArgThrSer   40

Qy 166 CCGCCTGTACGAGCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAGAGAAAGAAGTT   225
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Db   41 ProProValArgAlaAlaPheAlaLysGluLeuPheLeuGlyLysIleLysArgGluVal   60

Qy 226 TTCCCATTTCCAGAGAGTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCC   285
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Db   61 PheProPheProGluValSerGlnAsnGluLeuAsnGluIleAsnGlnPheLeuGlyPro   80

Qy 286 GTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAAGGGAAAATC   345
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Qy 346 CCAGATGAAAACTTTGGAGAAATTGAAGAGCCTAGGGTCTTTTGGGCTGCAAGTCCCAGAA   405
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Qy 466 ATGGATGGGTCCATCACTGTGACCCTGGCAGCCGACCCTATTGCCTCAAGGGGATC   525
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Qy 526 ATCTTGGCTGCCACTGGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGGCTCCGGGAG   585
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Qy   367  TTGAAGAGCCTAGGGTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGGCTTC  426
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Db   101  LeuLysSerGlyLeuPheGlyLeuGlnValProGluGlyTyrGlyGlyLeuGlyPhe    120

Qy   427  TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGGAGATCATGGTCCATCACTGTG  486
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Db   121  SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy   487  ACCCTGGCAGCGCACCAGCTATTGGCTCAAGGGGATCATCTGGCACTGGAGGAG        546
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Db   141  ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu  160

Qy   547  CAGAAAGCCAAATACTTGCTAAACTGGCTCCGGGAGGACCATTGAGCCTTCTGCCTC      606
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Db   161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyHisIleAlaAlaPheCysLeu    180

Qy   607  ACGGAGCCAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA    666
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Db   181  ThrGluProAlaSerGlySerAspAlaSerIleArgSerArgAlaThrLeuSerGlu    200

Qy   667  GACAAGAGCACTACATCCTCAAGGTCTGATTACTAATGGAGGACTGGCC            726
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Qy   727  AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGAC      786
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Db   221  AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240

Qy   787  AAAATCACAGACATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCAA    846
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Db   241  LysIleThrAspIleHisSerArgLysArgLeuTrpTrpSerHisAsnGlyLysProGlu 260

Qy   847  GATAAATTAGGCATTGGGGCTCCAACACTGTGAAGTCCATTTGAAAACACCAAGATA      906
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Db   261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   907  CCTGTGGAAAACATCCTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTC      966
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Db   281  ProValGluAsnIleLeuGluGlyValValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy   967  AACAGCGGCCGGTTCAGCATGGGCAGCGTCGTTGGCTCGGCTGCTCAAGAGATTGATTCGAA    1026
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Db   301  AsnSerGlyArgPheSerMetGlySerValValAlaGlySerValValGlyLeuIleGlu 320

Qy   1027 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTTGGA    1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321  MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnArgGlySerGluPheGly   340

Qy   1087 TTGATTCAGGAGAAATTTGACTGATGGCTCAGAAGGCTTACGTCATGGAGTATGACC     1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341  LeuIleGlnGluLysPheAspTrpTrpLeuArgArgLeuThrSerMetGluSerMetThr 360

Qy   1147 TACCTCACAGCAGGGATGCTGACCAACCTGGCTTCCCGACTGCTCCATCGAGGGCAGCC    1206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TyrLeuThrAlaGlyMetLeuThrAsnLeuAlaSerArgLeuLeuHisArgGlyGlnAla 380

Qy   1207 ATGGTGAAGGTGTTCAGCTCCGCACCAGCCGCCTGCAGTGTGTGAGGCGCTGCAGATC    1266
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381  MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy   1267 CTCGGGGGCTTGGCTACACAAGGACTATCCTACGAGGCCGCTATCGCGTGCACACCCGC    1326
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Db   401  LeuGlyGlyLeuGlyTyrThrArgAspTyrProValGluArgIleLeuArgAspThrArg 420

Qy   1327 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCCGCCTGACGGGT    1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleArgLeuThrGly 440

Qy   1387 CTGCAGGATGCGCGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG   1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441  LeuGlnHisAlaAlaArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy   1447 AGCACAGTCATCGATACCGTTCGCGGAGGCTTCGGGACTCCCTGGCCGAACTGTGGAC   1506
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RESULT 2
US-09-945-326-2
; Sequence 2, Application US/09945326
; Patent No. US20020127680A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Hunter, John Joseph
; TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MNI-187
; CURRENT APPLICATION NUMBER: US/09/945,326
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,831
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 4.0
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-326-2

Alignment Scores:
  Pred. No.:   Length: 621
  Score: 2.43e-249   Matches: 621
  Percent Similarity: 3153.00   Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00%   Indels: 0
  DB: 70.00%   Gaps: 0
                9

US-09-945-326-1 (1-2452) x US-09-945-326-2 (1-621)
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Db    1  MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaAlaArgAlaCysArgGlyLeu 20
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(sequence alignment continues)

us-09-945-326-1

US-09-945-326-1 (1-2452) x US-10-168-274-24 (1-621)

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Qy     67  ATGAGGGGCTGCGGGCTCTTCCTGCCACCACGCGTCGGCGCTCGTGCTGCCTGCCCGGGTCTG  126
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Db      1  MetSerGlyLeuPheLeuProLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu     20

Qy    127  GTGGTCTCTACCGGCAACCGGCGGCTACTGCGTGGAGACACTGCTGCTCCGCTTTGGC  186
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Qy    187  AAAGAGCTTTCCTAGGCAAATCAAGAAGAAAGAAGTTTCCCATTTCCAGAAGTTAGC  246
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Db     41  LysGluLeuPheLeuGlyLysLysLysLysGlyValPheProPheProGluValSer    60

Qy    247  CAAGATGAACTTAATGAAATCAATCAGTTCTTGGACACCGGTGGAAAAATTCTTCACTGAA  306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GlnAspGluLeuAsnGluIleAsnGlnPheLeuAspThrGlyValGlyLysPhePheThrGlu   80

Qy    307  GAGGTGACTCCGAAAAATGACCAGGAAGGAGAAAATCCCAGATGAAACTTGGAGAAA  366
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Db     81  GluValAspSerArgLysIleAspGlnGluGlyGluIleProAspGluThrLeuGluLys   100

Qy    367  TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAAGACATCATCAGTTGGCCTGGCTTC  426
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Db    101  LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGlyLeuTyrGlyGlyLeuGlyPhe   120

Qy    427  TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTG  486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal   140

Qy    487  ACCCTGCAGCGACCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCAGGAGGAG  546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141  ThrLeuGlnArgLeuLeuGlnAlaIleGlyLeuIleGlyIleIleLeuLeuAlaGlyThrGluGlu   160

Qy    547  CAGAAGGCCAAATACTTGCCTAAACTGGCTCCGGGAGCACATTGCCAGCCTTCTGCCTC  606
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Db    161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu   180

Qy    607  ACGGAGCCAGCCAGTGGAGCGATGCGAGCTCAATCCGGAGCAGAGCCACACTAAGTGAA  666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu   200

Qy    667  GACAAGAAGCACTACATCCTCAATGGCTCTGGATTACTAATGGAGGACTGGCC  726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201  AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla   220

Qy    727  AATATTTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATCAGTGAAAAGAC  786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221  AsnIlePheThrValPheAlaLysThrGluAlaValAlaAspSerArgValLysAsp   240

Qy    787  AAAATCACAGCATTCATAGATAGAAAGAGACTTTGGTGAGTCACTCAATGGGAAACCCGAA  846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrArgAsnGlyLysProGlu   260

Qy    847  GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA  906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle   280

Qy    907  CCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTC  966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281  ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu   300

Qy    967  AACAGCGGCCGGTTCAGCATGGGCAGCGTGCTGCTGGCCTGCTCAAGAGATTGATTGAA  1026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu   320

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321  MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly   340

Qy   1087  TTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACC  1146
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Db    341  LeuIleGlnGluLysLeuHisLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr   360

Db    461  SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp   480

Qy   1507  CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCAGTCTTGCGACACAGTGCCAACAAG  1566
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Db    481  LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuArgHisSerAlaAsnLys   500

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501  PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly   520

Qy   1627  AAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCCAACCTG  1686
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521  LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleGlnProGly  540

Qy   1687  TATGGCATGACGGCCGTGCTGTCGCGGGACCCAGCCCGTCCATCCGCATGGGCTCCGCAAC  1746
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TyrGlyMetThrAlaValLeuSerArgAspProSerArgSerIleArgIleGlyLeuArgAsn  560

Qy   1747  CACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGAAGCTTACTTGCAGAAATCTC  1806
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561  HisAspHisGluValLeuLeuAlaAsnThrPheCysValLysLeuThrCysArgAsnLeu   580

Qy   1807  TTCAGCCTCCTCCAGCTGGACAAGATATGCTTCCAGAAAACCTAGATGAGCAGATTAAGAAA  1866
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581  PheSerLeuLeuGlnLeuAspLysTyrAlaProGluAsnLeuAspGlnIleGluLysLys   600

Qy   1867  GTGTCCCAGCAGATCCTTGAGAGGCCGAGCCTATATCTGTGCCCACCCTCTGGACAGGACA  1926
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ValSerGlnGlnIleLeuGluGluLysLysArgAlaTyrIleCysAlaHisProLeuAspArgThr  620

Qy   1927  TGC  1929
            |||
Db    621  Cys  621
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RESULT 3
US-10-168-274-24
; Sequence 24, Application US/10168274
; Publication No. US2003012406A1
GENERAL INFORMATION:
  APPLICANT: INCYTE GENOMICS, INC.
  APPLICANT: YUE, Henry
  APPLICANT: LAL, Preeti
  APPLICANT: TANG, Y. Tom
  APPLICANT: HILLMAN, Jennifer
  APPLICANT: BAUGHN, Mariah R.
  APPLICANT: AZIMZAI, Yalda
  APPLICANT: LU, Dyung Aina M.
  TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
  FILE REFERENCE: PF-0754 PCT
  CURRENT APPLICATION NUMBER: US/10/168,274
  CURRENT FILING DATE: 2002-08-26
  PRIOR APPLICATION NUMBER: 60/172,367
  PRIOR FILING DATE: 1999-12-16
  NUMBER OF SEQ ID NOS: 54
  SOFTWARE: PERL Program
; SEQ ID NO 24
  LENGTH: 621
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
  OTHER INFORMATION: Incyte ID No. US2003012406A1 5540437CD1
US-10-168-274-24

Alignment Scores:
  Pred. No.:   2.43e-249   Length: 621
  Score: 3153.00   Matches: 621
  Percent Similarity: 100.00%   Conservative: 0
  Best Local Similarity: 100.00%   Mismatches: 0
  Query Match: 70.00%   Indels: 0
  DB: 14   Gaps: 0

Alignment Scores:
Pred. No.:
Score: 2.43e-249   Length: 621
Percent Similarity: 3153.00   Matches: 621
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 70.00%   Indels: 0
                                15   Gaps: 0

US-09-945-326-1 (1-2452) x US-10-112-944-420 (1-621)

Qy   67   ATGAGCGGCTGCGGGGCTCTTCTGCCGCCACCACGGCTGCGGCTGCTGCCGCGGGGTCTG   126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu   20

Qy 127   GTGGTCTTCACCGGAACCGGCGGCTACTGCCGCCACCCGCCCGTGTACGAGCTTTCGCC   186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21   ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla   40

Qy 187   AAAGAGCTTTCCTAGGCAAAATCAAGAAGAAAAGAGAGTTTTCCCATTTCCAGAAGTTAGC   246
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41   LysGluLeuPheLeuGlyLysLysLysGluValPheProPheProGluValSer   60

Qy 247   CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACACCGGTGGAAAAATTCTTCACTGAA   306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluProThrGlyGluGlu   80

Qy 307   GAGGTGACTCCGAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTGGAGAAA   366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81   GluValAspSerArgLysIleLysAspIleLysIleProAspGluThrLeuGluLys   100

Qy 367   TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAAGAAGAATATGTGGCCTGGGGCTTC   426
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101   LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyLeuGlyPhe   120

Qy 427   TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCACTGTG   486
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121   SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal   140

Qy 487   ACCCTGCCAGCGACCAGGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG   546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141   ThrLeuAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGluGlu   160

Qy 547   CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCACATTGGCGGCCTTCTGCCTC   606

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Db    521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1687 TATGGCATGACGGCCGTGCTGTCGCGGGGCCAGCCGCTCCATCCGACCATTGGGCTCCGCAAC 1746

Db    541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1747 CACGACCACCAGAGTTCTTCTTGCCAACACCTTCGTGGAAGCTTACTTGCAGAAATCTC 1806

Db    561 HisAspHisGluValLeuLeuLeuAlaAsnThrThrPheCysValGluAlaTyrLeuGlnLeuAsnLeuAla 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1807 TTCAGCCTCCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCCAGATTAAGAAA 1866

Db    581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAspAsnLeuAspGlnIleLeuLysLys 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1867 GTGTCCCAGACGATCCTTGAGAAGGCAGCCTATATCTGCGCCACCCTCTGACACAGGACA 1926

Db    601 ValSerGlnIleGlnLeuGluLysValGlyArgAlaTyrIleCysAlaAlaHisProLeuAspArgArgThr 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1927 TGC 1929

Db    621 Cys 621
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RESULT 5

Alignment Scores:
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Pred. No.:                                    Length:           621
Score:                    2.43e-249           Matches:          621
Percent Similarity:       3153.00             Conservative:     0
Best Local Similarity:    100.00%             Mismatches:       0
Query Match:              100.00%             Indels:           0
DB:                       70.00%              Gaps:             0
                          16
US-09-945-326-1 (1-2452) x US-10-408-765A-1059 (1-621)
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Qy     67 ATGAGCGGCTGCGGCCTGCCGGGGGCTCTTCCTGCGCCACCACGGCTGCGGCTCGTGCCTGCGCGCGGGTCTG 126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetSerGlyCysGlyLeuProGlyAlaLeuLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyGlyLeu 20

Qy    127 GTGGTCTCTACCGGCGAACCGGCCGGTACTGCGCACCAGCCGCCGCCTGTACGAGCTTTCGCC 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40

Qy    187 AAAGAGCTTTCTCTAGGCACAAATCAAGAAGAGAAGAAGTTTCCATTTCCAGAAGTTAGC 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 LysGluLeuPheLeuGlyGlyLysIleLysGluGluLysLysPheProPheProGluValSer 60

Qy    247 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGACCCGTGAAAAATTCTTCACTGAA 306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
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(Right-hand column continues:)

```
Db    161 GlnLysAlaLysTyrLeuProLeuGlyGluHisIleAlaAlaPheCysLeu 180
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    607 ACGGAGCCAGTGGGAGCGATGGCAGCCTCAATCCGGACGAGCAGACCACTAAGTGAA 666

Db    181 ThrGluProAlaSerGlyArgAspAlaAlaSerIleArgSerArgAlaThrArgAlaSerSerGlu 200
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    667 GACAAGAAGCACTACATCCTCCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC 726

Db    201 AspProLysHisTyrIleLeuLeuAsnGlySerLysSerValTrpIleThrArgAsnGlyGlyLeuAla 220
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    727 AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATTCTGATGATCAGTCAGTGAAAGAC 786

Db    221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysSerAsp 240
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    787 AAAATCACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAA 846

Db    241 LysIleThrAlaPheIleValGluArgAspAspPheGlyIleGlyValThrAsnGlyLysProGluGlu 260
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    847 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA 906

Db    261 AspLysLeuGlyIleLeuArgGlySerAsnThrCysGluValHisIlePheLeuAsnThrLysIle 280
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    907 CCTGTGGAAAACATCCTTGGACGAGTGCGGAGATGGTTTAAGGTGGCCATGAACATCCTC 966

Db    281 ProValGluAsnIleLeuGlyIleGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
          |||||||||||||||||||||||||||||||||||||||||||||
Qy    967 AACAGCGGCCGGTTCAGCATGGGCAGCGTCCTGGCTGGCTGCTCAAGAGATTGATTGAA 1026

Db    301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLeuLysArgLeuIleGlu 320
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1027 ATGACTGCTAGTAGCCTGCACAAGAAACAGTTAAACAAGAGGCTCAGTGAATTTGGA 1086

Db    321 MetThrAlaGluTyrAlaCysThrArgLysGlnLeuAsnLysArgLeuSerGluPheGly 340
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1087 TTGATTCAGGAGAAATTGCACTGATGGCTCCAGAGGCTTACGTCATGAGGAGTATGACC 1146

Db    341 LeuIleGlnGluLysLeuHisAlaLeuMetAlaGlnLnLysAlaTyrAlaValMetGluSerMetThr 360
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1147 TACCTTCACAGCAGGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGCAGCC 1206

Db    361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPhePheProAspCysSerIleGluAlaAla 380
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1207 ATGGTGAAGGTGTTCAGCTCCGAGGCGCGGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC 1266

Db    381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1267 CTCGGGGGCTTGGCTACACAAGGACTATCCGTACGAGGCCATACTGCGTGACACCCGC 1326

Db    401 LeuGlyGlyLeuGlyTyrThrArgGlyTyrProValProTyrGluGluArgIleLeuArgAspThrArg 420
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1327 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCCCGGATGTACATCGCCCTGACCGGGT 1386

Db    421 IleLeuLeuLeuPheGluGlyThrAsnGluIleLeuArgLeuLeuArgMetTyrIleAlaLeuThrGly 440
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1387 CTGCAGCATGCCGGCCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446

Db    441 LeuGlnHisAlaGlyArgIleLeuThrArgIleHisGluLeuLysGlnLnAlaLysVal 460
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1447 AGCACAGTCATGGATACCGTTGGCGGAGCTTCGGAGCTTCGGAGTCGGGAGGAGGACTGTGGAC 1506

Db    461 SerThrValMetAspThrValGlyGlyAlaSerGluLeuGlyTyrArgThrValAspAsp 480
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1507 CTGGGGGCTGACAGGGAACCAACCATATGAGGTGTGTGCACCCCAGTCTTCGCGACAGTGCCAACAAG 1566

Db    481 LeuGlyLeuThrGlyValHisGlyValValAlaHisProSerIleGluAlaAspSerAlaAsnLys 500
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1567 TTTGAGGAGAACACCTTGCTTCCGGCCGACCGTGGTGAGACACTGCTCCGCTTTGGC 1626

Db    501 PheGluGluAsnThrTyrCysPheGlyAlaArgThrValGluThrLeuLeuLeuArgPheGly 520
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   1627 AAGACCATGAGGAGGAACAGCTGTACTGAAGCGCGGAGATGGTTGGCCAACATCCTCAACCCTG 1686
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Qy   307 GAGGTGGACTCCCGAAAAATGACCAGGAGGGAAATCCAGATGAAACTTGAGAAA 366
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 GluValAspSerArgLysMetThrArgArgGluIleGlnMetLysLeuGluLys 100

Qy   367 TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAGATATGTGGGCCTGGGCTTC 426
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuLysSerLeuGlyLeuLeuGlyCysLysSerGlnLysArgTyrValGlyLeuGlyPhe 120

Qy   427 TCCAACACCATGTACTCAAGACTACTAGGGGAGGATCATCAGCATGATGGTTCCATCACTGTG 486
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SerAsnThrMetTyrSerArgLeuLeuGlyGluAspHisGlnHisAspGlySerIleThrVal 140

Qy   487 ACCCTGGCAGCCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCCTGGCACTGAGGAG 546
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrLeuAlaAlaAlaHisGlnAlaIleGlyLeuLysGlyLeuLeuAlaGlyThrGluGlu 160

Qy   547 CAGAAAGCCAAATACTTGCCTAAACTGGCTCCGGGGAGCACATTGCAGCCTTCTGCCTC 606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180

Qy   607 ACGGAGCCAGCAGTGGGAGGCGATGAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA 666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrGluProAlaSerGlySerAspGluAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy   667 GACAAGAAGCACTACATCCTCAAGGTCTGGATTACTAATGAGGAGGACTGGCC 726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 AspLysLysHisTyrIleLeuLysValTrpIleThrAsnGluGluAspTrpGlyLeuAla 220

Qy   727 AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATCGTGATCAGTGAAAGAC 786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePheThrValPheAlaLysThrGluValValAspArgAspGlnSerValLysAsp 240

Qy   787 AAAATACAGCATTCATAGTAGAAAAGAGACTTGGGTGGAGTCACTAATGGAAACCCGAA 846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAlaPheIleValGluLysArgLeuGlyValArgAspPheGlyGlyTyrLeuTyrAsnGluProGlu 260

Qy   847 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCATTTTGAAAAACACCAAGATA 906
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   907 CCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTC 966
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ProValGluLysHisProTrpArgGlyArgArgTrpValLysValAlaMetAsnIleLeu 300

Qy   967 AACAGGGGCCGGTTCAGCATGGGCAGCGTCGTGGCGTCAGATTGATTGAA 1026
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlySerValValAlaSerAspLeuLeuLysLeuArgLeuGlu 320

Qy  1027 ATGACTGCTGAGTACGCCCTGCACAAGGAAACAGTTAACAAGGACTCAGTGAATTGGA 1086
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrAlaGluTyrAlaLeuHisLysGluThrValAsnLysArgLeuSerGluPheGly 340

Qy  1087 TTGATTCAGGAGAAATTGCACTGACTGGCTCAGAGGCTTACGTCATGGAGTATGACC 1146
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysLeuHisTrpLeuAlaGlnArgLeuThrSerMetGluSerMetThr 360

Qy  1147 TACCTCACAGGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCGAGCC 1206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrGlyMetLeuAspLysProGlyPheProAspCysSerIleGluAlaGluAla 380

Qy  1207 ATGGTGAAGGTGTTCAGCTCCGAGGGCCGCCTGGCCAGTGTGTGAGTGAGGGCTGCAGATC 1266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 MetValLysValPheSerSerGluGlyArgLeuAlaSerValSerGluGlnIle 400

Qy  1267 CTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCCGCATACTGCCTGACACCCGC 1326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy  1327 ATCCTCCTCATCTTGCAGGGAACCAATGAGATTCTTCCCGGATGTACATCGCCCTGACGGGT 1386
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGluLeuThrArgAsnGluIleLeuAlaLeuThrGly 440

Qy  1387 CTGCAGCATGCGCGGGCCCATCCGCACCTACCAGGATCCACCAGGATCCTTAAACAGGCCAAAGTG 1446
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy        |||||||||||||||||||||||||||||||||||||||||||||||||||| 1506
Db   441 LeuGlnHisAlaGlyGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy  1447 AGCACAGTCATCGATACCGTTGGCCGGAGGCTTCGGAGACTTCGGAGACTGGCCGAACTGTGAC 1506
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrValGlyArgArgLeuArgArgLeuGlyArgThrValAsp 480

Qy  1507 CTGGGGCTGACAGGCAACCATGGAGTTGCACCCCAGTCTTGCCGACAGTGCCAACAAG 1566
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrGlyAsnHisGlyValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy  1567 TTTGAGGAGAACACCTACTGCTTCGGGCGACCGTGGAGACACTGCTCTCCGTTTGGC 1626
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGlnAsnThrTyrCysPheGlyArgThrValGluThrGluLeuLeuArgPheGly 520

Qy  1627 AAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGTGGCCAACATCCTCATCAACCTG 1686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrIleMetGluGluGlnLeuLeuValLeuLysLysArgValAlaAlaAsnIleLeuIleLeuAsnLeu 540

Qy  1687 TATGGCATGACCGCCGTGCTGTCGCGGGCCAGCCGCTCCATCCGCATTGGCTCCGAAC 1746
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560

Qy  1747 CACGACCACGAGGTTCTTGGCCAACACCTTCTGCGGTGGAAGCTTACTGCGAAATCTC 1806
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 HisAspHisGluValLeuLeuAlaAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy  1807 TTCAGCCTCTCCAGCTGGACAAGTAACCTAGATGAGCAGATTAAGAAA 1866
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLeuAsnLeuAspGluGlnIleLeuLysLys 600

Qy  1867 GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTCCCACCCTCTGACAGGACA 1926
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnGlnIleLeuGluGlyLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy  1927 TGC 1929
             |||
Db   621 Cys 621
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RESULT 6
US-10-408-765A-2053
; Sequence 2053, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2053
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2053

Alignment Scores:
Pred. No.:
Score: 2.43e-249   3153.00   Length: 621
Percent Similarity: 100.00%   Matches: 621
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 70.00%   Mismatches: 0
DB: 16   Indels: 0
                                                         Gaps: 0

US-09-945-326-1 (1-2452) x US-10-408-765A-2053 (1-621)

Left column

```
Qy    67  ATGAGCGGCTGCGGGCTCTTCTGCGCACCACGGCTGCGCGGCTCGTCGTGCCGGGGTCTG  126
          |||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MetSerGlyCysGlyLeuPheLeuCysThrThrArgLeuArgGlySerValValProGlyLeu  20

Qy   127  GTGGTCTCTACCGGCGAACCGGCGGCGGTACTGCCCGTACGCGGGGCCGCCCCGTCCGCC  186
          ||||||||||||||||||||||||||||||||||
Db    21  ValValSerThrAlaAsnArgArgLeuArgThrSerProProValArgGlyAlaPheAla  40

Qy   187  AAAGAGCTTTTCCTAGGCGAAAATCAAGAAGAAGAGTTTCCCATTTCCAGAAGTTAGC  246
          ||||||||||||||||||||||||||||||||||
Db    41  LysGluLeuPheLeuGlyLeuLysLysLysGluValPhePheProPheProGluValSer  60

Qy   247  CAAGATGAACTTAATGAAATCAATCAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAA  306
          ||||||||||||||||||||||||||||||||
Db    61  GlnAspGluLeuAsnGluIleAsnGlnPheLeuAspProValGluLysPhePheThrGlu  80

Qy   307  GAGGCTGGACTCCCGAAAAAATTGACCAGGAAGGGAAAATCCAGATGATGAAACTTGGAGAAA  366
          ||||||||||||||||||||||||||||||||||||
Db    81  GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspAspGluThrLeuGluLys  100

Qy   367  TTGAAGAGCTTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAGATATGGTGGCCTGGCTTC  426
          |||||||||||||||||||||||||||||||||||
Db   101  LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluMetValAlaTrpLeuGlyPhe  120

Qy   427  TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGACATGGTCCATCACTGTG  486
          ||||||||||||||||||||||||||||||||||
Db   121  SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal  140

Qy   487  ACCCTGCAGCGCCACCAGGCTATTGGCCTCAAGGGAGTCATCCTTGGCTCCTGGCACTGAGGAG  546
          |||||||||||||||||||||||||||||||||
Db   141  ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyValIleLeuAlaLeuAlaGlyThrGluGlu  160

Qy   547  CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGCAGCCTTCGCCTC  606
          ||||||||||||||||||||||||||||||||
Db   161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheAlaCysSerLeu  180

Qy   607  ACGGAGCCCAGTGGGAGCGATGGCAGCGAGCCTCAATCCGGAGCAGAGCCACACTAAGGTGAA  666
          |||||||||||||||||||||||||||||||||||
Db   181  ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGluGlu  200

Qy   667  GACAAGAAGCACTACATCCTCAATGCTCTCAAGGTCTGATTACTACAATACTAATGAGGAGGACTGGCC  726
          ||||||||||||||||||||||||||||||||||
Db   201  AspLysLysHisTyrIleLeuAsnGlyValTrpIleThrAsnGlyGlyLeuAla  220

Qy   727  AATATTTTACTGTGTTTGCAAAGAACTGAGGTCGTTCGTTGATTCTGATGGATCAGTGAAAGAC  786
          |||||||||||||||||||||||||||||||||
Db   221  AsnIlePheThrValPheAlaLysAsnThrGluValValAspSerAspGlySerValLysAsp  240

Qy   787  AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAA  846
          ||||||||||||||||||||||||||||||||||
Db   241  LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlyGlu  260

Qy   847  GATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA  906
          |||||||||||||||||||||||||||||||||
Db   261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluLysThrLysIle  280

Qy   907  CCCTGTGGAAAACATCCTCGAGAGAGTCGAGATGGGTTAAGGTGGCCATGAACATCCTC  966
          |||||||||||||||||||||||||||||||
Db   281  ProValGluAsnIleLeuGluGlyValGlyLysGlyPheLysValAlaMetAsnIleLeu  300

Qy   967  AACAGCGGCCGGTTCAGCTTCAGCATGCATGGGCAGCGTCCTGGCTGGCTCAAGAGAGATTGATTGAA  1026
          |||||||||||||||||||||||||||||||||
Db   301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLysLeuLeuArgGluIleGlu  320

Qy  1027  ATGACTGCTGAGTACGCCCTGCACAAGAGAAACAGTTAACAAGAGGCTCAGTGAATTTGA  1086
          |||||||||||||||||||||||||||||||
Db   321  MetThrAlaGluTyrAlaCysThrArgArgLysThrAlaGlnPheAsnLysLysSerGluPheGly  340

Qy  1087  TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTGCAGTATGACC  1146
          |||||||||||||||||||||||||||||||
Db   341  LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr  360
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Right column

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Qy  1147  TACCTCACAGCAGGATGCTGACCAACCTGCTTTCCCGACTGCTCCATGCTGCTCGAGGCAGCC  1206
          ||||||||||||||||||||||||||||||||||
Db   361  TyrLeuThrAlaGlyMetLeuThrAsnLeuLeuPheProAspCysSerMetLeuLeuGluAlaAla  380

Qy  1207  ATGGTGAAGTGTTCAGCTCCCAGGCCGCCCTGGCCAGTGTGTGAGTGAGGCGGCTCGAGATC  1266
          ||||||||||||||||||||||||||||||||||
Db   381  MetValLysValPheSerSerGluAlaAlaTrpProGlnCysValSerValSerGluGluGlnIleIle  400

Qy  1267  CTCGGGGGCTTGGCTACACAAGGACTATCCGTACGAGGCCGCATACTGCGGTGACACCCGC  1326
          ||||||||||||||||||||||||||||||||||
Db   401  LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgArgIleLeuLeuArgAspThrArg  420

Qy  1327  ATCCTCCTCATCTTCGAGGGAACCCATGAAGATGAGATTCCCGGATGTACACTGCCCTGACGGGGT  1386
          |||||||||||||||||||||||||||||||
Db   421  IleLeuLeuIlePheGluGluGlyThrArgAsnGluIleLeuArgMetTyrIleAlaLeuThrGly  440

Qy  1387  CTGCAGCATGCCGGCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG  1446
          ||||||||||||||||||||||||||||||||||
Db   441  LeuGlnHisAlaGlyAlaIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal  460

Qy  1447  AGCACAGTCATGGATACCGTTGGCCAGTCCTCCTGGCCGAGGACTGCCCTCCTGGCCGAACTGTGGAC  1506
          |||||||||||||||||||||||||||||||
Db   461  SerThrValMetAspThrValGlyArgLeuArgArgAspAspSerGlyArgThrValAsp  480

Qy  1507  CTGGGGCTGACAGGCCAACCATGGAGTGTGCACCCCAGTCTTGCGCACAGTGCCAACAAG  1566
          |||||||||||||||||||||||||||||||
Db   481  LeuGlyLeuThrGlyGlnProTrpSerValHisGlyValValValIleProSerLeuAlaAspSerAlaAsnLys  500

Qy  1567  TTTGAGGAGAACACCTACTGCTTCGGCGACCGTGGAGACACTGCTGCTGCCCGCTTGGC  1626
          |||||||||||||||||||||||||||||||
Db   501  PheGluGluAsnThrTyrCysPheGlyAspArgGlyAspThrValGluThrLeuLeuLeuArgPheGly  520

Qy  1627  AAGACCATCATGAGGAGCAGCGTGTCTGTGCGGGCTGGCCAACATCCTCATCAACCTG  1686
          |||||||||||||||||||||||||||||||
Db   521  LysThrIleMetGluGluGlnGlnValSerValArgValAlaAlaAsnIleLeuIleAsnLeu  540

Qy  1687  TATGGCATGACGGGCCGTGCTGTCCGGAGGCAGCCGCCTCCATCCGCCATTGGGCTTCCGCAAC  1746
          |||||||||||||||||||||||||||||||
Db   541  TyrGlyMetThrAlaValLeuSerArgArgGlnSerArgIleArgSerIleArgIleGluGlyIleGlyLeuArgAsn  560

Qy  1747  CACGACCACGAGGTTCTTGGCCAACACCTTCTGCCTGGAAGCTTACTTGCAGAATCTC  1806
          |||||||||||||||||||||||||||||||
Db   561  HisAspHisGluValLeuGluLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu  580

Qy  1807  TTCAGCCCTCTCAGCTGACAACAAGTCCTCCAGAAAAACCTAGATGAGCAGATTAAGAAA  1866
          |||||||||||||||||||||||||||||||
Db   581  PheSerLeuSerGlnLeuAspLysLysValTyrArgLeuProGlnAsnLeuAspGlnIleLysLys  600

Qy  1867  GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCACCCTTGCACAGGACA  1926
          |||||||||||||||||||||||||||||||
Db   601  ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgArgThr  620

Qy  1927  TGC  1929
          |||
Db   621  Cys  621
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```
; TYPE: PRT
; ORGANISM: Rat
US-10-362-537-9

Alignment Scores:
Pred. No.:
Score:                    1.16e-102
                          1365.00
Percent Similarity:       62.77%
Best Local Similarity:    46.05%
Query Match:              30.31%
DB:                       15

US-09-945-326-1 (1-2452)  x  US-10-362-537-9 (1-653)
```

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Qy    30  GGGAGACTGAGGCTGGGG---AACATCGGCAGCATGAGCGGCTCGGGCTCTT   86
          ||||| ||||||||| | ||        :: ||||| ||||||| ||||:::
Db    11  GlyArgGlnLeuLeuArgLeuGlyAlaArgSerSerArgSerAlaLeuGlnGlyGln   30

Qy    87  CCTCGGCCACCACGGCTCGTCGCCGGGTCTGTGGTCCTACCGGCGAACCG  146
          |||||||||||:::||:||        ||| ||||||| ||||:
Db    31  Pro-ArgProThrSerAlaGlnArg---------LeuTyrAlaSerGluAlaThrGl   46

Qy   147  GCGGCTACTCGC------------------ACCAGCCCGCCTGT  173
          : ||||                          ||| ||||||
Db    46  nAlaValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl   66

Qy   174  ACGAGCT----------TTCGCCAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGA  221
          ||||||          |||||      ||| ||||||||:::
Db    66  aArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGl   86

Qy   222  AGTTTTCCATTTCCAGAAGTTAGCCAAGATGAACTAATGA------------------AT  266
          :||||||||:::||       ||| ||||||||||            :
Db    86  nValPheProTyrProSerVal---------LeuAsnGluGlyGlnThrGlnPheLe  102

Qy   267  CAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAAT  326
          ||||||||||        :||| ||||||||||||||||||||||:
Db   102  uLysGluLeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaLysAs  122

Qy   327  TGACCAGGAAGGGAAAATCCAGATGAAATTGAAGAGCCTAGGGCTTTT  386
          ||       ||| :::||:|||||||      ||||| ||||||:
Db   122  nAspSerLeuGluLysValGluGluLysAspThrLeuGlnLeuLysGlyLeuGlyAlaPh  142

Qy   387  TGGGCTGCAAGTCCCAGAAGAAATATGGTGCCTGGCCTTCTCCAACACCATGTACTTCAAG  446
          |||||||||||||:::|| ||||||| ||||||||:
Db   142  eGlyLeuGlnValProSerGluLysGluGlyLeuGlyLeuSerAsnThrGlnTyrAlaAr  162

Qy   447  ACTAGGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGCCAGCCACCA  503
          ||||||||      | ||||        ::|||| ||||| ||||||
Db   162  gLeuAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuProLeuProAl  182

Qy   504  GGCTATTGGCTCAAGGGTCCAAGGGGATCATCTTGGCTGGCACTGGACAGAAAGCCAAATACTT  563
          ||||||||||:::|| ||||||||||| ||||| :::||:
Db   182  aLeuLeuGlyGlnArgGlySerIleIleTrpLeuGlyThrGlyGlnLysAlaGlnTyrLe  202

Qy   564  GCCTAAACTGGCTCCGGGGAGCACATTGCAGCCTTCGCCTCACGGAGCCAGCCAGTGG  623
          |||||||||||:::||:||  :::|| |||||||||:
Db   202  uProArgValAlaSerGlyValGlnAlaLeuAlaLeuAlaAlaPheCysGluThrGluSerGl  222

Qy   624  GAGGCGATGGAGATCATCAATCCGAGCAGAGCCTCAATGAAGAGTGAAGAACACTACAT  683
          ||||||||       ||||||||        ||||| ||||||||||||
Db   222  ySerAspValAlaSerIleArgSerArgSerAlaValProSerCysGlyTyrTyrTh  242

Qy   684  CCTCAATGGCTCCAAGGTCTGGATTACTAAGTGGAGACTGGCCAATATTTTTACTGTGTT  743
          |:::|||||||||||| ||||||| | ||||||||:::
Db   242  rLeuAsnGlySerLysValTrpIleThrLysTrpCysIleAlaAspIlePheThrValPh  262

Qy   744  TGCAAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGCAAAGACAAAAATCACAGCATT  800
          |||||||||||||||| |||        :|| ||| ::|||
Db   262  eAlaLysThrProIleLysGluAspAlaAlaThrGluLeuAlaValLysGluLysSerIleThrAlaPh  282

Qy   801  CATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCAT  860
          ||||||||||:::|| :::||||||||:||
Db   282  eAlaTyrThrProIleLysAspAlaAlaThrGluLeuAlaValLysGluLysSerIleThrAlaPh  302
```

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Qy   861  TCGGGGCTCCAACACTTGTGAGTCCATTTGAAGTCCAAGAATACCTGTGTGAAAACAT  920
          ||:::||||||     ||||:::|||||||:::
Db   302  eLysAlaSerAsnThrSerGluValTyrPheGluValLysValProLysGluAsnVa  322

Qy   921  CCTTGGAGAGGTCGGAGATGGGTTTAAGTGGCCATGAACATCCTCAACAGCGCCGGTT  980
          |||||||||||       | ||||||| ||||||||:::
Db   322  lLeuGlyGluValGlyAspGlyPheLysTrpProLysAsnIleLeuAsnAsnGlyArgPh  342

Qy   981  CAGCATGGGCAGCGTCGTGGCTGGCTGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTA 1040
          ||:||::||||| ||| ::::|||||||||||||:::
Db   342  eGlyMetAlaAlaThrLeuAlaGlyAlaThrMetLysAlaIleIleAlaAlaLysAlaAppHi  362

Qy  1041  CGCCTGCCAACGAAACAGTTAACAGAGACTCAGTGAATTTGGATTGATTCAGGAGAA 1100
          ::::||| ||||||       :::||:|||||| ||||||:
Db   362  sAlaThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLy  382

Qy  1101  ATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACGCAGG 1160
          ||||| ||||||||||||||||||||||:||||||:
Db   382  sLeuAlaAlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAl  402

Qy  1161  GATGCTGGACCAACCTGGCTTCCCGACTGCTCCATGGAGGCCATGGTGGTGAAGGTGTT 1220
          :::||||||||||| ||||||||||||:::
Db   402  aAsnMetAspGln--GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePh  421

Qy  1221  CAGCTCCGAGGGCCGCTGGCCAGTGTGAGTGAGGCCGGTGAGATCCTCGGGGGCTTGGG 1280
          |||||||||||:::|| ::::|||||||||||:
Db   421  eGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyMetGl  441

Qy  1281  CTACACAAGGGACTATCGTACGAGGCCATACTGCGTGACACCCGCATCCTCCTCATCTT 1340
          |:::|| |||||||:::||||||||:
Db   441  yPheMetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePh  461

Qy  1341  CGAGGAACCAATGAGATTCTCCGGATGTACATCGGCGTCTGCAGCATGCCGG 1400
          |||||||||:::||:|||||||||||||||:
Db   461  eGluGlyThrAsnAspLeuArgLeuPheValAlaLeuGlnLysCysMetAspLysGl  481

Qy  1401  CCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGT 1454
          |||||::::||:|| ::::|||||:
Db   481  yLysGluLeuThrGlyLeuValGlyLeuGlyAsnAlaLysLysAsnProLeuGlyAsnValGlyLeuLe  501

Qy  1455  CATGGATACCGTTGGCCGGAGGCTTCGGGACTTCGGGACTGTGGACCTGGGGGCT 1514
          :::::|| ||||||||||||||||||:
Db   501  uileGlyGluAlaSerLysSerGlnIleLeuArgGlyArgArgThrGlyIleGlySerGlyLeuSerIle  521

Qy  1515  GACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAGTTTGAGGA 1574
          |||       ::: ||||||||||||:
Db   521  User------GlyIleValHisProGluLeuSerGluArgSerGlyLeuLeuValGlu  538

Qy  1575  GAACAGCCACTGCTTCGGCCGGAGACCGTGGAGACCGTGCTGCTGCCCGCTTGGCAAGACCAT 1634
          ||||||| ||||||||||||||||||||||||||||||:::
Db   538  nAlaLeuGluGlnPheAlaThrValGluAlaLysLeuMetLysHisLysGlyLysGlyIl  558

Qy  1635  CATGGAGGAGCAGCTGTACTGAAGCGGGTGGCCAACAACCTGTATGGCAT 1694
          ||||||||||||||:::||:||||||:
Db   558  eValAsnGluGluGlnPheLeuGlnAspLeuLeuAlaIleAspLeuTyrAlaMe  578

Qy  1695  GACGGCCGTGCTGTCCCGGGGCCAGCTCCATCCGGCAGCTCCGCAACCACGACCA 1754
          ||||||||||||||||||||||||||||||:
Db   578  tValValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHi  598

Qy  1755  CGAGGTTCTCTTGGCCAACACCCTTCTGCCTGGAAGCT---------TACTTCCAGAATCT 1805
          ::::||||||     ::::|||||||:
Db   598  sGluLysMetLeuCysAspSerTrpCysIleAlaAlaThrArgIleArgGluAsnMe  618

Qy  1806  CTTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAAACCTAGATGAGCAGATTAAGAA 1865
          |||        ::: || ::::|||||:
Db   618  tAlaSerLeuGlnSerAsnProGln------GlnGlnGluGluProPheAsnPheArgSe  636

Qy  1866  AGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCAACCCTCTG 1917
          ::::||:| :::||||||:
Db   636  rIleSerLysAlaMetValGluAsnGlyLeuGlyLeuValThrSerAsnProLeu  653
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RESULT 8
US-10-362-537-10
; Sequence 10, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
;  APPLICANT: Takeda Chemical Industries, Ltd.
;  TITLE OF INVENTION: IRAP Binding Protein
;  FILE REFERENCE: 2774 USOP
;  CURRENT APPLICATION NUMBER: US/10/362,537
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: JP 2000-254263
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: JP 2000-276633
;  PRIOR FILING DATE: 2000-09-07
;  NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
;  LENGTH: 655
;  TYPE: PRT
;  ORGANISM: Mouse
US-10-362-537-10

Alignment Scores:
Pred. No.:                             Length:         655
Score:              2.99e-102          Matches:        287
                    1360.00            Conservative:   106
Percent Similarity: 66.05%             Mismatches:     184
Best Local Similarity: 48.24%          Indels:         18
Query Match:        30.20%             Gaps:           9
DB:                 15

US-09-945-326-1 (1-2452) x US-10-362-537-10 (1-655)
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```
Qy    169 CCTGTACGAGCT----------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAG 216
                              :|| :||| ||||||||||||||::|||:::::
Db     66 ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrIle 85

Qy    217 AAAGAAGTTTCCCATTTCCAGAAGTT---AGCCAAGATGAACTTAATGAAATCAATCAG 273
              ::|||||||||||||   :||||||          |||  ::  :||||||||||
Db     86 AspGlnValPheProTyrProSerValLeuSerGluGluGlnAlaGlnPheLeuLysGlu 105

Qy    274 TTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGACTCCCGAAAAATTGACCAG 333
              ||:||||     ||:|||||| ||  |||||||| |||
Db    106 LeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaLysAspAspAla 125

Qy    334 GAAGGAAAATCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTG 393
              ||||||||||||||||||| ||| :||||||||||||||||||||||||
Db    126 LeuGluLysValGluAspAspThrLeuGlnLeuLysGluGluGlyAlaPheGlyLeu 145

Qy    394 CAAGTCCAGAGAGAATATGTGGCCCTGGCTTCTCCAACACCATGTACTACTCAAGACTAGGG 453
              ||||||||||   |:||||  |:|:|||||||||:|:||||||
Db    146 GlnValProSerGluGluValGlyGlyLeuGlyLeuSerAsnThrGlnTyrArgLeuArgLeuAla 165

Qy    454 GAGATCATCAGCATG---GATGGTTCCATCACTGTGACCCTGGCAGCGCCACCAGGCTATT 510
              :: ||||||||||||  ::||||:||||||||||||||||||:||:|||
Db    166 GluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSerIle 185

Qy    511 GGGCCTCAAGGGGATCATCTTGGCTGCTGCTGGCTCGAGGAGCAGAAAGCCAAATACTTGCCTAAA 570
              |||||||||||||||||||||||   :||||||||||| |||||   ||||||||||||
Db    186 GlyPheLysGlyIleLeuLeuLeuTyrGlyThrLysAlaGlnLysArgGluLysProArg 205

Qy    571 CTGCGCTCCGGGAGCACATTGCAGCCTTCTGCCTCCACCGGAGGGAGCGAT 630
              :::||||||||::  :||||||||| ||| :|||||:||||:||||||
Db    206 ValAlaSerGlyGlnAlaLeuAlaAlaLeuAlaLeuAlaPheCysSerLeuThrProSerGlySerAsp 225

Qy    631 GCAGGCTCAATCCGGAGCAGAGCACCACCTAAGTGAAGACAAGAAGCACTACATCCTCAAT 690
              |||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db    226 ValAlaSerIleArgSerArgSerAlaIleProSerProCysGlyLysTyrTyrThrLeuAsn 245

Qy    691 GGCTCCAAGGTCTCGGATTACTAATGACGACTGCCAAATATTTTTACTGTGTTTGCAAAG 750
              |||||||||||||||||:||  :||||||||||||||||||||||||||||
Db    246 GlySerLysIleTrpIleSerAspAsnGlyGlyLeuGluAlaAlaIlePheThrValPheAlaLys 265

Qy    751 ACTGAGGTCGTTGAT--TCTGATGGATCAGTGAAAGACAAAATCAACAGCCATTCATAGTA 807
              |||  :|| :||    |||||||||||||||||||||||||||||||||||
Db    622 LeuGlnSerSerProGlnHis------GlnGluLeuPheArgAsnPheArgSerIleSer 639
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Db    266 ThrProIleLeuAspAlaAlaThrGlyAlaValValGluLysGluLysIleThrAlaPheValVal 285

Qy    808 GAAAGAGACTTTGGTGGAGTCACTAATGGAAACCGAGATAAAATAGGCATTCGGGGC 867
              |||| |:||||||:||||||||||||||||||| ::::
Db    286 GluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIleLysAla 305

Qy    868 TCCAACACTGTGAAGTCCATTTGAAAACAACCAAGATACCTGTGAAAACATCCTTGA 927
              ||||:||     ||||||::|||   :||:|
Db    306 SerAsnThrSerGluValTyrPheAspGlyValLysValProSerGluAsnValLeuGly 325

Qy    928 GAGGTCCGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGCCGGTTCAGCATG 987
              ||||||||||||||||| ||| ||||||||:|||| :|||||||||:|||
Db    326 GluValGlyAspGlyAspPheLysGlyLysPheGlyValAlaValAsnIleLeuAsnAsnGlyArgArgPheGlyMet 345

Qy    988 GGCAGGCGTCGTGGCTGGCGTGCTCAAGAGATGATTGAAATGACTGCTGAGTACGCCTGC 1047
              :| :||||||||||||||||||||| ||||||||||||| ::::
Db    346 AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysValAlaAspHisAlaThr 365

Qy   1048 ACAAGGAAACAGTTAACAGCGCTCAGTGAATTTGATTGATTGGATTGGATTGCA 1107
              :::::     |||||
Db    366 AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeuAla 385

Qy   1108 CTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGGATGCTG 1167
              |||||   |||||||||||||||||||||||  :: :||
Db    386 ArgMetAlaIleLeuLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsnMet 405

Qy   1168 GACCAACCTGGCTTTCCCGACTGCTTCCATGGAGGCCATGGTGAAGGTTGTTCAGCTCC 1227
              ||||| ||||||||||||||||  |||||||||||||||||||||||||||
Db    406 AspGln--GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePheCysSer 424

Qy   1228 GAGGGCCGCCTGGCAGTGTGTGAGTGAGGCGGCTGCAGATCCTCGGGGGCTTGGGCTACACA 1287
              |||||||||||  :|| :::::  |||||:||:
Db    425 GluAlaAlaTrpLysValAlaAspGluCysIleGlnIleMetGlyMetGlyPheMet 444

Qy   1288 AGGGACTATCCGTACGAGAGGCATACTGCGTGACACCCGCATCCTCCTCATCTTCGAGGGA 1347
              :::::  ||||||
Db    445 LysGluProGlyValGluValValLeuArgAspIleArgIlePheArgIlePheGluGly 464

Qy   1348 ACCAATGAGATTCCCGGATGTACATCGGCGCCTGACCGGGGTCTGCAGCATGCCGGCCCGCATC 1407
              |||||||||||||||||||||||||||||||||||||||||||||||
Db    465 AlaAsnAspIleLeuArgLeuPheValAlaLeuAlaLeuGlnGlyCysMetAspLysLysGlyLysGlu 484

Qy   1408 CTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCAGCACAGTCATGGAT 1461
              |||||||||||||||||||| :::  |||||
Db    485 LeuThrGlyLeuGlyLeuGlyAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly 504

Qy   1462 ACCGTTGGCCGAGCTTGCGAGGCTTGGGACTCCCTGGCGACCTGTGACCTGGGCTGACCAGGC 1521
              :::|||||||||||||||||||||||||||||||||||||||
Db    505 GluAlaGlyLysGlnLeuAlaArgArgThrGlyIleGlyIleGlyLeuSerGlyLeuSer--- 523

Qy   1522 AACCATGAGGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAGTTTGAGGAGAACACC 1581
              |||||||||||||||||||||||||||||| |||
Db    524 ------GlyIleValHisProGluLeuSerArgSerGlyLeuLeuAlaValGlnAlaLeu 541

Qy   1582 TACTGCTTCGGCCGACCGTGGAGGACACTGCTGCGCTCCGCCTTTGGCCAAGACCATCATGGAG 1641
              |||||||||||||:: :||||||||||||||||||||:|:
Db    542 AspGlnPheAlaThrValValGluAlaLeuValLysHisLysGlyIleValAlaAsn 561

Qy   1642 GAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACGGCC 1701
              |||||||||::: :|||||||||||||||||||||||||||||||||
Db    562 GluGlnPheLeuGluLeuGlnIleArgLeuAlaLeuAlaAspProLeuTyrAlaMetValVal 581

Qy   1702 GTGCTGTCGCGGGCAGCAGAGCCGCGCTCCATGGCCATTGGGCTCCGAACCACCACGAGGTT 1761
              |||||||||||| :::::
Db    582 ValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGluLys 601

Qy   1762 CTCTTGGCCAACACCTTCTGCGTGGAAGCT-------TACTTGCAGAATCTTCAGC 1812
              :::::::||||||||||:::||||||||||
Db    602 MetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAlaSer 621

Qy   1813 CTCTTCCAGTCGACAAGTATGCTCCAGAAGACAAAACTAGATGAGCAGATTAAGAAAGTGTCC 1872
              ||| |||  :||  ::::
Db    622 LeuGlnSerSerProGlnHis------GlnGluLeuPheArgAsnPheArgSerIleSer 639
```

Qy   1873 CAGCAGATCCTTGAGAAGGCAGCCTATATCTGTGCCACCCTCTG 1917
           ::: ||||:::|| ::   ::||||||
Db   640 LysAlaMetValGluAsnGlyGlyLeuValThrGlyLeuAsnProLeu 654

RESULT 9
US-10-362-537-11
; Sequence 11, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Bovine
US-10-362-537-11

Alignment Scores:
Pred. No.:   5.08e-101   Length: 655
Score: 1345.00   Matches: 285
Percent Similarity: 65.51%   Conservative: 110
Best Local Similarity: 47.26%   Mismatches: 194
Query Match: 29.86%   Indels: 14
DB: 15   Gaps: 9

US-09-945-326-1 (1-2452) x US-10-362-537-11 (1-655)

Qy   133 TCTACCGGCAACCGGCGCTACTGCGCACCAGCCGCCCGCCTGTACGACGCTTTCGCCAAAGAG 192
          ||| |||:::: ||| :::   :::::||||||
Db   57 SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly 76

Qy   193 CTTTTTCCTAGGCAAAATCAAGAAGAAGAGTTTCCCATTTCCAAGAGT---AGCCAA 249
          ||| ||||:::|| :::::::
Db   77 ThrPheLysGlyGlnLeuThrThrAspGlnValPheProSerValLeuAsnGlu 96

Qy   250 GATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAG 309
          |||:::   :::|||||| |||||||
Db   97 AspGlnThrGlnPheLeuGlyLysGluLeuValGlyProValThrArgPhePheGluGluVal 116

Qy   310 GTGGACTCCCGAAAAATTGACCAGGAAGGGAAAAТCCCAGATGAAACTTTGGAGAAATTG 369
          ||| ||| ||| :::   :: |||:::||
Db   117 AsnAspAlaAlaLysAspMetLeuGlyValArgValGluGluThrThrMetGlnGlyLeu 136

Qy   370 AAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTTCTCC 429
          ||| |||:::|| |||||||::||
Db   137 LysGlyLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyLeuGlyValGlyLeuCys 156

Qy   430 AACACCATGTACTCAAGACTAGGGGAGATCATCAGCATG---GATGGGTCCATCACTGTG 486
          |||:::|||||| ||| ||| :::   :::
Db   157 AsnThrGlnTyrAlaArgLeuValGluValGlyMetTyrAspLeuValGlyIleIle 176

Qy   487 ACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG 546
          ||| ||| ||| ||| :::
Db   177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyLyPheLeuLeuPheGlyThrLysAla 196

Qy   547 CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGCAGCCTTCTGCCTC 606
          ||| :::|||||| ||||||||| ||| |||:::
Db   197 GlnLysGlyLysGluLysTyrLeuProLysLeuAlaSerGlyValGluThrIleAlaAlaPheCysLeu 216

Qy   607 ACGGAGGCCAGTGGGAGCGGATGGCCGGTCGTGTCCGGAGCAGCCACTAAGTGAA 666
          |||:::|||||||| ||||||||
Db   217 ThrGluProSerGlySerGlySerAspAlaAlaSerIleArgSerAlaValProSerPro 236

Qy   667 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC 726

```
Db   593 HisProThrAlaGlnHisGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaAla 612

Qy  1792 ---TACTTGCAGAATCTTCTTCAGCCTCCTCAGCTGGACAAGTATGCTCCAGAAAACCTA 1848
              :::|||    ::|||    |||   ||:||    |||:    ||||||||||||
Db   613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlu---Leu 630

Qy  1849 GATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC 1908
              |||    :::||||:    ::|||||||||||    ::: :::
Db   631 PheArgAsnPheLysSerIleSerLysAlaLeuValGluArgGlyValGlyValThrSer 650

Qy  1909 CACCCTCTG 1917
         ::|||||||
Db   651 AsnProLeu 653

RESULT 10
US-10-362-537-1
; Sequence 1, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 1
;   LENGTH: 655
;   TYPE: PRT
;   ORGANISM: Human
US-10-362-537-1

Alignment Scores:
Pred. No.:                           Length:       655
Score:           4.72e-99            Matches:      297
Percent Similarity:   1321.00        Conservative: 109
Best Local Similarity: 61.52%        Mismatches:   213
Query Match:     45.00%              Indels:       41
DB:              29.33%              Gaps:         13

US-09-945-326-1 (1-2452) x US-10-362-537-1 (1-655)

Qy    21 GCTAAGAAGGGAGACTGAGGCTGAGGCTGGGAACATCGGGCAGCATGAGCGGCTGCGG 80
            ||||||||||||||||||||    |||
Db     8 AlaSerLeuGlyArgGlnLeuLeuArgLeuGly-----GlyGlySerSerArgLeuThr 25

Qy    81 GCTCTT---------------------CCTGCGCACCACGGCTCGGCGTCGTGCCTGCCG 119
         ||||||                          ||:||||
Db    26 AlaLeuLeuGlyGlnProArgProGlyProAlaArgArg------------------Pro 39

Qy   120 GGGGTCGTGGTCGTCTC--------------------------TACCGCGAACCGGGG 149
         ::|||||||                                  ::: |||
Db    40 TyrAlaGlyGlyAlaAlaGlnLeuAlaLeuAspLysSerAspSerHisProSerAspAla 59

Qy   150 GCTACTGCGCACCAGCCCGCC----------TGTACGAGCTTTGCCAAAGAGCTTTTCCT 200
         ::|||||    |||              ||:|||||
Db    60 LeuThrAlaLysLysProAlaLeuAlaGluSer-LysSerSerPheAlaValGlyMetPheLy 79

Qy   201 AGGGAAAATCAAGAAGAAGAAGAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAA 260
         ||||||||    :::|||||||    ||    :::
Db    80 sGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGluGluGlnTh 99

Qy   261 TGAA--ATCAATCAGTTCTTGGGACCCGGTGGAAAAATTCTTCACTGAAGAGGTGGACTC 317
             :: ::: :::    |||    ||||    ::|||    :::
Db   100 rGlnPheLeuLysGluLeuValGluLeuProValSerArgPheAlaGluPheGluValAlaAsnAspPr 119

Qy   318 CCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAAATTTGGAGAAATTGAAGAGCCT 377
         ||||||                    ::::
Db   119 oAlaLysAspAlaAsnAspAlaLeuGlyMetValGluMetValGluThrThrTrpGlnGluThrTyrGluLe 139
```

```
Db    498  aGlyLeuLeuGlyLeuGlyGluAlaGlyLysGlnLeuArgArgArgArgAlaGlyAlaGlyLeuGlySerGl  518
                |||::::::               |||:::::|||||
Qy

Db   1506  CCTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAA  1565
                |||::||:||   :::|||||||:::  :::
Qy    518  yLeuSerLeuSer---------GlyLeuValHisProGluLeuSerArgSerGlyGluLe   535

Db   1566  GTTTGAGGAGAACACCTACTGCTTCGGCCGACGCTGGACACTGCTCCGGTTGG  1625
                :::::::|||||||   ||||||||
Qy    535  uAlaValArgAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIleLysHisLy  555

Db   1626  CAAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCT  1685
                |||::::|||||||                |||:::|||
Qy    555  sLysGlyIleValAsnGluGlnPheLeuLeuLeuGlnArgLeuAlaAspGlyAlaIleAspPle  575

Db   1686  GTATGGCATGACGGCCGTGCTGTGCGGGGCCAGCCGCTCCATCCGCCATTGGGCTCCGCAA  1745
                |||||                |||||||:::
Qy    575  uTyrAlaMetValValLeuSerArgAlaSerArgSerLeuSerGluGlyHisProTh     595

Db   1746  CCAGACCACCAGAGGTTCTCTTGGCCAACACCTTCTGCCTGAA---------GCTTACTTGCA  1799
                ||||||||   |||||                :::
Qy    595  rAlaGlnHisGluLysMetLeuCysAspThrTrpCysIleGluAlaAlaAlaAlaArgIleAr  615

Db   1800  GAATCTCTTCAGCCTCCTCTGACAAGTAACGTATGCTCCAGAAAAACCTAGTAGAGCAGAT  1859
                :::                ||
Qy    615  gGluGluMetAlaAlaLeuGlnSerAspProTrpProGlnGlnGlu---LeuTyrArgAsnPh  634

Db   1860  TAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCACCCTCTG  1917
                |||                 :::  :::|||||
Qy    634  eLysSerIleSerLysLysValGluValAlaLeuValArgGlyValValThrSerAsnProLeu  653
```

RESULT 11
US-10-408-765A-534

; Sequence 534, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 534
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-534

Alignment Scores:
Pred. No.:
Score: 4.72e-99   Length: 655
                      1321.00   Matches: 297
Percent Similarity: 61.52%   Conservative: 109
Best Local Similarity: 45.00%   Mismatches: 213
Query Match: 29.33%   Indels: 41
                      16   Gaps: 13

```
US-09-945-326-1 (1-2452) x US-10-408-765A-534 (1-655)

Db    21  GCTAAGAAGGGGAGACTGAGGCTGGGGAACATCGGGCAGCAGTGAGCGGCTGCGG  80
              |||||                       |||||
Qy

Qy     8  AlaSerLeuGlyArgGlnLeuArgLeuGly------GlyGlySerSerArgLeuThr  25

Db    81  GCTCTT----------------CCTCGCCACCACGGCTGCGGCTGTGCCTGCCG  119
              |||                                ||||:::|||
Qy    26  AlaLeuLeuGlyGlnProArgProGlyProAlaArg------Pro  39
```

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-320

Alignment Scores:
Pred. No.:                                    Length:          655
Score:               2.59e-98                 Matches:         296
                     1312.00                  Conservative:    109
Percent Similarity:  61.36%                   Mismatches:      214
Best Local Similarity: 44.85%                 Indels:          41
Query Match:         29.13%                   Gaps:            13
DB:                                           16

US-09-945-326-1 (1-2452) x US-10-408-765A-320 (1-655)

Qy    21  GCTAAGAAGGGAGACTGGAGGCTGAGGCTGGGAACATCGGCGGCATGAGCGGCGGCTGCGG    80
              |||||      ::||||||||||||||||||||||||||||||::  |||||||||
Db     8  AlaSerLeuGlyArgGlnLeuArgLeuGly------GlyGlySerSerArgLeuThr    25

Qy    81  GCTCTT--------------------------CCTGCGCCACCACGGCTGCGGCTGCGGCTGCGG   119
              |||||                        |||||||||||||||||||||||| ------Pro  39
Db    26  AlaLeuLeuLeuGlyLeuGlnProArgProGlyAlaArgArg------Pro

Qy   120  GGGTCTTGGTGTGTCTC----------------------------------TACCCGGACCGCGGCG   149
              :::::::                                            :::  |||
Db    40  TyrAlaGlyGlyValAlaAlaGlnLeuAlaAlaLeuAlaAspLysSerAspSerHisProSerAspAla   59

Qy   150  GCTACTGCGCCACCAGCCGCC----------TGTACGAGCTTCGCCAAAGAGCTTTTCCT   200
              |||                      |||||
Db    60  LeuThrArgLysLysProAlaAlaGlyAlaGluSer--LysSerPheAlaValGlyMetPheLy    79

Qy   201  AGGCAAAATCAAGAAGAAAGAGAGTTTCCCATTCCAGAAGTTAGCCAAGATGAAGAACTTAA   260
              ||||||::::        ::  ::||||  ||||||   :||||||||||
Db    80  sGlyGlnLeuThrArgAspGlnValPheProTyrProSerValLeuAsnGluGlnTh    99

Qy   261  TGAA---ATCAATCAGTTCTTGGACCCGTGGAAAATTCTTCACTGAGAGGGTGGACTC   317
              ||||                ::                ::|||||
Db   100  rGlnPheLeuLysGluGluValGluProValSerArgPheGluPheProGluValAlaAspPr   119

Qy   318  CCGAAAAATTGCACCAGGAAGGAGAAAATCCAGATGAAACTTGAGAAATTGAGCAGGCCT   377
              ||:::                   ::: ||||||||||
Db   120  oAlaLysAsnAspAlaLeuGluMetValGluGluThrThrTrpGlnTyrLeuLysGluLe   139

Qy   378  AGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCGGCTTCCCAACACCAT   437
              |||||||     :::|||||||||||||||||
Db   140  uGlyAlaPheGlyLeuProSerGluLeuGlyGlyLeuCysAsnThrGl   159

Qy   438  GTACTCAAGACTAGGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGC   494
              :::|||:::||||                  :::
Db   160  nTyrAlaArgLeuValGluIleValGlyMetHisAspLeuValGlyIleThrLeuGl   179

Qy   495  AGCGCCACCAGGCTATTGGCCTCAAGGGGATCATCTGGCTGGCCACTGAGGAGCAGAAAGC   554
              :::|||||||||::        ::
Db   180  yAlaHisGlnSerIleGlyIleLeuLeuGlyLeuPheCysThrLysAlaGlnLysGl   199

Qy   555  CAAATACTTGCCTAAACTGGCTCCGGGAGCACATTGCAGCCTTCTGCTCCACGGAGCC   614
              |||||                   :::||||||||||||||||
Db   200  uLysTyrLeuProLysLeuAlaSerGlyGluThrValAlaAlaPheCysLeuThrGluPr   219

Qy   615  AGCCAGTGGACGGGATGCAGCGTCCAATCCGAGCGAGCCACCAAGTGAAGAACAAGAA   674
              ||||||||||||||||        ||||||||||||||||
Db   220  oSerSerGlySerAspAlaAlaSerIleArgThrSerAlaValProSerAlaValLeuLy   239

Qy   675  GCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGGGAACTGGCCAATATTT   734
              ::::||                       ::::
Db   240  sTyrTyrThrLeuAsnGlySerLysSerLeuTrpIleSerAsnGlyGluLeuAspIlePh   259

Qy   735  TACTGTGTTGCAAAGACTGAGGTCGTTGAT---TCTTGATGGATCAGTCAGAGAACAAAT   791
              :::||                    |||||||
Db   260  eThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValLysLysLysIl   279

Qy   792  CACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTACTACTGAGGAAACCCGAAGATAA   851
              :::||||                      |||
Db   280  eThrAlaPheValValGluArgGlyPheGlyIleThrHisGlyProGluLysLy   299
```

RESULT 13
US-10-369-493-5444
; Sequence 5444, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5444
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5444

Alignment Scores:
Pred. No.:   Length: 613
Score: 5.32e-90   Matches: 272
Percent Similarity: 1210.50   Conservative: 109
Best Local Similarity: 61.16%   Mismatches: 205
Query Match: 43.66%   Indels: 37
DB: 26.88%   Gaps: 14
                          15

US-09-945-326-1 (1-2452) x US-10-369-493-5444 (1-613)

```
Qy    85  TTCCTGCGCACCAGGCTGCGGCTCGTGCCTGCCGGGGTCGGTGGTCTCTACCGCGAAC  144
              |:::||||||| ||||||| |||:  |||::  ||||||||||||||||
Db    16  PheIleArgLeuSerHisSerAlaAlaAlaAlaLys----------AspAlaLysPro   31

Qy   145  CGGCGGCTACTGCGCACCAGCCCGCCTGTACGAGAGCTTTCGCCAAAGAGCTTTTCCTAGGC  204
              :::::||||||| |||     ::: ||| ||       :::|||
Db    32  LysLysValAlaAlaAlaValAspSerPro------SerPheValMetAsnLeuPheArgGly   49

Qy   205  AAAATCAAGAAGAAGAAAGAAGTTTCCATTTCCAGAGTTAGCCAAGATGAACTTAATGAA  264
              |||    ::|||||||||||||  |||||||||:::|||
Db    50  LysAlaValThrAspGlnValPhePrdTyrProLeuAsnMetThrAspGluGlnLysGlu   69

Qy   265  ---ATCAATCAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGA  321
              ::|||||||  |||  ||| ||||| |||:::
Db    70  ThrLeuGlyMetValMetSerProLeuGluLysMetLeuValLeuGluValAsnAspValVal   89

Qy   322  AAAATTGACCAGGAAGGAGGAAAATCCCAGATGAAAACTTTGGAGAAAATTGAAGAGCCTAGGG  381
              |||||||||| |||||| |||:::
Db    90  LysAsnAspGluThrSerAspIleProArgAlaValLeuAspGlnPheAlaAlaGluLeuGly  109

Qy   382  CTTTTTGGGCTGCAAGTCCAGAAGAAATATGTGGCTGGCTTCTCCAACACCATGTAC  441
              ||||||:::||||| ||||| |||||:: |||::
Db   110  ThrPheGlyValLeuValProProGluLeuGlyLysGlyPheAsnSerGlnMet  129

Qy   442  TCAAGACTAGGGGGAGATCATC---AGCAATGGATGGGGTCCATCACTGTGACCCTGGCAGCG  498
              :::||||||||||||  :::  ::|||||| ||||||||||
Db   130  AlaArgValAlaGlyLleValGlyAlaTyrAspGlyAlaPheGlyValMetGlyAla  149

Qy   499  CACCAGGCTATTGGCCTCCAAGGGGATCATCTTGGCTCGGCCACTGAGGAGCAGAAAGCCCAAA  558
              |||||||| ||||||| |||||||||||
Db   150  HisGlnSerIleGlyTyrLysGlyLleLeuLeuGluGlyLleThrAspAlaGlnLysGlnLys  169

Qy   559  TACTTGCTAAACTGGCGTCCGGGGAGCACATTGCAGCCCTTCGCCTCGCCGGAGCCAGCC  618
              :  ||||||||||||||::||
Db   170  TyrLeuProAspLeuAlaThrGlyArgLysPheAlaAlaPheAlaLeuThrGluProThr  189

Qy   619  AGTGGGAGCGGATGCAGCCTCAATCCGGACGAGCAAGTGAAGACAAGAAGCAC  678
              :::||||||| ::: ||||||||||||
Db   190  ThrGlySerAspAlaSerValArgThrArgAlaGluLeuSerAlaAspGlyLysHis  209
```

```
Qy   852  ATTAGGCCATTCGGGGCTCCAACACTTGTGAAGTCATTTGAAAAACCAGATACCTGT  911
              |:::||||| ||||||| |||::  ::: |||
Db   299  sMetGlyIleLysAlaSerAsnThrAlaGluValPhePheAspGlyValArgValProSer  319

Qy   912  GGAAAACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAG  971
              |||||||:::|||||||| ||||||| |||
Db   319  rGluAsnValLeuGlyLeuGlyValGlySerGlyAspGlyPheLysValAlaMetAsnIleLeuAsnAs  339

Qy   972  CGGCCGGTTCAGCATGGGCAGCGCTGCGTGGTCGCTGGCTGCTCAAGAGATTGATTGAAATGAC  1031
              :|||||||| ||  :::::    ||||||  :::|||
Db   339  nGlyArgPheGlyMetAlaAlaLleAlaLeuAlaGlyThrMetArgGlyLleLeuAlaAlaLysAl  359

Qy  1032  TGCTGAGTACGCCCTGCACAAGGAAACAGTTAACACAGAGGCTCAGTGAATTTGGATTGAT  1091
              |||::  ::||||| |||||||| ||||||||||||
Db   359  aValAspHisAlaThrArgThrGlnPheGlyLeuLysIleHisAsnPheGlyLeuIl  379

Qy  1092  TCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCT  1151
              |||||| ||||||||||||||||||||:::
Db   379  eGlnGluLysGluLeuAlaArgValMetLeuGlnTyrValThrGluSerMetAlaTyrMe  399

Qy  1152  CACACAGCAGGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGCAGCCATGGT  1211
              :::||||||  ::|||  |||  :::|||
Db   399  tValSerAlaAsnMetAspGln---GlyAlaThrAspPheGlnIleIleGluAlaIlese  418

Qy  1212  GAAGGTGTTCAGCTCCGAGGCCGCCTGGCCAGTGTGGTGAGTGAGGCCGTCAGATCCTCGG  1271
              |||||| |||::: ||||||||| |||||::
Db   418  rLysIlePheGlySerGluAlaAlaTrpLysValThrArgAspGluCysIleGlnIleMetGl  438

Qy  1272  GGGCTTGGGCTACACAGGGACTATCCGTACGAGGCGCATACTGCGTGACACCGCATCCT  1331
              ||||| ||  ::: ||||||||||||||||
Db   438  yGlyMetGlyPheMetLysGluProLeuGlyValGluArgValLeuArgAspLeuArgIlePh  458

Qy  1332  CCTCATCTTCGAGGGAACCAATGAGATTCTCCGATGTACATCGCCCTGACGGGTCTGCA  1391
              ||||||||||| :::||||||:::|||||||||||
Db   458  eArgIlePheGluGluPheGluGlyGlyThrAsnAspIleLeuArgLeuAlaLeuGlyLlyGlyCysMe  478

Qy  1392  GCATGCCGGCGGCATCCTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGT  1445
              ||||||   ||||| |||||||
Db   478  tAspLysGlyLysGluLeuSerGlyLeuGlyLleSerAlaLeuLysAsnProPheGlyAsnAl  498

Qy  1446  GAGCAGCAGTCATGATCATGCCGGCTTGGCCGGAGGCTTCGGGACTCCCTGGCCGAACTGTGGA  1505
              :::||||||||| |||||||||||
Db   498  aGlyLeuLeuGlyLleGlyLysGlyGlnLeuArgArgAlaGlyLleValLeuSerGl  518

Qy  1506  CCTGGGGCTGACAGGCAACCATGAGTGTGTGCACCCCAGTCTTGCCGGACAGTGCCAACAA  1565
              |||:::|||  |||||||  |||  |||||||
Db   518  yLeuSerLeuSer--------GlyLeuValHisProGluSerArgSerGlyGluLe  535

Qy  1566  GTTTGAGGGAACACCTACTGCTTCGGCCGGCGTGGAGCACTGCTGCTCCGCTTTGG  1625
              |||||||||||| ::: |||
Db   535  uAlaValArgAlaLeuGluGlnPheAlaThrValGluValLleuLysLeuHisLy  555

Qy  1626  CAAGACCATGGCCTGTGACTGAGGAGCAGCTGGTGCCAACATCCTCATCAACCT  1685
              |||:::||||||| ||||||||||||||
Db   555  sLysGlyLleValAsnGluGlnPheLeuLeuGlnArgLeuAlaLeuAspGlyAlaAlaIleAspPhe  575

Qy  1686  GTATGGCATGGACGGGCCCGTGCTGTCCTTCATCCGCATTGGGCCTCCCGAA  1745
              |||||| ||||||:::  :::|||
Db   575  uTyrAlaMetValValLeuAsnGluArgLeuSerArgSerArgSerGluSerGluArgGlyHisProTh  595

Qy  1746  CCACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCCGTGAA------GCTTACTTGCA  1799
              |||:::||||||||||||| ||||||||
Db   595  rAlaGlnHisGluLysMetLeuCysAspThrTrpCysIleGluAlaAlaAlaArgIleAr  615

Qy  1800  GAATCCTTCTTCCAGCCCTCTCCAGCTGACAAGTATGCTCCAGAAAACCTAGATGAGCAGAT  1859
              :::  ||||||||||||||
Db   615  gGluGlyMetAlaAlaLeuGlnSerAspProTrpGlnGlu---LeuTyrArgAsnPh  634

Qy  1860  TAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCCTATATCGTGCCCACCCCTG  1917
              :  :::||||  |||||||| |||||||||||
Db   634  eLysSerIleSerLysAlaGlyLleLleArgGlyLyValValThrSerAsnProLeu  653
```

us-09-945-326-1.rapb

```
Qy  1753 CACGAGGTTCTTGGCCAACACCTTCTGCGGTGGAAGCTTACTTGCAGAATCTTCTTCAGC 1812
                   ::::|||                 :::||              :::::       |||
Db   556 PheGluArgLysValAla---ThrTyrTyrValAspLysAlaMetLys--------Ser 571

Qy  1813 CTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGTAGCAGAATTAAGAAAGTGTCC 1872
                   :::::                |||            ||      :::::
Db   572 SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAsnAlaSerLysValAlaThr 591

Qy  1873 CAGCAGATCCTTGAGAGGCAGCCTATATCTGTGCC-------------------CAC 1911
                   ::: |||                                              |||
Db   592 IleGluSerLeuAlaLysGlu-----ValCysGlyAsnGlyGlyLeuThrLeuGlnHis 609

Qy  1912 CCTCTGAC 1920
         ||| ||:|
Db   610 ProValGlu 612
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RESULT 14
US-10-408-765A-1442
; Sequence 1442, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1442
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1442

Alignment Scores:
Pred. No.:   Length: 188
Score: 3.43e-69   Matches: 188
Percent Similarity: 954.00   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 21.18%   Gaps: 0

US-09-945-326-1 (1-2452) x US-10-408-765A-1442 (1-188)

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Qy  1366 ATGTACATCGCCCTGACGGGTCTCGCAGCATGCCGGCCCATCCTGACTACCAGGATCCAT 1425
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetTyrIleAlaLeuThrGlyLeuAlaAlaCysArgProIleLeuThrThrArgIleHis 20

Qy  1426 GAGCTTAAACAGGCCAAAGTGAGCACAGTCATGGATACCGTTGGCCGGAGGCTTCGGGAC 1485
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAsp 40

Qy  1486 TCCCTGGGCCGAACTGTGGGACTGGGACCTGGGGCTGCAGGGCAACCATGGAGTTGTGCA 1545
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 SerLeuGlyArgThrValAspLeuGlyLeuGlyThrGlnGlyAsnHisGlyValValHis 60

Qy  1546 CTTGCCGACAGTGCCACAAGTTGAGGAGAACACCTACTGCTTCGGCCGGACCGTGGAG 1605
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu 80

Qy  1606 ACACTGCTGCTCCGCTTGGCAAGACCATCATGGAGGAGGAGCAGCTGGTACTGAAGCGGGTG 1665
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGluGlnLeuValLeuLysArgVal 100

Qy  1666 GCCAACATCCTCATCAACCTGTATGGCAACGACGCCCCGTGTCGCGGCCCAGCCGCTCC 1725
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1666 GCCAAATCCTCATCAACCTGTATGGCATGAGGACGGCCGTGCTGTCGCGGGCCAGCCGCTCC 1725
          |||||||||||||||||||||||||||||||||||||||
Qy   101 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 120

Qy   1726 ATCCGCATTGGCTCCGCAACCACGACCACGAGGTTCTTGGCCAACACCTTCTGCGTG 1785
          |||||||||||||||||||||||||||||||||||||||
Db   121 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuValLeuAlaAsnThrPheCysVal 140

Qy   1786 GAAGCTTACTTGCAGAATCTCTTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAAC 1845
          |||||||||||||||||||||||||||||||||||||||
Db.   141 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn 160

Qy   1846 CTAGATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGT 1905
          |||||||||||||||||||||||||||||||||||||||
Db   161 LeuAspGluGlnIleLysLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCys 180

Qy   1906 GCCCACCCTCTGACAGGACATGC 1929
          |||||||||||||||||||||||
Db   181 AlaHisProLeuAspArgThrCys 188

Search completed: May 2, 2005, 15:56:48
Job time : 318.192 secs

RESULT 15
US-10-408-765A-2052
; Sequence 2052, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 66008.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2052
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2052

Alignment Scores:
Pred. No.:   3.43e-69   Length: 188
Score: 954.00   Matches: 188
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 21.18%   Indels: 0
DB: 16   Gaps: 0

US-09-945-326-1 (1-2452) x US-10-408-765A-2052 (1-188)

Qy   1366 ATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCGCCATCCTGACTACCAGGATCCAT 1425
          |||||||||||||||||||||||||||||||||||||||
Db   1 MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyAlaIleLeuThrThrArgIleHis 20

Qy   1426 GAGCTTAAACAGGCCAAAGTGAGCACAGTCATGGATACCGTTGGCCGGAGGCTTCGGGAC 1485
          |||||||||||||||||||||||||||||||||||||||
Db   21 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAsp 40

Qy   1486 TCCCTGGGCCGAACTGTGGACCTGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGT 1545
          |||||||||||||||||||||||||||||||||||||||
Db   41 SerLeuGlyArgThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSer 60

Qy   1546 CTTGCGGACAGTGCCAACAAGTTGAGGAGAACACTACTGCTTCGGCCGGACCGTGGAG 1605
          |||||||||||||||||||||||||||||||||||||||
Db   61 LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu 80

Qy   1606 ACACTGCTGCTCCGCTTTGGCAAGAACCATCATGAGGAGAACAGCTGGTACTGGAGCGGGTG 1665
          |||||||||||||||||||||||||||||||||||||||
Db   81 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGluAsnSerTrpTyrTrpSerGlyVal 100

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:      May  2, 2005, 14:27:05 ; Search time 79.2709 Seconds
                                      (without alignments)
                                      5952.335 Million cell updates/sec

Title:            US-09-945-326-1
Perfect score:    4504
Sequence:         1 cgtgtgtgtgtccctgcggc..........actgttaaaaaaaaaaaa 2452

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0

Searched :        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09945326/runat_02052005_135411_22364/app_query.fasta_1.4686
-DB=PIR -QFMT=faEtan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN_1_1.225 @runat_02052005_135411_22364 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
          1: pir1:*
          2: pir2:*
          3: pir3:*
          4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3149	69.9	621	2	JC7892	acyl-CoA dehydroge
2	1365	30.3	655	2	A54872	acyl-CoA dehydroge
3	1321	29.3	655	2	S54183	acyl-CoA dehydroge
4	1210.5	26.9	613	2	T15905	hypothetical prote
5	821	18.2	594	2	F84085	butyryl-CoA dehydr
6	815.5	18.1	594	2	C70021	butyryl-CoA dehydr
7	711.5	15.8	650	2	A70817	probable fadE10 pr
8	699	15.5	382	2	B87302	acyl-CoA dehydroge
9	691.5	15.4	384	2	B83443	probable acyl-CoA
10	690	15.3	379	2	G84124	acyl-CoA dehydroge
11	682	15.1	378	2	D69658	acyl-CoA dehydroge
12	682	15.1	381	2	AC3556	butyryl-CoA dehydr
13	678	15.1	381	2	B87472	acyl-CoA dehydroge
14	658	14.6	380	2	F84124	acyl-CoA dehydroge
15	652.5	14.5	379	1	S55421	acyl-CoA dehydroge
16	652	14.5	387	2	D75417	acyl-CoA dehydroge
17	648	14.4	379	2	T45286	butyryl-CoA dehydr
18	644	14.3	456	2	AF3637	butyryl-CoA dehydr
19	630	14.0	389	2	C70979	probable fadE25 pr
20	629.5	14.0	381	2	E75458	acyl-CoA dehydroge
21	626	13.9	380	2	F98299	probable acyl-CoA
22	626	13.9	380	2	A12983	acyl-CoA dehydroge
23	625.5	13.9	379	2	T47262	butyryl-CoA dehydr
24	625.5	13.9	379	2	F97233	butyryl-CoA dehydr
25	617.5	13.7	387	2	A83393	probable acyl-CoA
26	615	13.7	419	2	T15088	hypothetical prote
27	613	13.6	380	2	T44811	acyl-CoA dehydroge
28	611.5	13.6	402	2	D69530	probable acyl-CoA
29	610.5	13.6	381	2	B83791	butyryl-CoA dehydr
30	609	13.5	389	2	B87001	probable acyl-CoA
31	606	13.5	380	2	G69893	butyryl-CoA dehydr
32	604	13.4	432	1	A55680	acyl-CoA dehydroge
33	603.5	13.4	375	2	F83326	probable acyl-CoA
34	594.5	13.2	422	2	H75382	acyl-CoA dehydroge
35	593	13.2	397	2	B69378	probable acyl-CoA
36	588.5	13.1	398	2	B75411	acyl-CoA dehydroge
37	587.5	13.0	423	2	A37033	isovaleryl-CoA deh
38	586	13.0	397	2	H84225	isovaleryl-CoA deh
39	585.5	13.0	382	2	AE3492	isovaleryl-CoA deh
40	585.5	13.0	424	1	C34252	isovaleryl-CoA deh
41	583	12.9	412	2	A30605	acyl-CoA dehydroge
42	579	12.9	412	2	B30605	acyl-CoA dehydroge
43	579	12.9	412	2	T16568	hypothetical prote
44	576.5	12.8	421	2	AD2984	acyl-CoA dehydroge
45	576.5	12.8	421	2	C98299	probable acyl-CoA

ALIGNMENTS

RESULT 1.
JC7892
acyl-CoA dehydrogenase (EC 1.3.99.3) - 9 - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C;Accession: JC7892
R;Zhang, J.; Zhang, W.; Zou, D.; Chen, G.; Wan, T.; Zhang, M.; Cao, X.
Biochem. Biophys. Res. Commun. 297, 1033-1042, 2002
A;Title: Cloning and functional characterization of ACAD-9, a novel member of human acyl-
A;Reference number: JC7892; MUID:22246103; PMID:12359260
A;Accession: JC7892
A;Molecule type: mRNA
A;Residues: 1-621 <ZHA>
A;Cross-references: UNIPROT:Q9H845; GB:AF327351
C;Experimental source: Dendritic cells
C;Comment: This enzyme, which belongs to a family of mitochondrial enzymes that catalyzes
-long-chain acyl-CoA and has specific activity toward palmitoyl-CoA (C16:0).
A;Genetics:
A;Gene: acad-9
A;Map position: 3q26
C;Keywords: oxidoreductase

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Alignment Scores:
Pred. No.:              1.98e-196       Length:           621
Score:                  3149.00         Matches:          620
Percent Similarity:     99.84%          Conservative:     0
Best Local Similarity:  99.84%          Mismatches:       1
Query Match:            69.92%          Indels:           0
DB:                     2               Gaps:             0

US-09-945-326-1 (1-2452) x JC7892 (1-621)

Qy   67 ATGAGCGGCTGCGGGGCTCTTCCTCGCACCACAGGCTGCTGCGCTGCCTCGCCGGGGTCTG 126
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Db    1   MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaArgAlaCysArgGlyLeu  20

Qy  127 GTGGTCTCTACCGGCGAACCCGGCGGCTACTGCGCACCAGCCGCCGCCGCCTGCAGAGCTTTCGCC 186
         |||||||||||||||||||||||||||||||||||
```

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Db    21  ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla  40

Qy   187  AAAGAGCTTTCCTAGGCAAAATCAAGAGAAGAAGAGAGCTTTCCCAATTTCCAGAAGTTAGC  246
               ||||||||||||||||||  |||||||||  |||||||||
Db    41  LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer  60

Qy   247  CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA  306
               ||||||||||||||||||  ||||||||  |||
Db    61  GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu  80

Qy   307  GAGGTGACTCCCGAAAAATTGACCAGGAAGGGAAAATCCAGATGAAACTTTGGAGAAA  366
               ||||||||||||||||||||||||||||  ||||
Db    81  GluValAspSerArgLysIleAspGlnGlnGlyLysIleProAspGluThrLeuGluLys  100

Qy   367  TTGAAGAGCCTAGGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGGCTTC  426
               ||||||||||||  ||||||||||||||||||
Db   101  LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe  120

Qy   427  TCCAACACCATGACTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCACTGTG  486
               ||||||||||||||||||||||||||||
Db   121  SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal  140

Qy   487  ACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGATCATCTTGGCTGCTGGCACTGAGGAG  546
               ||||||||||||||||||||||||||||||||
Db   141  ThrLeuAlaAlaHisGlnAlaIleAlaGlyLeuLeuLysGlyIleIleLeuAlaGlyThrGluGlu  160

Qy   547  CAGAAAGCCAAATACTTGCCTAAACTGGCTCCGGGGAGCACAATTGCAGCCTTCTGCCTC  606
               |||||||||||||||||||||||||||||||
Db   161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu  180

Qy   607  ACGGAGAAGCACTACATCCTCAAGTGCTGATTACTAATGGAGGACTGGCC  666
               |||||||||||||||||||||||||||||||||
Db   181  ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu  200

Qy   667  GACAAGAAGCACTACATCCTCAAGTGCTGATTACTAATGGAGGACTGGCC  726
               ||||||||||||||||||||||||||||||
Db   201  AspLysLysHisTyrIleLeuLysTrpIleThrArgAsnGlyGlyLeuAla  220

Qy   727  AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATCAGTGAAAGAC  786
               ||||||||||||||||||||||||||||||
Db   221  AsnIlePheThrValPheAlaLysThrGluValAspIleLeuAspGlnSerValLysSerVal  240

Qy   787  AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAA  846
               |||||||||||||||||||||||||
Db   241  LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGluGlu  260

Qy   847  GATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA  906
               ||||||||||||
Db   261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle  280

Qy   907  CCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGCCATGAACATCCTC  966
               ||||||||||||||||
Db   281  ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValProMetAsnIleLeu  300

Qy   967  AACAGCGGCCGGTTCAGCATGGGCATGGGTTCGTCGTGCTGCTCAAGAGATTGATTGAA  1026
               ||||||||||||||||||||||||||||
Db   301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu  320

Qy  1027  ATGGCTGCGAGTACGCCGTGCCACAGGAAAACAGTTAACAAGAGGCTCAGTGAATTTGGA  1086
               |||||||||||||||||||||||||||
Db   321  MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly  340

Qy  1087  TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTACGGAGAGTATGACC  1146
               ||||||||||||||||||||||||||||||
Db   341  LeuIleGlnGluLysPheAlaLeuMetAlaGlnArgLeuLysAlaGlnArgMetThr  360

Qy  1147  TACCTCACAGCAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCATCGAGGCAGCC  1206
               ||||||||||||||||||||||||||||
Db   361  TyrLeuThrArgAlaGlyMetLeuAspGlnProGlyPheProAlaAspCysSerValAlaAla  380

Qy  1207  ATGTGAAGGTGTTCAGCTCCGAGGCCGCTGCAGTGTGTGAGTGAGGCGCTGCAGATC  1266
               |||||||||||||||||||||||||
Db   381  MetValLysPheSerGluAlaAlaAlaTrpGlnCysValSerGluValLeuGlnIle  400
```

```
Qy  1267  CTCGGGGGCTTGGCTCACACAAGGACTATCCGTACCAAGGCCATACTGCCGTGACACCCGC  1326
               |||||||||||||||||||||||||||
Db   401  LeuGlyGlyLeuGlyTyrLeuGlyTyrProTyrGluArgIleLeuArgAspThrArg  420

Qy  1327  ATCCTCCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT  1386
               |||||||||||||||||||||||||
Db   421  IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly  440

Qy  1387  CTGCAGCATGCGGCCGCCATCCTGACTACCAGGATCCATCATGAGCTTAAACAGGCCAAAGTG  1446
               |||||||||||||||||||||||||
Db   441  LeuGlnHisAlaGlyAlaArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal  460

Qy  1447  AGCACAGTCATGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCCAACTGTGGAC  1506
               ||||||||||||||||||||||||||
Db   461  SerThrValMetAspThrValGlyArgLeuArgLeuArgAspSerLeuGlyArgThrValAsp  480

Qy  1507  CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAG  1566
               ||||||||||||||||||||||||||
Db   481  LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys  500

Qy  1567  TTTGAGGAGACACACTTACCTGCTTGGCCGGACCGTGGAGACACTGCTGCTCCGGTTTGGC  1626
               ||||||||||||||||||||||||||
Db   501  PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly  520

Qy  1627  AAGACCATCATGAGGAGCAGCTGGTACTGGAAGCGGGTGGCCAACATCCTCATCAACCTG  1686
               |||||||||||||||||||||||||||
Db   521  LysThrIleMetGluGluGlnLeuGlnLeuLeuLysArgValAlaAsnIleLeuIleAsnLeu  540

Qy  1687  TATGGCATGACGGCCGTGCTGTCCGCGGCCATTCCGATCCGCTCCGTGGGCTCCGCAAC  1746
               |||||||||||||||||||||||||||
Db   541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgGlyAsn  560

Qy  1747  CACGACCACGAGGTTCTTCTTGCCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC  1806
               ||||||||||||||||||||||||||||
Db   561  HisAspHisGluValLeuLeuAlaAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu  580

Qy  1807  TTCAGCCTCTCCAGCTGACAAGTAGTGCTCCAGAAAACCTAGTAGGAGCAGAGTTAAGAGAA  1866
               |||||||||||||||||||||||||||||
Db   581  PheSerLeuSerGlnLeuAspLysLysTyrAlaProGlyAsnLeuAspGlnIleLeuLysLys  600

Qy  1867  GTGTCCCAGCCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTGGACCAGGACA  1926
               ||||||||||||||||||||||||||||||
Db   601  ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProGlyLeuAspArgThr  620

Qy  1927  TGC 1929
          |||
Db   621  Cys 621
```

```
Alignment Scores:

Pred. No.:                              Length:           655
Score:               1.2e-80            Matches:          303
Percent Similarity:  62.77%             Conservative:     110
Best Local Similarity: 46.05%           Mismatches:       202
```

```
Query Match:   30.31%      Indels:   43
DB:            2            Gaps:     13

US-09-945-326-1 (1-2452) x A54872 (1-655)

Qy    30  GGGAGACTGAGGCTGGGG---AACATCGGCAGCATGAGCGGCTCGGGGTCTT   86
          ||||||||||||||||       :: ||||||   |||::
Db    11  GlyArgGlnLeuLeuArgLeuGlyAlaArgSerSerAlaAlaLeuGlnGlyGln   30

Qy    87  CCTCGGCACCACGGCGTCGCGGCTCGTGCCTGCCGGGTCTGGTCTCCACCGCAACCG   146
          |||||||::|||||  |||           :::
Db    31  Pro-ArgProThrSerAlaGlnArg--------LeuTyrArgAlaSerGluAlaThrGl   46

Qy   147  GCGGCTACTCGCGC----                 -ACCAGCCCGCCTGT   173
          : |||||:||                          ||
Db    46  nAlaValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl   66

Qy   174  ACGAGCT----------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGA   221
          ||      ||||||      :::|||  |||
Db    66  aArgAlaGluSerLysSerPheAlaValGlyMetPheLysMetLysGlnLeuThrAspGl   86

Qy   222  AGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAACCTAATGA----------AT   266
          :|||||||::||    |||                              :
Db    86  nValPheProTyrProSerVal--------LeuAsnGluGlyLyGlnThrGlnPheLe   102

Qy   267  CAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAGAGAGGTGGACTCCGAAAAAT   326
          :     ||||||||  :||||| ||:       :::::|||
Db   102  uLysGluLeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaLysAs   122

Qy   327  TGACCAGGAGGGGAAATCCCAGATGAAATTTGAGAAAATTGAAGAGCCTAGGGCTTTT   386
          |||             ||||:   |||||||||
Db   122  nAspSerLeuGlyLeuValGluGluAspThrLeuGlnLeuLeuLysGluGluValAlaPh   142

Qy   387  TGGGCTGCCAAGTCCCAGAAGAATATGGTGCCTGGCTTCTCCAACACCATGTACTCAAG   446
          ||||||||||:::||||         :::||
Db   142  eGlyLeuGlnValProSerGluGlyLeuGlyLeuLysLeuGlyLeuProSerSerGl   162

Qy   447  ACTAGGGGAGATCATCAGCATG---GATGGCTCCATCACTGACCCTGGCAGCCACCA   503
          ||||||||                  :::||||
Db   162  gLeuAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGl   182

Qy   504  GGCTATTGGCTCAAGGGGATCATCCTGGCTGCGGCCACTGAGGACAGAGAAAGCCAAATACTT   563
          |::||||||    ||||||||||:::
Db   182  nSerIleGlyPheLysGlyIleLeuLeuAlaAlaAlaThrGluAspArgGluLysGlnLysTyrLe   202

Qy   564  GCCTAAACTGGCGTCCGGGAGCACCATTGCAGCCTTCTGCCTCACGGAGCCCAGTGG   623
          ||::||||||:::||||  |||           :::::|||
Db   202  uProArgAlaValAlaSerGlyGlnLeuAlaAlaPheCysLeuThrGluProSerGl   222

Qy   624  GAGGCATGGCAGCTCAATCCGGGAGCAGAGCCCACACTAAGTGAAGACAAGAAGCACTACAT   683
          ||||||||      ||||:::||
Db   222  yAspValAlaSerIleArgSerSerAlaValProSerProCysSerGlyTyrTyrTh   242

Qy   684  CCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTTACTGTGTT   743
          ||:||||||:::|||||    ||||||
Db   242  rLeuAsnGlySerLysTrpIleLeuSerAsnGlyGlyValLeuAlaAspIlePheThrValPh   262

Qy   744  TGCAAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGAGAAATCACAGCATT   800
          |||||||||||||::::                    :::
Db   262  eAlaLysThrProIleLeuAspAlaAlaThrGluAsnValAlaVallLeuThrAlaPh   282

Qy   801  CATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCAT   860
          ||||||||||||||||  ||||||        :::::
Db   282  ySerAspValAlaSerIleArgSerSerAlaValProSerProCysSerGlyTyrTyrTh   242

Qy   861  TCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCACCAGATACCTGTGGAAAACAT   920
          |:::||||||||||||::|||
Db   302  eLysAlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnVa   322

Qy   921  CCTTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGGCCGTT   980
          |:::|||||||||||||||::||||||||||
Db   322  lLeuGlyGlyValGluGluAspGlyPheLysProGlyAspLysValAlaAlaAsnGlyArgPh   342
```

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Qy   981  CAGCATGGCAGCCGTCGTGGCTGGGTGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTA  1040
          |||               :::||||| |||||||      :::::||
Db   342  eGlyMetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleIleGluAlaLysAlaAspHi   362

Qy  1041  CGCCTGCACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAA  1100
          |||||||        :::|||||||      ||||||||
Db   362  sAlaThrArgThrGlnPheGlyLysValIleGlnGluGluLy   382

Qy  1101  ATTTGCACTGATGGCTCAGAGGCTTACGTCATGGGAGTATGACCTACCTCACAGCAGG  1160
          |||||||||        ||||||| :::
Db   382  sLeuAlaArgMetAlaIleLeuLeuTyrValThrGluSerMetAlaTyrMetLeuSerAl   402

Qy  1161  GATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGCGGCAGCCATGGTGAAGGTGTT  1220
          :::|||||||  :::||||          ||||||||
Db   402  aAsnMetAspGln----GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePh   421

Qy  1221  CAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGGCGTGAGGGTGGTCCCGGGGGCTTGGG  1280
          |        ||||||||    ||||:::||||||||
Db   421  eGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetGl   441

Qy  1281  CTACACAAGGGACTATCGTACGAGCCGCATACTGGTGACACCGCATCCTCCTCATCTT  1340
          ||:::      :::|||||||||||:::|||||
Db   441  yPheMetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePh   461

Qy  1341  CGGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCCTGACGGGTCTCCAGCCATGCCGG  1400
          |||||||||||||:::|||||          :::|||||||
Db   461  eGluGlyThrAsnAspIleLeuArgLeuPheAlaAlaLeuGlyLeuGlyCysMetAspLysGl   481

Qy  1401  CCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGT  1454
          ||:::|||||||||||      ||||||          :::||||||
Db   481  yLysGluLeuThrGlyLeuGluGlyAsnAlaLeuLysAsnProLeuGlyLeuLeuLeu   501

Qy  1455  CATGGATACCGTTGGCCGGAGCCTTCCCAAGCTTCCCTGGGCCGAACTGGACGCTGGGGCT  1514
          ||:::           :::||||||||||||
Db   501  uIleGlyGluGluLysLysGlnLeuArgLeuArgArgThrGlyIleGlyGlyGlyLeuSerLe   521

Qy  1515  GACAGGCAACCATGAGTTGTGCACCCCAGTGCTTGCCGGACAGTGCCAACAAGTTTGAGGA  1574
          ||:::                :::||||||||
Db   521  uSer--------GlyIleValHisProGluLeuSerGlyArgSerGlyGluLeuAlaValGl   538

Qy  1575  GAACACCACCTGCTTCCGGCCGATGACGCTGCTCCGCTTTGGCAAGACCAT  1634
          |||||||||||::: |||||||||
Db   538  nAlaLeuGluGlnPheAlaIleThrValGluValGluLysLysMetLysHisGlyIl   558

Qy  1635  CATGGAGGAGCAGCTCGTACTGAAGCGGGTGCCAACATCCTCATCAACCTGTATGGCAT  1694
          ||:::||||||||      :::||||||||
Db   558  eValAsnGluGlnPheLeuLeuLeuGlnArgLeuLeuAspGlyAlaIleAlaAspLeuTyrAlaMe   578

Qy  1695  GACGGCCGTGCTGTCGCGGGACAAGAGCCTCATCCGCATTGGGCTCCGCAACCACGACCA  1754
          |||||||||||::::||||||
Db   578  tValValLeuSerArgAlaSerArgLeuSerGluGlyTyrProThrAlaGlnHi   598

Qy  1755  CGAGGTTCTCTTGGCCAACACCTTCTGCTGGAAGCT-----TACTTGCAGAATCT  1805
          ||:::           ||||||           :::|||||||
Db   598  sGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMe   618

Qy  1806  CTTCAGCCTCTTCAGCTGGACAAGTATGCTCCAGAAAACCTAGAGCAGATTAAGAA  1865
          |:::            :::      ||:::
Db   618  tAlaSerLeuGlnSerAsnProGln--------GlnGlnGluLeuProheArgAsnPheArgSe   636

Qy  1866  AGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTCCCAACCTCTG  1917
          |:::||||||||          :::
Db   636  rIleSerLysAlaMetValGluAsnGlyValGlyLeuValThrSerAsnProLeu   653
```

RESULT 3
S54183

acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain specific - human
C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S54183
R;Andresen, B.S.
submitted to the EMBL Data Library, April 1995
A;Reference number: S54183

A;Accession: S54183
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-655 <AND>
A;Cross-references: UNIPROT:P49748; EMBL:X86556; NID:g790446; PID:g790447
C;Genetics:
A;Gene: GDB:ACADVL; VLCAD
A;Cross-references: GDB:1248185; OMIM:201475
A;Map position: 17p11.2-17p11.1
C;Keywords: oxidoreductase

Alignment Scores:

Pred. No.:	8.62e-78	Length: 655
Score:	1321.00	Matches: 297
Percent Similarity:	61.52%	Conservative: 109
Best Local Similarity:	45.00%	Mismatches: 213
Query Match:	29.33%	Indels: 41
DB:		Gaps: 13

US-09-945-326-1 (1-2452) x S54183 (1-655)

```
Qy    21  GCTAAGAAGGGGAGACTGAGGCTGGGAGGCTGAGCTGGGGAACATCGGGCAGCATGACGGCTGCGG    80
              ||||  |||||  ||||||||  ||||||||  ||     ||||||
Db     8  AlaSerLeuGlyArgLeuArgLeuGly------GlyGlySerSerArgLeuThr    25

Qy    81  GCTCTT------------CCTGCGCCACCGGCTCGCCGGCTCGTCGTGCCTGCCG   119
              |||||:                                     :||||||||
Db    26  AlaLeuLeuGlyGlnProArgProGlyProAlaArgArg---------Pro    39

Qy   120  GGGTCTCGGTGGTCTC-----------------TACCGGAACCGGCGG   149
              ::||||                                ::
Db    40  TyrAlaGlyGlyValAlaAlaGlnLeuAlaLeuAspLysSerAspSerAspAla    59

Qy   150  GCTACTGCGCACCAGCCCGCC-------TGTACGGAGCTTTCGCCAAAGAGCTTTTCCT   200
              ||||  ||||||:|:||||                ::||||||||
Db    60  LeuThrArgLysProAlaLysAlaGluSer-LysSerPheAlaValGlyMetPheLy    79

Qy   201  AGGCAAAAATCAAGAAGAAAGAAGAGTTTTCCATTTCCAGAGTTAGCCAAGATGAACTTAA   260
              ||||||||||||||||                   :::||
Db    79  sGlyGlnLeuThrArgAspGlnValPheProTyrProSerValLeuAsnGluGlnInTh    99

Qy   261  TGAA--ATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGGTGGACTC   317
              :  :::  ||||  :: ||||||   ||||||||   ::||||
Db    99  rGlnPheLeuLysGluLeuValGluProValSerArgPhePheGluGluValAsnAspPr   119

Qy   318  CCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAAACTTTGAGAAATTGAAGAGAGCCT   377
              ||||||||||||||:     :: :  || :||:||||||
Db   119  oAlaLysAsnAspAlaLeuMetValGluThrThrArgPheGluPheGlnLysLysGluLe   139

Qy   378  AGGGCTTTTGCCTGCAAGCTGCTGCAAGAATATGGTGGCCTTCTCCAACACCAT   437
              :|||||||||||||  ||||||||||||||||||||||
Db   139  uGlyAlaPheProLysLeuAlaSerGlyValGlyValGlyValLeuCysAsnThrGl   159

Qy   438  GTACTCAAGACTAGGGGGAGATCATCAGCATG--GATGGGTCCATCACTGACCCTGGC   494
              :: ||||||||||||||  :: :||||||||  ||| |||||
Db   159  nTyrAlaArgLeuValGluIleGlyMetHisIleAspLeuValGlyIleThrLeuGl   179

Qy   495  AGCGCCACCAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGACAGAAAGC   554
              |||||||||||||||||||||:  :||||||  ||:
Db   179  yAlaHisGlnSerIleGlyPheLysGlyIleIleLeuAlaGlyThrLysAlaGlnSerGl   199

Qy   555  CAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGAGCCTTCTGCCTCACGGAGCC   614
              :::||||||||||||||||||||||||||||  ||||
Db   199  uLeuTyrProLysLeuAlaSerGlyValGlyThrValAlaAlaAlaPheCysLeuThrGlu   219

Qy   615  AGCCAGTGGGAGCCGGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAA   674
              |||||||||||||||||||||||||||||  :: |||||
Db   219  oSerSerGlySerAspAlaAlaSerIleArgThrSerAlaAlaProSerProCysGlyLy   239

Qy   675  GCACTACATCCTCAATGGCTCTGGATTACTAATGGACGGACTGGCCAATATTTT   734
              |||||  |||||||||||  :::|||  |||||||||::||||
Db   239  sTyrTyrThrLeuAsnGlySerLysLeuTrpIleSerAsnGlyGlyLeuAlaAspIlePh   259
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```
Qy   735  TACTGTGTTGCAAAGACTGAGGTCGTTGAT---TCTGATGATCAGTGAAGACAAAT   791
              ||||||||||||||||                :::  |||||||||||:|||||
Db   259  eThrValPheAlaLysThrProValThrAspPro-ValAlaValLysGluLysLySIl   279

Qy   792  CACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAAGATAA   851
              |||||||||||||||||||||||||||||||::|||||||
Db   279  eThrAlaPheValValGlyArgGlyPheGlyGlyIleThrHisGlyProProGluLySLy   299

Qy   852  ATTAGGCATTCGGGGCTCCAACACTGTGAAGTCCATTTGAAAACACCAGATACCTGT   911
              :::||:|  |||||||::|||||||||||||||||||||||
Db   299  sMetGlyIleLysAlaSerAsnThrAlaGluValPheAspGlyValArgValProSe   319

Qy   912  GGAAAACATCCTTGGAGAGGTCGGAGAGTGGGTTAAGGTGGCCATGAACATCCTCAACAG   971
              |||||||||||||:::||||||||||  ||||||||||||
Db   319  rGluAsnValLeuGlyValGlyValGlySerGlyPheLysGlyValAlaMetHisIleLeuAsnAs   339

Qy   972  CGGCCCGGTTCAGCATGGGCAGCGTCGTGGGTGGCTGCTCAAGAGATTGATTGAAATGAC   1031
              :::||||||||||  ||||||::|:||||||||  ||:||
Db   339  nGlyArgPheGlyMetGlyAlaAlaLeuAlaLeuAlaGlyThrMetArgGlyIleIleGluAlaLysAl   359

Qy  1032  TGCTGAGTACGCCTGCACAAGAAACAGTTTAACAGAGGCTCAGTGAATTTGATTGAT   1091
              :::||  |||||||||||||||||||||||||||||||||||
Db   359  aValAspHisAlaThrAsnArgThrGlnPheGluGluValIleHisAsnPheGlyLeuIl   379

Qy  1092  TCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGAGAGTGATGACCTACCT   1151
              |||||||||||  |||  ||||||  |||||||||||||||||
Db   379  eGlnGluLysGluLeuAlaArgMetValMetLeuGlnTyrValThrGluSerMetAlaTyrMe   399

Qy  1152  CACAGCAGGGATGCTGACCAACACCTGGCTTTCCCGACTGCTCCATCGAGGGCAGCCATGGT   1211
              |||||||||||||||  ||||||||  ||  :::||
Db   399  tValSerAlaAsnMetAspGln---GlyAlaThrAspPheGlnIleIleAlaAlaIleSe   418

Qy  1212  GAAGGTGTTCAGCTCCGAGGCCGCCGCCCAGTGTGTGAGGCCGTCGAGATCCTCGG   1271
              ||||||||||||||||||:|||||||                :::||||||
Db   418  rLysIlePheGlySerGluAlaLeuAlaTrpLysValThrAspGluCysIleGlnInIleMetGl   438

Qy  1272  GGGCTTGGGCTACACAAGGGACTATCCGTACGAGGCCATACTGCGTGACACCCGCATCCT   1331
              ||||||||||||||||||  :::: :::||||||
Db   438  yGlyMetGlyPheMetLysGluProGlyAlaValLeuArgValLeuArgAspHisArgIlePh   458

Qy  1332  CCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGGTCTGCA   1391
              ||:  |||||||||||||  :::|||||||||
Db   458  eArgIlePheGluGlyThrAsnGluIleLeuArgLeuTyrIleAlaLeuGlnGlyCysMe   478

Qy  1392  GCATGGCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG-----GCCAAAGT   1445
              |||||||                                  ||||||
Db   478  tAspLysArgProHisLeuSerAlaLeuAsnLysGlyLeuAsnAl   498

Qy  1446  GAGCACAGTCAGTCATGATACCGTTGGCGGAGGCTTCGGGAGCCTCCCTGGCCGAACTGTGGA   1505
              ||||||||||||||||||||||||  |||||:||||||||||
Db   498  aGlyLeuLeuLeuGlyLeuGlnLeuGlnArgArgArgAlaGlyLeuGlySerGl   518

Qy  1506  CCTGGGGTCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTCGCGACAGTGCCAACAA   1565
              ||  ||||||||||||||||||||||||  :: :::||||
Db   518  yLeuValHisProGluLeuSerArgSerGlyGluGlu   535

Qy  1566  GTTTGAGGAGAACACCTACTGCTTCGGCGACCGTGGAGCACTGCTGCTCCGCTTGG   1625
              ||||||||||||||  |||||||:||||||||
Db   535  uAlaValArgAlaLeuGluGlnGluPheAlaThrValGluGlnPheThrLysAlaGlnIleLysLysHisLy   555

Qy  1626  CAAGACCATCATGAGGAGGAGCCAGTGGTACTGAGCGGGTGGCCAACATCCTCATCAACCT   1685
              ||||||:   :||||||||||||  ||||||||
Db   555  sLysGlyIleValAlaAsnGluLeuArgLeuArgLeuGlyLeuAlaIleAspAsppLe   575

Qy  1686  GTATGGCATGACGGCCGTGCTGTCGGAGCCCGCCATTGGGCTCCGCAA   1745
              ||||  ||||||||||||||||||||||||
Db   575  uTyrAlaMetValValLeuSerArgAlaSerLeuSerGlyArgGluGluHisProTh   595

Qy  1746  CCACCACCACGAGGTTCTTCTGGCCAAGACACTTCTCCGTGGAA------GCTTACTTGCA   1799
              ||||||||||||||:   :::|||||                :::||||
Db   595  rAlaGlnHisGluLysMetLeuCysAspThrTrpCysIleGluAlaAlaAlaArgIleAr   615

Qy  1800  GAATCTCTTCAGCTCTCCTCAGCTTGGACAAGTATGCTCCAGAAAAACCTAGAGAGCAGAT   1859
```

```
Db  615  :gluGlyMetAlaAlaLeuGlnSerAspProTrpGlnGlnGlu---LeuTyrArgAsnPh  634
              :::              |||              :::         |||
Qy 1860  TAAGAAAGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCACCCTCTG   1917
         :::|||||||   ::||||    |||   ::: ||  :::::||||||
Db  634  eLysSerIleSerLysValGluValGlyValValThrSerAsnProLeu  653

RESULT 4
T15905
hypothetical protein E04F6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R;Pauley, A.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z18427
A;Accession: T15905
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-613 <PAU>
A;Cross-references: UNIPROT:Q19057; EMBL:U28943; NID:g861333; PID:g861335; PIDN:AAA68357
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:E04F6.5
A;Introns: 55/3; 90/2; 195/3; 233/3; 472/2; 518/1; 567/3

Alignment Scores:
Pred. No.:
Score:                    1210.50           Length:          613
Percent Similarity:       61.16%            Matches:         272
Best Local Similarity:    43.66%            Conservative:    109
Query Match:              26.88%            Mismatches:      205
DB:                                         Indels:           37
                                            Gaps:              2

US-09-945-326-1 (1-2452) x T15905 (1-613)

Qy   85  TTCCTGCGCACCACGGCTGGCCGGCTCGCCTGCCGCGGGGTCGGTCGTGTGTCTCTACCGCGGAAC   144
             :::|||              :::
Db   16  PheIleArgLeuSerHisSerAlaAlaAlaAlaLys---------AspAlaLysPro  31

Qy  145  CGGCCGCTACTGCGCCACCAGCGCCGCCTGTACGAGCGTTTCGCAAAGAGCTTTCCTAGGC   204
         ::::::::::   |||:::              :::|||
Db   32  LysLysValAlaAlaAlaAspValAlaSerPro------SerPheValMetAsnLeuArgAsnLeuPheArgArgGly  49

Qy  205  AAAATCAAGAAGAAAGAAGAAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA   264
            :::||||||||||:::|||
Db   50  LysAlaValThrArgAspGlnValPheProTyrProLeuAsnMetThrAspGluGlnLysGlu  69

Qy  265  ---ATCAATCAGTTCTTGGGACCCTGGAAAAATCTTCACTGAGAGAGGTGGACTCCCGA   321
                :::       :::|||||||
Db   70  ThrLeuGlyMetValMetSerProLeuGluLysMetSerValGluValGluAlaAlaAsnAspValVal  89

Qy  322  AAAATTGACCAGGAAGGGAGAAATCCCAGTGAAACTTTGGAGAAATTGAACAGGCCTAGGG   381
         |||:::||||||              :::|||
Db   90  LysAsnAspGluThrSerAspIleProArgAlaValLeuAspGlnPheLysAlaValLeuGluLeuGly   109

Qy  382  CTTTTTGGGCTGCAAGTCCAGAAGAAGAATATGGTGCCTGGCTTCTCCAACACCATGTAC   441
         ||||||   :::|||||||   :::||:::
Db  110  ThrPheGlyValLeuValProProGluLeuGlyTyrSerGlyLysPheAsnAsnSerGlnMet   129

Qy  442  TCAAGACTAGGGGAGATCATC---AGCATGGATGGTTCCATCACTGTGACCCTGGCAGCG   498
            :::||||||||||||:::||||||
Db  130  AlaArgValAlaGluIleValGlyAlaTyrAspGlyLeuuGlyPheAspGlyLeuValMetGlyAla   149

Qy  499  CACCAGGCTATTGGCTCAAGGGATCATCTTGGCTGGCACTCTGGACGAGACAGAAAGCCAAA   558
         :::|||:::||||||   |||::::::||||||
Db  150  HisGlnSerIleGlyTyrLysGlyLeuLeuLeuGluGluGlyPheArgLysHisAspAlaAlaGlnIleLysLys   169

Qy  559  TACTTGCCTAAACTGGCTGCGGTCCGGGGAGCCACATTGGAACCGCCTCTGCCTCACGGAGCCAGCC   618
         ||||||||||||   :::|||   |||||||:::
Db  170  TyrLeuProAspLeuAlaThrGlyLysArgLysGlyPheAlaLeuThrAlaPheAlaLeuuThrLeuuThrProThr   189

Qy  619  AGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCCACCACTAAGTGAAGACAAGAAGCAC   678
         :::|||||||||||||||||||||||||||:::|||
Db  190  ThrGlySerAspAlaSerValArgThrArgAlaGluLeuSerAlaAspGlyLysHis   209

Qy  679  TACATCTCAATGGCTCCAAGGTCTGATTACTAATGGAGGACTGGCCAATATTTTACT   738
         |||:::|||||||   :::|||||||   :::||||||||
Db  210  TyrValLeuAsnGlyGlyLysIleTrpIleSerGluAsnGlyPheAlaAspValPheThr   229

Qy  739  GTGTTTGCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGACAAAATCACAGCA   798
         |||||||   :::|||||||||   ||
Db  230  ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysAspLysMetSerAla   249

Qy  799  TTCATAGTAGAAAGAGACTTGGTGGAGTCACTAATGGAAACCCGAGATAAATTACGC   858
         |||:::     |||||||||:::||   |||:::   |||
Db  250  PheIleValGluArgAlaPheGlyGlyValThrSerGlyTyrProGlnGluGlyLysMetGly   269

Qy  859  ATTCGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAC   918
         |||:::||||||   |||||||   :::|||   :::|||
Db  270  IleLysGlySerAsnThrThrGluValHisPheAspAsnLeuLysIleProValGluAsn   289

Qy  919  ATCCTTGGAGAGTCGGAGATGGTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGg   978
         :::||||||:::   |||:::|||||||:::
Db  290  LeuLeuGlyLysGluGlyGlyGluGlyPheLysGlyPheLysValAlaAlaMetAsnIleLeuAsnAsnGlyArg   309

Qy  979  TTCAGCATGGGCAGCCGTCGTGGCTGGCGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAG  1038
         :::|||:::   |||::::::
Db  310  PheGlyTyrIleProAlaAlaCysThrGlyAlaMetLysHisCysIleGlnLysThrValAsp   329

Qy 1039  TACGCCTGCACAAGGAAACAGTTAACAAGAGGCTCAGTGAATTGGATTGATTCAGGAG  1098
         :::|||   |||||||:::
Db  330  HisIleThrThrArgValGlnPheGlyLysLeuGlnPheGlyAsnIleGlnGluGlu   349

Qy 1099  AAATTGCACTGATGGTCAGAGAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCA  1158
         |||   |||:::   |||   |||   |||:::
Db  350  LysLeuValGluMetIleSerLysSerLeuTyrArgAlaThrGluSerIleValTyrMetLeuSer   369

Qy 1159  GGGATCGTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCCATGGTGAAGGTG  1218
         :::|||:::
Db  370  SerAsnMetAspArg---GlyTyrLeuLysGluTyrGlnIleuGlnIleuAlaIleGlyLysLysVal   388

Qy 1219  TTCAGTCGAGGCCGCTGGACGTGTGAGTGAGTCGCTGCGTGAGGCCGTCGAGGGGCTTG  1278
         :::|||||||   :::
Db  389  LeuAlaSerGluAsnAlaTrpIleuLeuValCysAspSerAspAlaIleGlnValHisGlyIleyMet   408

Qy 1279  GGCTACACAAGGGACTATCCGTACGAGGGCATACTGCCTGCGACACCCGATCCTCCTCATC  1338
         :::   |||   :::|||||||   |||
Db  409  GlyPheMetArgGluThrGlyLeuLeuValArgArgLeuAspProLeuuArgLeuuArgIleArgIle   428

Qy 1339  TTCGAGGGAACCAATGAGATTCTTCACTGAGAGGTGGACTCCCGA  1398
         |||:::|||||||   ||
Db  429  PheGluGlyLeuAlaAsnAspValLeuArgLeuPheIleAlaLeuThrArgValAlaGlnHisAla   448

Qy 1399  GGGCCGATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTCATG  1458
         |||:::
Db  449  GlyLys---------HisLeuAlaGluGlnAla------SerGlyValGly   460

Qy 1459  GATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGACCTGGGCTGACA   1518
         :::
Db  461  GlyLeuIleGlyLeuAlaValSerArgValThrGly---------GlyAsnThr   475

Qy 1519  GGC---AACCATGGA--GTTGTGCACCCCAGTCTTGCCGACAGTGCCAACAAGTTTGAG   1572
         |||:::    :::|||||||
Db  476  GlySerAsnPheGlyIleValValAlaAspSerAlaSerLeuGlnAspSerAlaLeuValLeuAsp   495

Qy 1573  GAGAACACCTACTGCTTGGCTACGGAGCGGGTGGCCAACATCCTCGCCTTTGGCAAGACC   1632
         ::   :::
Db  496  GlnGlnIleAlaLeuPheGlyGlnThrValGlnLeuLeuLeuMetLysHisLysLysGly   515

Qy 1633  ATCATGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTCTATGGC   1692
         ::
Db  516  IleIleAspArgGlnTyrGluMetHisSerArgValAlaAspAlaAlaIleAsnIleTyrSer   535

Qy 1693  ATGACGGGCCGTGCGTCGCGGGAACCGGCCAGCCGCCTCCATCCGACCACGAC   1752
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Db   127 GlyAlaAsnGluAspGlnLysLysLysTyrLeuProAspLeuAlaThrGlyAlaArgIleAla  146
         |||        ||||:::|||||||
Db   555 SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLeuLysAsnLysSerSerAlaAsp

Qy   595 GCCTTCTGCCTCACCGAGCCCAGTGGGAGCCAGCGATGCAGAATCTCTTCAGC 654
         ||||||||||||||||||||          |||:::|||
Qy  1753 CACGAGGTTCTTCTGCCAACACCTTCGTCTTGGGAAGATCTTCAGC  1812

Db   147 AlaTyrAlaLeuThrGluProSerSerGlySerAspAlaLeuGlyAlaLysThrThrAla  166
         :::::            |||:::|||
Db   556 PheGluArgLysValAla---ThrTyrTyrValAspLysAspLysAlaMetLys------Ser  571

Qy   655 ACACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAAT 714
         ||||||||||||||||||||||||||
Qy  1813 CTCTTCAGCTGGACAAGTATGCTCCAGAAAAACCTAGATGAGCAGATTAAGAAAGTGTCC  1872

Db   167 ValLeuAsnGluAlaGlyThrHisTyrValLeuAsnGlyGluLysGlnTrpIleThrAsn  186
         |||:::|||
Db   572 SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAsnAlaSerLysValAlaThr  591

Qy   715 GGAGGACTGGCAATATTTACTGTGTTTGCAAGACTGAGGTGTCGTCGTTGATTCGTGATGAA 774
         ||||||||||||          |||:::
Qy  1873 CAGCAGATCCTTGAGAAGGCAGGCCTATATCTGCC------------------CAC 1911

Db   187 SerAlaPheAlaAspValPheIleValTyrAlaLysIle------------AspGly  201
         :::|||
Db   592 IleGluSerLeuAlaLysGlu------ValCysGlyAsnGlyGlyLeuThrGlnHis  609

Qy   775 TCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAAGACTTGGTGAGTCACTAAT 834
                  :::||||||||||||:::|||
Qy  1912 CCTCTGGAC 1920

Db   202 ------GluHisPheSerAlaPheIleValGluLysAspPheGluGlyValSerThr  218
         |||:::
Db   610 ProValGlu  612

Qy   835 GGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAA 894

Db   219 GlyProGluGluLysGlyMetGlyIleLeuGlySerThrArgThrLeuIleLeuGlu  238

Qy   895 AACACCAAGATACCTGTGGAAAACATCCTTGGAGAGTCGGAGATGGGTTTAAGGTGGCC 954

Db   239 AspAlaLeuValProLysGluAsnIleLeuGlyGluValGlyLysGlyHisValIleAla  258

Qy   955 ATGAACATCTCAACGACGGCCGGTTCAGCATGGGCAGCGTCGTCGTCGGCGTGCTCAAG 1014

Db   259 PheAsnIleLeuAsnAlaGlyArgTyrLysLeuGlyValGlyCysIleGlyGlySerLys  278

Qy  1015 AGATTGATTGAAATGACTGCTGAGTACGCCTGCAAGGAAACAGTTAACAAGGAGGCTC 1074

Db   279 ArgGlyIleGluLeuAlaAlaLysTyrAlaAlaAsnGluArgLysGlnPheLysGlnProIle  298

Qy  1075 AGTGAATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATG 1134

Db   299 AlaLysPheThrLeuIleLeuGlnLysAsnLeuAlaAsnMetAlaValThrTyrThrTyrAlaAla  318

Qy  1135 GAGAGTATGACCTACCTCACCCAGCAGGGATGCTGACCCAA------------------1173

Db   319 GluSerSerIleTyrArgThrGlyGlyLeuPheGluLeuProPheAlaGluTyrArgGlyLeuGlyLeuSerGlu  338

Qy  1174 ------------------CCTGGCTTCCCGACTGCTGCTCCATCGAGGCA  1203

Db   339 GluGlnGlnLysAspGlyArgArgGluValAlaAlaLysLeuAlaIleAlaGluTyrAlaIleAlaGluCys  358

Qy  1204 GCCATGGTGAAGGTGTTCAGCTGCCAGGCCCCTGGCAGTGTGAGTGAGCGCGTCGCAG 1263

Db   359 SerLeuAsnLysValValGlySerGluAlaLeuAspPheValAlaAlaAspGluAlaValGln  378

Qy  1264 ATCCTCGGGGGCTTGGGCTACCACAAGGGACTATCCGTACGCGCCGATACTGCGTGACACC 1323

Db   379 IleHisGlyLyTyrGlyPheMetAlaGluTyrGluValGluArgMetTyrArgAspSer  398

Qy  1324 CGCATCCTCCTCATCTTGAGGGAAGGAAGGAAAATGACCAGGAAGGGAAAATCCCAGATGAA 1383

Db   399 ArgIleAsnArgIlePheGluGlyThrAsnGluIleLeuAsnArgLeuLeuValProGlyThr  418

Qy  1384 GGTCTGCAGCATGCC------GGCCCGCATC---CTGACTACCAGGATCCATGAGCTTAAA 1434

Db   419 IleLeuArgLysAlaGluLysGlyGluLeuProPheLeuGluLeuGlyAlaThrAlaLeuGln  438

Qy  1435 CAGGCCAAAGTGAGCAAGTACAGTCATGAGTCCGGCCGGAGGCTTCGGGACTCCCTGGGC 1494

Db   439 GluGluLeuMetMetLeuMetProGlnValGly------------------450

Qy  1495 CGAACTGTGACCTGGGCTGACAGCAGGCTGACCAGGAGTTGTGTGCACCCCAGTCTTGCGGAC 1554

Db   450 ------------------450

Qy  1555 AGTGCCAACAAGTTGAGGAGGAACACCTACTGCTTCGGCCGAGACCGTGGAGACACTCTG 1614
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RESULT 5

F84085

butyryl-CoA dehydrogenase BH3486 [imported] - Bacillus halodurans

C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84085
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-594 <STO>
A;Cross-references: UNIPROT:Q9K784; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB072
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3486

Alignment Scores:	
Pred. No.:	
Score:	2.35e-45
Percent Similarity:	821.00
Best Local Similarity:	50.00%
Query Match:	33.17%
DB:	18.23%
	2

Length:	594
Matches:	207
Conservative:	105
Mismatches:	210
Indels:	102
Gaps:	13

US-09-945-326-1 (1-2452) x F84085 (1-594)

```
Qy   199 CTAGGCAAAATCAAGAAGAAAGAAGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTT 258
                       :::||||||
Db    16 LeuAspGlyIleLeuAspAspAlaAspLysValPhe------------ThrProIleAspPhe 30

Qy   259 AATGAAATCAATCAGTTCTTGGACCCCGTGGAAAAATTCTTCACT------------303
                       |||          :::|||
Db    31 ThrGluGluHisGluMetIleGlyLysThrThrGluGlyPheValValAlaAsnGluValVal 50

Qy   304 ------GAAGAGGTGGACTCCCGAAAAATGACCAGGAAGAGGGAAAATCCCAGATGAA 354
                   :::|||:::|||:::|||
Db    51 ProValLeuAspGluIleLeuGluAsnHisGlnPheAsp------------IleSerArgArg 66

Qy   355 ACTTTCGAGAAATTGAAGAGCCTAGGGCTTTTTGGGCTGCCAAGTCCCAGAAGAATTATGGT 414
                   |||          |||:::
Db    67 LeuLeuThrGlnIleAlaGlyLeuGluLeuGlyLeuLeuGlyLeuAlaAspProValProGluGluTyrArgGly 86

Qy   415 GGCCTGGCTTCTCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATCAGGATGGG 474
                   |||          |||:::|||
Db    87 GlyLeuGlyLeuAspLysLysSerSerSerIleIleThrGluLysGlyPheSerGluArgAlaGlyGly 106

Qy   475 TCCATCACTGTGACCCTGGCACGCGCCACCAGGCTATTGGCCTCAAGGGGGATCATCTTGGCT 534
                       :::::::|||
Db   107 GlyPheSerLeuSerTyrArgGlyTyrAlaHisValGlyTyrIleLeuGlySerLeuProIleValPhePhe 126

Qy   535 GGCACTCGAGGAGCGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGCA 594
```

```
Db    45  IleGluGlnAspValLeuProHisIle------------------------------------------                         53
Qy   301  ACTGAAGAGGTGGACTCCGAAAAATTGACCAGGAACGGAAAAATCCCAGATGAAACTTG                                     360
              ::::::::::::::::     ::::  :::::::    :::::::
Db    54  ---AspAspIleGluAsnHisGlnPheGluHisSerValArgLeu----------Leu                                     68
Qy   361  GAGAAATTGAAGAGCTAGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGGCTG                                        420
              :::||  |||::|||||:::|||| |||::|||:::  |||::|||
Db    69  LysLysAlaGlyGluLeuGlyLeuLeuGlyAlaAspValProGluGluTyrGlyGlyLeu                                   88
Qy   421  GGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATC                                    480
              ::||||:::| |:| |:|||::|||:::  :::||||||  :::|:|||  :||||
Db    89  GlyLeuAspLysSerAlaAlaIleThrGluLeuThrGluGluArgAlaGlySerPhe                                      108
Qy   481  ACTGTGACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGGCACT                                     540
              :::::::::: |||||||||::|||::::  |||::  ::|||::::||||
Db   109  SerLeuSerTyrTyrGlyAlaHisValGlyIleIleGlySerLeuProIleValPheGlySer                                128
Qy   541  GAGGAGCAGAAAGCCAAATACTTGCTAAACTGGCTCCGGGGAGCACATTGCCAGCCTTC                                     600
              |||||||||||:::  :::|::|  ::||||:||:::::||::|||| :::||:||
Db   129  GluGluGlnLysLysLysTyrLeuProLeuAlaSerArgGlyAlaSerIleAlaAlaTyr                                   148
Qy   601  TGCCTCACGGAGCCAGCCGATGGAGCCATCCAATCCGAGCAGAGCCACACTA                                            660
              |||:|||| ||||||||::|||::|| :::|:|||||:::  |||||:||:::
Db   149  AlaLeuThrGluProGlySerGlySerAspAlaLeuGlyLeuGlyArgIleLeuAlaValLeu                                168
Qy   661  AGTGAAGACAAGAAGCACTACATCCTCAATGCCTGGATTACTAATGGAGGA                                             720
              :||:||||||:::|||||:::||:::|||:||:::|||:::||::
Db   169  AsnGluAlaGlyThrHisTyrHisTyrValLeuThrGlyGluLysGlnTrpIleThrAsnSerAla                            188
Qy   721  CTGGCCAATATTTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATGATCAGTG                                            780
              |||::|||:::  |||||||||  ||||||     |||||||||
Db   189  PheAlaAspValPheValValTyrAlaLysVal----------------AspGly------                                  201
Qy   781  AAAGACAAAATCACAGCATTCATAGTAGAAGAGACTTGGTGGAGTCACTAATGGAGAA                                      840
              ||||||||||:::  ::||||||||:::::|||||:::||||||||||
Db   202  ---AspLysPheSerAlaPheIleValGluLysGluProGlyValSerThrGlyPro                                      220
Qy   841  CCCGAAGATAAATTAGGGCTCCAACACTTGTGAAGTCCATTTGAAAAACACC                                            900
              |||::|:::  :::::::|:::|||||:::  |:|:|||||||||
Db   221  GluGluLysLysMetGlyIleLysGlySerSerThrArgThrLeuIleLeuAspGlnAla                                  240
Qy   901  AAGATACCTGTGGAAAACATCCTTGAGAGTCGGAGATGGGTTAAGGTGGCCATGAAC                                       960
              ::|:|||:::  |||||::||:::|||||:::::|||||:::  ||:|||||:
Db   241  GluValProLysGluAsnLeuLeuLysGlyLeuGlnLeuIleAlaIleGlyLysGlyIleHisValIleLeuAlaPheAsn               260
Qy   961  ATCCTCAACAGCGCCGGTTCAGCATGGGACGCGTCGGTGGGCTGGGCTGCTCAAGAGATTG                                  1020
              :::  :::||::|||::::|||||::||:::  :::|||::|||::|||||:::
Db   261  IleLeuAsnIleGlyArgTyrLysLeuAlaValGlyThrIleGlyAlaSerLysArgVal                                  280
Qy  1021  ATTGAAATGACTGCTGAGTACGCCTGCCACAAGGAGAAACAGTTAACAGAGGCTCAGTGAA                                  1080
              :::::::::|||  :::||||||:::||:||::|:||:||:::
Db   281  IleGluLeuSerAlaAlaTyrAlaAlaTyrAlaAsnGlnAsnArgGlnPheLysProIleAlaGly                             300
Qy  1081  TTTGGATTGATTCAGGAGAAATTGCACTGATGCTTCAGAAGGCTTACGTCATGGAGAGT                                    1140
              |||  |:::  |||||:::|||:::||||:::|:||||||:::|||||||:||:::
Db   301  PheSerLeuThrGlnLeuIleGlnGluGlyIleGlyThrMetAlaSerArgLeuTyrAlaMetGluSer                          320
Qy  1141  ATGACCTACCTCACAGCAGGGGATGCTGGACCAA--------------------------                                  1173
              :::  |||||:::  |||:||::|::
Db   321  SerValTyrArgThrValGlyLeuPheGluAspAsnMetSerGlnPheThrAlaGluAsp                                  340
Qy  1174  --------------------CCTGGCTTCCCGAGCTGCTCCATCGAGCAGCAGCCATG                                     1209
                                  ::::||||||||     :::::::|::::|
Db   341  LeuLysAspGlyArgGlnIleAlaLysSerIleAlaGluTyrAlaIleGluCysSerLeu                                  360
Qy  1210  GTGAAGGTGTTCAGCTCGCAGTGTGGTGAGTGAGGAAGTGGTGCAGATCCTC                                           1269
              :::||::|::|:::  |::||::|:::|:::|||  |::|||:::||:|||
Db   361  AsnLysValPheGlySerGluThrGlyTyrIleLeuAspTyrIleValGlnIleHis                                     380
Qy  1270  GGGGGCTTGGGCTACAACAAGGGACTATCCGTACGAGCCGCCATATCGCCTGACACCCGATC                                1329
              :::  :::||||||:::  :::|||:::|||||::|||::|||:::|||
Db   381  GlyGlyTyrGlyPheMetGlnGlyTyrArgGlyAlaValGluArgAlaTyrArgAspSerArgIle                            400
```

```
Db   451  ---AspGluProLeuGluGlnGluLysTyrLeuLeuSerMetAlaLysLysValPheLeu                                  469
Qy  1615  CTC----------------------CGCTTGGTCAAGACCATCACCATGATGGCAGCTGGTA                                 1653
              :::                      :::||||  :||:::  ::::::  |||||
Db   470  MetIleAlaGlyThrGlyAlaGlnThrTyrGlyLysGlnGlnGlnGlnGluGlnGlnLeu                                  489
Qy  1654  CTGAAGCGGTGGCCAACATCCTCATCAACCTGATACGCATGGCGGCCGCCGCTGTCGCGG                                    1713
              :::||| |:|||:::|||:::  ::::::|||  :||:||||:::||:||:||||
Db   490  LeuAlaAsnValAlaAspIleValSerAspPheSerMetGluSerValIleLeuArg                                     509
Qy  1714  GCCAGGCCGCTCCATC--CGCATTGGGCTCCGCAACCACCAGACCAGAGGTTCTTGGCC                                    1770
              ||||||||::||||     :::||||::|||::|||:::  |||||:::|:|:||
Db   510  ThrGluLysAlaIleLeuArgArgAsnGlyLeuAlaGluGlnLysLeuAlaLeuThr                                     529
Qy  1771  AACACCTTCTGCGTGAAGCTTAC------------------------------------                                   1794
              :::|||::|:|||||:::  ::
Db   530  GlnValPheCysGlnGluAlaPheAsnArgIleAlaHisAlaAlaLysGluSerLeuVal                                  549
Qy  1795  --------------------TTGCAGAATTCTTCAGC---CTCTCCAGCTGACAAG                                       1830
                                  |||||:::  :::|||   :|||||:::||::||
Db   550  AlaMetGlnSerGlyAspThrLeuArgThrMetThrSerIleLeuArgLysLeuThrArg                                  569
Qy  1831  TATGTCCAGAAAAACCTAGATGAGCAGATTAAGAAAGTGTCCAGGAAGTCCTTGAGAAG                                    1890
              :::  |||||||||  ::::|||:|||||  ::::||:::  ::::|||::::|||
Db   570  HisThrProIleAsnValIleLysLysArgGluIleLeuAlaGlyArgIleLeuAlaGluAla                                589
Qy  1891  CGAGCTATATC                                                                                   1902
              :::||||| |||
Db   590  GluArgTyrVal                                                                                 593
```

RESULT 6
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C70021
butyryl-CoA dehydrogenase homolog yusJ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte r
  C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
  A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
  Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler
  iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
  Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
  A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauuel
  y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
  Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
  akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
  T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C70021
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-594 <KUN>
A;Cross-references: UNIPROT:O32176; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15271.
A;Experimental source: strain 168
C;Genetics:
A;Gene: yusJ
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Alignment Scores:
Pred. No.:         5.35e-45            Length:           594
Score:             815.50              Matches:          201
Percent Similarity: 49.58%             Conservative:     97
Best Local Similarity: 33.44%          Mismatches:       202
Query Match:       18.11%              Indels:           101
DB:                2                   Gaps:             12

US-09-945-326-1 (1-2452) x C70021 (1-594)
Qy  241  GTTAGCCAAGATGACTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTC                                     300
             ::::   ||||||  |||
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Score:                  711.50       Matches:       204
Percent Similarity:      49.32%      Conservative:  123
Best Local Similarity:   30.77%      Mismatches:    242
Query Match:             15.80%      Indels:         94
DB:                          2       Gaps:           18

US-09-945-326-1 (1-2452) x A70817 (1-650)
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Qy   178 GCTTTCGCCAAAGAGAGCTTTCCTAGGCAAAATCAAGAAGACAAGAAGAGAGTTTCCATTTCCA 237
             :::|||||||||||||::: :::: ||||||||||||| ||||| ::: ||||||||
Db    28 SerPheAlaLysGlyGluLeuPheLeuGlyLeuLeuHisProPhePro 47

Qy   238 GAAGTTAGCCAAGATGAACTAATGAAATCAATCAGTTCTTGGGACCCGTGAAAAATTCC 297
             ::: ||| |||||| ||| ::: :::||
Db    48 LysProSerAspAlaGluAlaThrGluAlaPheLeuValLysLeuArgLeuArgGluPhe 67

Qy   298 TTCACTGAGAGGTGACTCCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAAACT 357
             ::: ||| :::
Db    68 Leu---AspThrValAspGlySerValIleGluArgAlaAlaAlaGlnIleProAspGluTyr 86

Qy   358 TTGGAGAAATTGAAGACCTAGGCTTTTGGGCTCAAGTCCCAGAAGAATATGGTGGC 417
             :::|| ||||||||||::: ||||||||:::|||||
Db    87 ValLysGlyLeuLeuAlaGluLeuGlyCysPheGlyLeuLysIleProSerGluTyrGlyTyrGly 106

Qy   418 CTGGGCTTCTCCAACACCATGTACTACTCAAGA---CTAGGGGAGATCATCAGCATGGATGGG 474
             ||| :::
Db   107 LeuAsnMetSerGlnValAlaValAlaTyrAsnArgValLeuMetMetValThrThrValHisSer 126

Qy   475 TCCATCACTGTGACCCTGGCAGCCTATGGCCTC---AAGGGGATCATCTTG 531
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Db   127 SerLeuGlyAlaLeuLeuSerAlaHisGlnSerIleGluValProGluProLeuLysLeu 146

Qy   532 GCTGGCACTGGAGGACGAGAAGCCAAATACTTGCCTAAACTGGCCTCCGGGGAGCACATT 591
             ||||||| ::::::: |||||| :::
Db   147 AlaGlyThrAlaGlyGlnLysLysArgArgPheLeuProArgCysAlaAlaAlaGlyAla---Ile 165

Qy   592 GCAGCCTTCTGCCTCACGAGCACCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGA 651
             ::||||||| ||||||| :: :::||
Db   166 SerAlaAlaPheLeuLeuThrGluProAspValGlySerAspProAlaAlaArgMetAlaSerThr 185

Qy   652 GCCCACTAAGTGAAGACAAGAAGACTACATCCTCAATGGCTCTGGATTACT 711
             ::: |||:::||||:::||| :: |||||:::|||
Db   186 AlaThrProIleAspGlySerLysThrThrSerSerGlnTrpLeuTrpThrThr 205

Qy   712 AATGAGGACTGGCCAATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATTCTGAT 771
             |||||| :::::::
Db   206 AsnGlyValValAlaAlaAspLeuValValMetAlaArg-----ValProArgSerGlu 223

Qy   772 GGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAAGAGACTTTGGTGGAGTCACT 831
             ||| :::  ||:::||||:::|||::: ||||||
Db   224 GlyHis---ArgGlyGlyIleSerAlaPheValValGluAlaAspSerProGlyIleThr 242

Qy   832 AATGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTAAGTCCATTT 891
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Db   243 ValGluArgArgAsnLysPheMetGlyLeuArgGlyIleLeuAsnGlyValThrArgLeu 262

Qy   892 GAAAACACCAGATACCTGTGAAAACATCCTTGGAGAAACATCCTTGGAGATGGGTTTAAGGTG 951
             :::::: ||||||:::
Db   263 HisArgValArgValProLysAspAsnLeuIleGlyLysAspGlyLeuLysIle 282

Qy   952 GCCATGAACATCCTCCAACAGCGGCCGGTTCAGCATGGGCCAGCGTCGTGCTGTGGCCTGCTC 1011
             :::::: :: ::: |||||||:::
Db   283 AlaLeuThrThrLeuAsnAlaGlyLeuArgLeuSerLeuProAlaIleAlaThrGlyValAla 302

Qy  1012 AAGAGATTGATTGAAATGACCCTGACGTACGCCTGCACAAGGAAAACAGTTTAACAGAGG 1071
             ||| :::  |||:::
Db   303 LysGlnAlaLeuLeuIleAlaAlaArgGluTrpSerValGlnArgValGlnTrpGlyLysPro 322

Qy  1072 CTCAGTGAATTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTC 1131
             ::: |||:::|||
Db   323 ValGlyGlnHisGluAlaValAlaAlaSerLysIleSerSerPheIleAlaAlaThrAsnTyrAla 342

Qy  1132 ATGGAGAGTAGTAATGACCTACCTCACAGCAGCAGGGATGCTGGACCAACCTGGCTTTCCGACTGC 1191
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Qy  1330 CTCCTCATCTTCGAGGGAACCAATGAGATTCTTCCGGATGTACATCGCCTGACGGGTCTG 1389
             |||||||||||||:: :::||| :::
Db   401 AsnArgIlePheGluPheGlyLeuThrAsnGluIleLeuAsnArgLeuIleValProSerThrPheLeu 420

Qy  1390 CAGCATGCC------GGCCGCATC---CTGACTACCAGGATCCATGAGCTTAAACAGGCC 1440
             ::: ||| ::: ||||||
Db   421 LysLysAlaLeuLysGlyGluLeuPheGluLeuProLeuPheGlyLeuLysSerLeuGlnSerLeuGlnGlu 440

Qy  1441 AAAGTGAGCACAGTCATGGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACT 1500
             ::: ::: ||| |||
Db   441 LeuMetMetLeuMetProGluGluProGly--- 450

Qy  1501 GTGGGACCTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCC 1560
             ::::::
Db   451 ---------SerGlyValLeu- 454

Qy  1561 AACAAGTTTGAGGAGGAGAACACCTACTGCTTCTCGGCCGGACCGTGGAGACACTGCTGCTC--- 1617
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Db   455 ---------GluGlnGluLysTyrIleValLysValAlaLysGlnAlaAlaAlaLysLeuPheAla 471

Qy  1618 ---------CGCTTTGGCAAGACCATCATGAGGAGGAGCAGCTGGTACTGAAG 1659
             ||||||:::||
Db   472 AlaGlyLeuAlaLeuAlaGlnInLysTyrGlyLysAlaIleAspArgGluGluArgGlnInLeuLeuVal 491

Qy  1660 CGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACGCGCGTGCGTGCCGGGGCCAGC 1719
             ||||||| ::: :::
Db   492 AsnValAlaAspIleValSerAsnValTyrAlaMetGluSerAlaValAlaValLeuArgThrGlu 511

Qy  1720 CGCTCCATCCGCATT--GGGCTCCGCAACACCAGAGTTCTCTTGGCCCAACACC 1776
             ::::::||| ::::::
Db   512 LysAlaIleAlaAlaGlnInGlyAlaLysGluLysAlaAlaAlaAlaGlyIleLysValLeuTyrThrGluIle 531

Qy  1777 TTCTGCGTGGAAGCTTACTTGCAG------------------ 1800
             |||:::
Db   532 PheValGlnLeuGluAlaPheAsnGluIleGluLysAlaLysHisAlaAlaGluSerLeuIleAlaMet 551

Qy  1801 ---------AATCCTTCAGCCTTCTCAGCTGGACAAGTATGCT 1836
             ||| ::: :::
Db   552 GluGluGlyGlyAspSerLeuArgMetLeuSerAlaLeuArgGlyMetLeuSerAlaLeuArgGlyLeuThrArgValThr 571

Qy  1837 CCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCCAGCAGATCCTTGAGAAGGCGAGCC 1896
             :::||||:::  :::::: |||  :::
Db   572 ProLysAsnValIleGlnLysLysArgGluAlaAlaAlaAlaGlyIleLysPheGluAlaGluAlaGluLys 591

Qy  1897 TAT 1899
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Db   592 Tyr 592
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RESULT 7
A70817
probable fadE10 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70817
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference: A70500; MUID:98295987; PMID:9634230
A;Accession: A70817
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-650 <COL>
A;Cross-references: UNIPROT:Q10535; GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA1767
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: fadE10

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Alignment Scores:
Pred. No.:       3.09e-38       Length:       650
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acyl-CoA dehydrogenase, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonz
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <STO>
A;Cross-references: UNIPROT:Q9AB07; GB:AE005673; NID:g13421592; PIDN:AAK22414.1; GSPDB:GM
C;Genetics:
A;Gene: CC0427
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:   1.7e-37   Length: 382
Score: 699.00   Matches: 155
Percent Similarity: 58.31%   Conservative: 80
Best Local Similarity: 38.46%   Mismatches: 124
Query Match: 15.52%   Indels: 44
DB: 2   Gaps: 8

US-09-945-326-1 (1-2452) x B87302 (1-382)

Qy   253 GAACTAATGAATCAATCAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAAGAGTG 312
             ||| || || :: || :|| || |||| |||||
Db   4 AspLeuGluThrArgGluGlnLeuIleAspPheValAlaArgPheValAlaArgLeu 23

Qy   313 GAC------TCCCGAAAAATGACCAGGAGGAAGGAAAATCCAGATGAAAACTTTGGAGAAA 366
         ||| :::||||||||||::||
Db   24 ArgProIleGluAlaGlnIleAlaLysAsnAspAlaValProAspAlaValIleGluGlu 43

Qy   367 TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCAAGAAGAATATGGTGGCCTGGCTTC 426
         ::|||:|||| | :||:|| || | |||||
Db   44 MetLysGlyLeuGlyLeuGlyPheGlyLeuThrIlePheProGluGlyGlyLeuGly-- 62

Qy   427 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGTGGTCCATCACTGTG 486
         |||:||| | ||| | ::|| | ||||::| ||| |||
Db   63 ------------------------------------LeuThrMetGluGluGluValVal 71

Qy   487 ACCCTGGCAGCGCACCAGGCT------------------------ 507
         :::|| ||| || ||||
Db   72 AlaIleGluLeuGlyLeuArgAlaSerProAlaPheArgSerValPheGlyThrAsnValGly 91

Qy   508 ATTGGGCTCAAGGGATCATCTTGGCTGGCCACTGAGGAGCAGAAAGCCAAATACTTTGCCT 567
         |||| || :::||::|||| |||| |||| ||| | |||
Db   92 IleGlySerGlnGlyLeuValMetPheGlyAsnAspGluGlnIleAlaLysTrpLeuPro 111

Qy   568 AAACTGCGTCCGGGGAGCACATTGAACCTTCTGCCTCAGCCTCCACGGCCAGTGGGAGC 627
         |:::||| || ||:|| | | || |:|| || |
Db   112 GlyIleAlaSerGlyAlaValAlaValIleThrSerPheAlaLeuThrGluProGluAlaGlySer 131

Qy   628 GATGCAGCCTCAATCCGGAGCAGAGCCACTAAGTGAAGAGCACTACATCCTC 687
         ||||||||| |:::|| |||| || || | |
Db   132 AspSerAlaAlaValGlnThrArgAlaThr------ArgAspGlyAspTyrIleLeu 149

Qy   688 AATGGCTCCAAGGTCCGGATTACTAATGAGGAGCTGTGGCCCAATATTTTACTGTGTTCA 747
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Db   150 AsnGlySerLysValArgTyrIleThrAsnAlaGlyLeuPheThrValMetAla 169

Qy   748 AAGACTGAGGTCGTTGATTCTGATGATGATCAGTGAAAAGACAAAATCACAGCATTCATAGTA 807
         ::||| || | ||||::|: |
Db   170 ArgThrAsn--ProAspAlaLysGlyGlyAla------GlyValSerAlaPheLeuVal 186

Qy   808 GAAAAGAGACTTTGGTCGGAGTCACTAATGGACAATAAAAATAGGACATTCGGGGC 867
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Db   187 ProArgAspLeuProGlyLeuThrValGlyLysMetGlyLysProGluLysGlyGlnGly 206

Db   343 LeuAsnAspAlaValValGluGlyLeuLeuSerSerGlnMetAlaAspGlu---GlyArgAsnAspIle 361
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Qy 1192 TCCATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCGCAGATCGCCGAGGCCGCTGGCAGTGTGAGT 1251

Db   362 ArgIleGluAlaLysAlaLeuAlaLysLeuTrpSerSerGluMetAlaCysLeuValGlyAsp 381
             |||||| :||| ||||||| :||| || || |
Qy 1252 GAGGGCCTGCAGATCCTCGGGGCCTGGGCTAC------ 1284

Db   382 GluLeuLeuGlnIleLeuArgGlyValGlyTyrGluThrAlaGluLeuAlaAlaArg
             ||| ||| |||
Qy 1285 ---ACAAGGACTATCCGTACGAGGCCATACTGCGTGACACCCGCATCCTCCTCATCTTC 1341

Db   402 GlyGluArgAlaValProValGluGlnMetValArgAspLeuArgIleAsnArgIlePhe 421
             ||||| ||| |:: ::||| | |||||||
Qy 1342 GAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT----------CTG 1389

Db   422 GluGlySerSerGluIleMetArgLeuLeuIleAlaArgGluAlaArgGluAlaAlaHisAlaLeu 441
             |||||| ||| :|| | | |||:|| ||||| | | || ||||
Qy 1390 CAGCATGCCGCCGGCCGACCTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGC 1449

Db   442 ThrAlaAlaGlyAspLeuAlaAsnProLysAla---AspLeuArgGlnLysAlaAlaAla 460
             ||: ||| ::: ||: :|| ||| | |||| | ||| ||| || |
Qy 1450 ACAGTCATGATACCGTTCGGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGACCTG 1509

Db   461 AlaAla-- 462
             |||||
Qy 1510 GGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCG-------------- 1551

Db   463 GlyAlaSerGlyPheTyrAlaLysTrpAlaLysTrpLeuProLysPheGlyGluGlyGlnLeu 482
             ||| |:|| ||||| || :| ||| ||
Qy 1552 ---GACAGT 1557

Db   483 ProThrThrTyrArgGluPheGlyAlaLeuAlaThrHisLeuArgPheValGluArgSer 502
             ||| ||| | |:||||| |||::|| | |||
Qy 1558 GCCACAAGTTGAGGAGAACACCTACTGCTTCGGCGACCTGCTGCTC 1617

Db   503 SerArgLysAsnAspAlaPhe------TyrGly------MetAla 515
             |:|||| || |:|| |||||
Qy 1618 CGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGGAGGCGGTGGCCAACATCCTC 1677

Db   516 ArgTrpGlnAlaSerLeuGluLysGluLeuLysGlyPheLeuGlyPheLeuGlyValAspIleGly 535
             |||||| | | : ||| || |::|| | ||||
Qy 1678 ATCAACCTGTATGGCATGGCATGACCGCCGTGCTGCGCGGCCGCCGTCCATCCGCATTGGG 1737

Db   536 AlaGluLeuPheAlaIleSerArgAlaAlaCysValArgGluAlaGlnArgThrAlaAsp 555
             |||| |||| :::||| | |||| |:|| |
Qy 1738 CTCCGCAACCAACGACCAGAGTTCTCTTGGCCAACACCTGTGC---------------- 1782

Db   556 ProValGluGlyValGlyGlnIleAlaTyrGluLeuAlaLeuAlaPheCysSerGlnGlnAlaThrLeu 575
             ||| | |:|| : |||||:::|
Qy 1783 ---GTGGAAGCTTACTGCAGAATCTCTCAGCTGTCGACAAGTATGCTCCA 1839

Db   576 TrpLeuGluGlnIleGlyProTrpIleGlyThrLeuGlyProTrpLeuSer------ 586
             |||| |||| || ||| :|| |::|||:||
Qy 1840 AAACCTAGATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAGCGA--GCC 1896

Db   587 --AsnThrAspSerIleAspProValArgLeuAlaAsnAspAlaValLeuGlyLysArgTyrThr 605
             ::||| | || ||||||| :|||
Qy 1897 TATATCTGTGCCCACCCTCTGGACAGGACATGCTGAGGGAGGACAGTGTCCCCCTGCTA 1956

Db   606 TrpLeuGluGlnIleGlyIleLeuGlyProTrpGlyProTrpIleAlaSerThr 625
             ||| |||| || | : |||||
Qy 1957 CCGCCCG------------------CCCCTACCCATGGCCCGTTGCTGGATGACTGTTACTCTTTT 2004

Db   625 pGluProGlyProSerThrGluAlaAsnLeuAlaArgArgPheLeuThrValSerProSer 645
             ::: ||| || ||| | |||:|::
Qy 2005 TTCAGAA 2011

Db   645 rSerGlu 647
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Qy 2005

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Qy    868 TCCAACACTTGTGAAGTCCATTTGAAAAACACCAAGATACCTGTGAAAAACATCCTTGGA 927
          ::::::    :::|||  :::::|||  ||||||
Db    207 AlaHisIleHisAspValThrPheAspAsnValArgValProAlaTrpAsnArgLeuGly 226

Qy    928 GAGGTCGGAGATGGGTTTAAGGTGTTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATG 987
          |||:::||||||||||||  :::  :::|||::: ||||||
Db    227 AlaGluGlyGluGlyPheLysValAlaMetGlnValAlaMetGlnValLeuAspArgArgLeuHisIle 246

Qy    988 GGCAGCGTCGTGCTGCTGGCCGTGCTCAAGAGATTGATGAAATGACTGCTGAGTACGCCTGC 1047
          ::::|||||||  :::||||||
Db    247 AlaAlaValCysValGlyValAlaGluArgLeuIleAlaAspCysValAlaTyrAlaSer 266

Qy   1048 ACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTGGATTGATTCAG---------- 1095
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Db    267 GluArgLysGlnPheGlyGlnProIleAlaSerPheAlaMetIleAla 286

Qy   1096 ---GAGAAATTTGCACTGATGGCTTACGTCAGGAGTATGACCTACCTC 1152
          ::: ||||||::::::||||||
Db    287 AspSerLysThrGluAlaLeuAlaLeuAlaLysAlaLeuValLeuGluThrAlaArgLysArg 306

Qy   1153 ACAGAGGGATGCTGACCAACCTGGCTTTCCCGACTGCTCCATGCAGGCAGCCATGGTG 1212
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Db    307 AspAlaGlyVal---------------------AsnValThrLeuGluAlaAlaSerSer 319

Qy   1213 AAGGTGTTCAGCTCCGAGGGCCGCCTGGCAGTGTCGTCAGTGAGGCGCTGCAGATCCTCGGG 1272
          ||||||||||||  :::::::|||||||||||
Db    320 LysLeuPheAlaSerGluMetValGlyTyrValAlaAspArgAlaValGlnValPheGly 339

Qy   1273 GGCTTGGCTACACAAGGGACTATCCGTACGAGCCGCATACTGCCGTGACACCCGCATCCTC 1332
          ||||||  :::::::|||||||||||
Db    340 GlyAlaLeuAlaThrGluGlyTyrProTyrArgLeuTyrArgAspValArgIlePhe 359

Qy   1333 CTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCCGCCTGACGGGTCGCAG 1392
          :::|||||||||||
Db    360 ArgIleTyrGluGlyTyrSerGlnValGlnThrSerGlnValGlnLeuLeuIleLeuAlaArgGluThrLeuLys 379

Qy   1393 CATGGCCGGC 1401
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Db    380 ArgGlyGly 382
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Qy      8 LeuAsnLeuLeuLeuAspSerIleArgGlnPheValArgGluSerLeuValProHisGlu 27

Qy    319 CGAAAAAATTGACCAGGAAGGGAGAAATCCCAGTGAATGAAACTTTGGAGAAATTGAAGAGGCCTA 378
          ::::::|||::: :::||||||::: ::::::||||||
Db     28 GlnGluValAlaGluThrAspArgIleProGluAlaIleIleIleAlaArgMetArgGluMet 47

Qy    379 GGGCTTTTGGGCTGCCAAGTCCAGAAGAATATGGTGGCCTTCTCCAACACCATG 438
          ::::|||::::::|||||||
Db     48 GlyLeuPheGlyLeuSerIleProGluAlaTyrGlyGlyLeuGly----------- 62

Qy    439 TACTCAAGACTAGGGGAGATCATCAGCATGGGGTCCATCACTGTGACC----------- 489
          ::::::|||:::  :::::::::::
Db     63 ---------------ValThrMetGluGluGlyValSerIleAlaPheGluLeu 75

Qy    490 CTGGCAGCCGCCACCAGGCTATTGGCCTCCAAG 519
          :::  :::||||||
Db     76 GlyArgThrSerProAlaPheArgSerLeuLeuGlyThrAsnAsnGlyIleGlySerGln 95

Qy    520 GGGATCATCTTGGCTGCACTGAGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCC 579
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Db     96 GlyIleValIleAspGlyThrGluGlnLysArgArgTyrLeuProArgLeuAlaSer 115

Qy    580 GGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCAGTGGGAGCGGATGCAGCCTCA 639
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Db    116 GlyGluLeuLeuSerSerPheCysGluThrGluProAspSerGlySerAspAlaAlaSer 135

Qy    640 ATCCGGAGCAGAGCCACACTAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAG 699
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Db    136 LeuLysThrThrAlaVal------ArgAspGlyGluHisTyrValLeuAsnGlyThrLys 153

Qy    700 GTCTCGATTACTAATGGAGACTGGCCAATATTTTTACTGTGTTTTGCAAAGACTGAGGTC 759
          ::::::|||||||||||
Db    154 ArgPheIleThrAsnAlaProGlnAlaGlyTyrIleTyrThrValMetAlaArgThr------ 171

Qy    760 GTTGATTCTGATGGATCAGTGAAAGACAAA---------ATCACAGCATTCATAGTAGAAAAGA 813
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Db    172 --------AspProAlaIleArgGlyValGlyIleSerAlaPheValGlyIleGlyAlaArg 188

Qy    814 GACTTTGGTGGAGTCACTAATGGAACCCGAAGAGATAAATTAGGCATTCGGGGCTCCAAC 873
          :::::::::: ||||||:::  :::
Db    189 GlyThrProGlyLeuSerLeuGlyLysProAspArgLysMetGlyGlyMetGlyGlyAlaHis 208

Qy    874 ACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGAAAAACATCCTTGGAGAGGTC 933
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Db    209 ThrCysAspValIlePheAspAspCysArgValProAlaSerGlnLeuIleGlyGlyVal 228

Qy    934 --GGAGATGGGTTTAAGGTGCCATGAACATCCTCAACACGGCCGGGTTCAGCATGGGC 990
          ::: ||||||:::
Db    229 GluGlyValGlyPheLysThrAlaMetLysValLeuAspLysArgLeuHisIleAla 248

Qy    991 AGGCTCGTGGCTGGCCTGGTCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCCTGCACA 1050
          ||||| :::::::||||||
Db    249 AlaValCysValGlyValAlaGluArgMetLeuGluAspAlaLeuArgTyrAlaLeuGlu 268

Qy   1051 AGGAAACAGTTAACAAGAGGCTCAGTGAATTTGATTGATTCAGAGAAATTTGCACTG 1110
          ||||||||||||::: :::::: ::::::|||||||
Db    269 ArgLysGlnPheGlyGlnProIleAlaGluPheGlnLeuIleLeuAlaMetLeuAlaAsp 288

Qy   1111 ATGGCTCAGAGGCTTACGTCATGGAGAGATGACTACCTCACAGCAGGGATGCTGGAC 1170
          :::||||||
Db    289 SerLysAlaGluAlaTyrAlaAlaArgCysMetValIleAspAlaAlaArgGlnArgGlyAsp 308

Qy   1171 CAACCTGGCTTCCCGACTGCTCCATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAG 1230
          :::::::|||  :::::::::|||||||
Db    309 GluGly-------ArgAspValGlyThrGluValAlaSerCysAlaLysLeuPheAlaSerGlu 326

Qy   1231 GCCCGGCTGGCAGTGTGAGTGAGGCGCTGCAGATCCTGCGATACTGCAGGCAGAGGATGCTGGAC 1290
          :::  :::|||||||
Db    327 MetCysGlyGlyTyrArgValAlaAlaArgAlaValGlnIlePheGlyGlyAlaLeuGlyTyrIleGly 346

Qy   1291 GACTATCCGTACGAGCCGCATACTGCGTGACACCCGCATCCTCCTCACTGAAGAGGTG------GACTCC 1350
          ||||||::: :::  :::|||||||
Qy    265 ATCAATCAGTTCTTGGGCACCGTGGAAAAATTCTTCACTGAAGAGGTG------GACTCC 318
```

```
RESULT 9
B83443
probable acyl-CoA dehydrogenase PA1631 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83443
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
   adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
   .; Lory, S.; Olson, M.V.
   Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <STO>
A;Cross-references: UNIPROT:Q9I391; GB:AE004590; GB:AE004091; NID:g99947587; PIDN:AAG0502
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1631
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:                        Length:           384
Score:          5.22e-37          Matches:          147
                691.50            Conservative:     82
Percent Similarity:  58.87%       Mismatches:       121
Best Local Similarity: 37.79%     Indels:           39
Query Match:    15.35%            Gaps:             8
DB:

US-09-945-326-1 (1-2452) x B83443 (1-384)
```

```
Db    347  AspTyrGlyIleGluArgPheTyrArgAspValArgLeuPheArgIleTyrGluGlyThr 366
                ||||| ::::| ||||||
Qy   1351  AATGAGATTCCGGATGTACATCGCC 1377
                ||||| :::::| ||||||
Db    367  ThrGlnIleGlnIleLeuLeuIleAla 375
```

```
                                                       Db    196  GlyLysLysGluLysGlyMetGlyLeuHisGlySerAsnThrThrGluLeuPheGlu 215
                                                                     |||||| |||:: ||||:|
Qy    895  AACACCAAGATACCTGTGGAACAAACATCCTTGGAACGTCCGGAGAGGTGGTTTAAGGTGGCC 954
                                                                     ::: :::||||:|||||||||
Db    216  AspAlaLeuValProLysGluAsnLeuLeuGluLeuGlyLysAspGlyTyrLysPheAla 235
```

RESULT 10

```
G84124
acyl-CoA dehydrogenase mmgC [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G84124
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
Nucleic Acids Res. 28, 4317-4331, 2000
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G84124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:Q9K6D0; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB075
A;Experimental source: strain C-125
C;Genetics:
A;Gene: mmgC
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:               6.51e-37        Length:         379
Score:                   690.00          Matches:        147
Percent Similarity:      61.39%          Conservative:   74
Best Local Similarity:   40.83%          Mismatches:     125
Query Match:             15.32%          Indels:         14
                                         Gaps:           6
```

US-09-945-326-1 (1-2452) x G84124 (1-379)

```
Qy    298  TTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAAGGAAATCCCAGATGAAACT 357
                ||| |||||| ||:::||||||:
Db     27  PheValGluGluMetGluThr------------------AsnAspThrPheProMetHisIle 41
```

RESULT 11

```
D69658
acyl-CoA dehydrogenase mmgC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69658
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleri
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y.,M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpscra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69658
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-378 <KUN>
A;Cross-references: UNIPROT:P45857; GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14346.]
A;Experimental source: strain 168
C;Genetics:
A;Gene: mmgC
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:               2.15e-36        Length:         378
Score:                   682.00          Matches:        157
Percent Similarity:      56.33%          Conservative:   70
Best Local Similarity:   38.96%          Mismatches:     130
Query Match:             15.14%          Indels:         46
```

DB:

US-09-945-326-1 (1-2452) x D69658 (1-378)

```
DB:                              Gaps:   2                    8

Qy    172  GTACGAGCTTCGCCAAAGAGAGTTTTCCTAGGCAAAATCAAGAAGAGAGAGTTTCCCA  231
                ::: ::::::::||||| :::|||                    :::|||
Db     14  ValArgAspPheAla------------------------ArgLysGluIleAlaPro   24

Qy    232  TTTCCAGAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCAGTTCTTGGGACCCGTGGAA  291
                ||||| :                                            
Db     25  AlaAlaGluIle--------------------------------------------  28

Qy    292  AAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAAAAATCCAGAT  351
                                   :::  :::|||   :::::::::|||
Db     29  -------------------------------MetGluLysThrAspGluPheProPhe  37

Qy    352  GAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAATAT  411
                ::: ::::::::|||:::::||||:                   :::|||
Db     38  GlnLeuIleLysLysMetGlyLysHisGlyLeuMetGlyIlePheProValProGlnTyr  57

Qy    412  GGTGGCCTGGGCTTCTCCAACACCATGTAC---TCCAAGACTAGGGAGGAGATCATCAGCATG  468
                ||||| :::                   :::  :||||
Db     58  GlyGlyLeuAlaGlyAlaLeuSerTyrIleLeuAlaIleHisGluIleSerArgIle  77

Qy    469  GATGGGTCCATCACTGTGACCCTGGCACCCGGCTATTGGGCCTCAAGGGGATCATC  528
                :::::: ||||| :::                    :::
Db     78  SerAlaAlaValGlyValIleLeuSerValHisThrSerValGlyThrAsnProIleLeu  97

Qy    529  TTGGGCTGGCACTGAGGAGCGAAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCAC  588
                                    :::::::::|||||||||||||
Db     98  TyrPheGlyAsnGluGlnIleLysMetLysTyrIleProAsnLeuAlaSerGlyAspHis  117

Qy    589  ATTGCAGCCTTCTGCTCACGGAGCCAGTGGAGCGATGCAGCCTCAATCCGGAGC  648
                :::                   ||||||||||||::
Db    118  LeuGlnLeuAlaPheAlaLeuThrGluProHisSerGlyAlaGlySerAspArgThr  137

Qy    649  AGAGCCACACTAAGTGAAGAGCAACAAGAGACTACATCTCCAATGGCTCTGGATT  708
                ::: |||||||||||||||::::::
Db    138  ThrAlaIleLeuLysAsnGlyLys----------TyrLeuLeuAsnGlySerLysIlePhe  155

Qy    709  ACTAATGGACGCTGGCCAATATTTTACTGTGTTTCAAAGACTGAGGTCGTTGATTCT  768
                ||||||||||| :::: :::::|||   :::
Db    156  ThrAsnGlyGlyAlaAlaAspIleTyrIleTyrPheAlaLeuThr----------Ala  171

Qy    769  GATGGATCAGTGAAAGACAAAAGACATTCATAGTAGAAAGAGACTTTGGTGGAGTC  828
                    ::: ||||||||||||||:::::
Db    172  ProAspGlnArgHisSerAlaPheIleVaGluLysArgAsnThrProGlyPhe  191

Qy    829  ACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGGCTCCAACACTTGTGAAGTCCAT  888
                ::::::::::::::: :::::::||||||
Db    192  ThrValGlyLysLysGluArgLysValGlyLeuTyrGlyIleArgGlyLeuArg  211

Qy    889  TTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAAGTTCGGAGAGTGGTTTAAG  948
                ||||||||:::::||||:::
Db    212  PheAspAsnAlaGluValProGluLysIleLeuGlyGluValArgArgValGlyPheHis  231

Qy    949  GTGGCCATGAACATCCTCACACGCGCCGTTGCCGGATGGCCAGCGTCGTGGCGCTG  1008
                :::::::::::|||||||:::::
Db    232  IleAlaMetAsnAlaAsnLeuAsnValGlyArgIleGlyTyrIleGluAlaAlaLeuGlyIle  251

Qy   1009  CTCAAGAGATTGATTGAAATGAACTGCTGAGTGAGTGGTCCATCACTGTGACCCTGACCCAGGCTATTGGC  1068
                ::: ::::::::|||| :::::
Db    252  AlaGluAlaAlaLeuAlaLeuHisGluHisGlyTyrArgAlaLysGlnValGlnPheGlyArg  271

Qy   1069  AGGCTCAGTGAATTTGATTGAATTGGATTCCACTGAGTGGCTCAGAAGGCCTTAC  1128
                :::                   :::
Db    272  ProIleAlaAlaAsnGlnIleLeuSerPheLysPheLeuAlaAspMetAlaThrArgAlaGlu  291

Qy   1129  GTCATGGAGAGTATGAACATCCTCACCTACCGCTCTGCACCAGGGATCTGCTTTCCCGAC  1188
                ::: |||                   :::
Db    292  AlaAlaArgHisLeuValTyrHisSerLeuValThrArgGlyLeu--LeuHisAsnArgGlyLeu--Asn  309

Qy   1189  TGCTCCATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCCCAGAGCCGCCAGTGTGTG  1248
                :::
Db    634  GCCTCAATCCGGAGCAGCAGAGCCGCCACCTACTAAGTGAAGACAAGAAGAGCACTACATCCTCAATGGC  693
```

310 CysGlyLysGluAlaSerMetAlaLysGlnPheAlaSerAspAlaAlaValLysAlaLeu 329

1249 AGTGGAGGCGCTGCAGATCCTCGGGGCTTGGCTCACAAGAGGACTATCCTACGAGGGC 1308
           :::::||:||::||||||| ||:::::::|||:::::||||||
330 ---AspAlaValGlnIleTyrGlyGlyTyrGlyTyrMetLysAspTyrProValGluArg 348

1309 ATACTGCGTGACACCCGCATCCTCCATCTTCGAGGGACCAATGAGATTCTCCGGATG 1368
           :::::   :::::
349 LeuLeuArgAspAlaLysAlaValThrGlnIleTyrGluGluGlnArgLeu 368

1369 TACATCGCC 1377
         ||:::
369 IleIleSer 371

RESULT 12
AC3536
butyryl-CoA dehydrogenase (EC 1.3.99.2) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3536
R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesso
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <KUR>
A;Cross-references: UNIPROT:Q8YDG3; GB:AE008918; PIDN:AAL53454.1; PID:g17984354; GSPDB:GN
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0213
A;Map position: II
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: oxidoreductase

```
Alignment Scores:
Pred. No.:                                   Length:           381
Score:                 2.15e-36              Matches:          151
Percent Similarity:    682.00                Conservative:      73
Best Local Similarity: 60.70%                Mismatches:       131
Query Match:           40.92%                Indels:            14
DB:                    15.14%                Gaps:               7
                       2
```

US-09-945-326-1 (1-2452) x AC3536 (1-381)

```
Qy    286  GTGGAAAAATTCTTCACTGAAGAGTG--------GACTCCCGAAAATTGACCAGGAA  336
                :::::::::||||||             :::::::::::
Db     16  ValArgPheValArgGluArgLeuValLeuProAlaGluSerArg---ValGluGluThr  34

Qy    337  GGGAAAATCCAGATGAACATTCTGGAGAAGTTTCGGAGAGCCTAGGGCTTTTTGGGCTGCAA  396
                :::::::::|||||||||||:::::::
Db     35  AsnArgIleProAspAspIleLeuIleLeuAlaAspGlyLysIleGluMetArgAlaMetGlyLeuPheGlyLeuSer  54

Qy    397  GTCCCAGAAGAATATGGTGGCCTTCTCCAACACCATGTACTCACCAAGACTAGGG---  453
                ::::::::||||||||||||||:::::
Db     55  IleProGluGluTyrGlyGlyLeuGlyLeuThrMetGluGluLeuThrMetGluGlyValGlyValGlyPhe  74

Qy    454  GAGATCATCAGCATGATGGGTCCATCACTGTGACCCTGGCACCCGGCTATTGGC  513
                :::                    :::
Db     75  GluLeuGlyTyrThrSerProAlaPheArgSerValIleGlyThrAsnGlyIleGlyGly  94

Qy    514  CTCAAGGGGGATCATCTTGGCTGCACTGAGTGGCTCAGAAGGCCAAATACTTGCCTAAACTG  573
                ||||||||||             :::::
Db     95  SerGlnGlyIleIleAlaAlaGlyThrAspSerMetAlaThrArgAlaGlu  114

Qy    574  GCGTCCGGGGAGCACATTGCAGCCTTCTGCTCACGGAGCCAGTGGAGCGATGCA  633
                :::  |||                   :::::
Db    115  AlaSerGlyAlaGlyIleIleAlaLeuAlaSerPheAlaLeuThrGluProHisAspValGlySerAspAla  134

Qy    634  GCCTCAATCCGGAGCAGCAGAGCCGCCACCTACTAAGTGAAGACAAGAAGAGCACTACATCCTCAATGGC  693
```

Pred. No.:
Score: 678.00   Length: 381
Percent Similarity: 59.13%   Matches: 149
Best Local Similarity: 38.30%   Conservative: 81
Query Match: 15.05%   Mismatches: 135
DB: Indels: 24
                                                              Gaps: 7

US-09-945-326-1 (1-2452) x B87472 (1-381)

```
Qy  265 ATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAGAGGTGGACTCCGAAAA 324
            :::          ::::::::::::::||
Db    7 LeuSerAlaLeuIleAspValIleGlnArgPheValAlaGluArgLeuArgIleGlu 26

Qy  325 ---------ATTGACCAGGAAGGGAAAATCCCAGATGAAACTTGAGAAATTGAGAGGCTA 378
             :::   ::: |||   ::::::::::||
Db   27 GlyLeuValSerGlyThrAspGlyLysProGlySerIleIleGluGluMetLysGlnLeu 46

Qy  379 GGGCTTTTGGGCTGCAAGTCCAGAAGAATATGGTGCCTGGCTTCTCCAACACCATG 438
         ||||||||||||          :::||||||
Db   47 GlyLeuPheGlyLeuLeuSerIleProGlySerTyrGlyGlyLeuGlyLeuGluGluGlu 66

Qy  439 TACTCAAGACTAGGGGAGATCATCAGCATG---------GATGGGTCCATCACTGTGACC 489
            :::||||::                   :::||
Db   67 GluAlaArgVal------IleValAlaPheCysHisThrAlaProAlaPheArgSerThr 84

Qy  490 CTGGCAGCGCCACCAGTCATTGGCTCAAGGGGATCATCTTCGCTGCACTGAGGAGCAG 549
          ||          :::  :::||| |||||
Db   85 PheGlyThrAsnValGlyIleGlyLeuValMetPheGlyAspGluAlaGln 104

Qy  550 AAAGCCAAATACTTGCCTAAACTGGGCTCCGGGAGGACAATTCAGCCTTCTGCCTCACG 609
         ||||||||||                   :::||||||
Db  105 LysAlaAlaArgTyrLeuProSerIleAlaSerGlyGluThrIleThrAlaAlaLeuThr 124

Qy  610 GAGCCAGCCAGTGGAGCGGATGCAGCCTCAATCCGAGCAGCAGCCACTAAGTGAGAC 669
         ||          :::||||||
Db  125 GluAlaGluAlaGlySerAspSerAlaSerValGlnThrArgAlaVal------ArgAsp 142

Qy  670 AAGAAGCACTACATCCTCAATGCGCTCGGATTACTAATGGAGGACTGGCCAAT 729
          :::          :::||||||
Db  143 GlyAspHisTyrValLeuAsnGlyValLysArgTyrIleThrAsnAlaGlyArgAlaAsn 162

Qy  730 ATTTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATCAGTAGAAAGACAAA 789
          :::          :::||||||
Db  163 LeuPheThrValMetAlaArgThrAspProAsnThrLysGlyGlyAla------Gly 179

Qy  790 ATCACAGCATTCATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAACCCAGAGAT 849
          ::::::||||::||||||
Db  180 ValSerAlaPheLeuValProAlaAspLeuProGlyLeuSerValGlyLysProGluLys 199

Qy  850 AAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAAACACCAGAATACCT 909
          ::::::::||||||
Db  200 LysMetGlyGlnGlyAlaHisIleHisAspValValPheGluAspValArgValPro 219

Qy  910 GTGGAAAACATCCTTGAGAGTCGGAGGATGGTTTAAGGTGGCCATGAACATCCTCAAC 969
         |||||||||:::    ::|||||||::   ::::::||||||
Db  220 ValGluAsnArgLeuGlyLeuAlaGluGlyGlyGlyIlyPheThrValAlaMetArgValLeuAsp 239

Qy  970 AGCGGCCGGTTCAGCATGGGCCAGCGTCGTGGGCTGCTGCTCAAGAGATTGATTGAAATG 1029
          |||                   :::||||||
Db  240 ArgGlyAlaArgValHisIleSerAlaValCysValGlyValAlaGluLeuAlaAsp 259

Qy 1030 ACTGCTGAGTACGCCTGCACAGAGAAAACAGTTAACAAGAGGCTCAGTGAATTGGATTG 1089
          :::||||||||||                   :::||||||
Db  260 CysValAlaArgGlyAlaTyrAlaSerGluArgLysGlnPheGlyLeuProIleAlaSerPheGlnLeu 279

Qy 1090 ATTCAG----------GAGAAATTTGCACTGATGGCTCAGAGGCTTACGCATG 1134
          |||          :::||||||
Db  280 IleGlnAlaMetIleAlaAspSerLysThrGluAlaLeuAlaAlaLeuLysAlaLeuValPhe 299

Qy 1135 GAGAGTATGACCTACCTCACAGCAGGGATGTCGGACCAACCTGGCGTTTCCGACTGCTCC 1194
          :::                   :::|||
Db  300 ------------------------------------------AlaAsnValThr 312
```

```
Db  135 GlyAlaValAlaArgThr------ThrAlaGluArgAspGlyAspTyrIleIleAsnGly 152
          :::          :::||||||
Qy  694 TCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTTTACTGTGTTGCAAAGACT 753
          ::|||          :::
Db  153 ThrLysArgPheIleThrAsnAlaProAlaValGlyValAlaPheThrLeuMetAlaArg--- 171

Qy  754 GAGGTCGTTGATTCTGATCAGTAGAAAGACAAAATCACAGCATTCATAGTAGAAAGA 813
          :::          :::||||||
Db  172 ---------MetGlyGlySerGlyProSerGlyIleSerAlaPheLeuValAlaGluArg 187

Qy  814 GACTTTGGTGAGTCACTAATGGGAAACCCAGAGATAAATTAGGCATTCGGGGCTCCAAC 873
          |||          :::::::||
Db  188 AspLeuProGlyLeuThrValGlyThrProAspHisLysMetGlyGlnArgGlyThrGln 207

Qy  874 ACTTGTGAAGTCCATTTGAAAAACACCAGAATACCTGTGGAAAACATCCTTGAGAGGTC 933
          ||||::::          :::::||
Db  208 ThrCysAspValTyrLeuGluValArgProAlaThrSerIleIleGluGluGlyValVal 227

Qy  934 --GGAGATGGGTTAAGGTGGCCATGAACATCCTCAACACGGGCCGGTTCAGCATGGGC 990
           ::: :::          :::||
Db  228 GluGluLysPheGlyPheThrAlaMetLysValLeuAspArgGlyAlaArgValHisIleSer 247

Qy  991 AGCGGCCGGTGCTGGGCTGTGCTCAAGAGATTGATTGAAAGATGACTGCTGAGCCCTGCACA 1050
          ||||||          :::   :::|||
Db  248 SerValCysAlaGlyValGlyThrAlaGlyGlyProIleGluGluGluValGlyLeuGlySer 267

Qy 1051 AGGAAAACAGTTTAACAAGAGGCTCAGTGAATTTGATTGATTCAGGAGAAATTTGCACTG 1110
          ||| :::          :::||||||
Db  268 ArgValGlnProHisGlyLysArgIleAlaGluGluHisGlnGlnIleMetLeuAlaMetLeuAlaAsp 287

Qy 1111 ATGGCTCAGAGGACGTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGGATGTCGGAC 1170
          ||          :::||||||
Db  288 MetSerThrGluAlaThrArgAlaGlyArgCysMetValLeuAspAlaAlaArgAlaPheAsp 307

Qy 1171 CAACCTGGCTTCCGACTGCTCCATCGAGGCAGCCATGTGAAGTGTTCAGCTCCGAG 1230
          ::: :::
Db  308 GluSerAsnVal---AspIleIleAlaGluLysArgAlaSerLysSerLysValPheCysSerSerGlu 326

Qy 1231 GCCGCCTGCCAGTGTGTGAGTGAGCGCGTCGAGTCCTCGGGGGCTTGGCTACACAAGG 1290
          |||          :::||||||
Db  327 MetValGlyTyrArgAlaValAlaAspAsnAlaValAlalleGlnIleHisGlyGlySerGlyTyrMetGln 346

Qy 1291 GACTATCCGTACGAGCGCCATACTGCGTGACACCCCGATCCTCCTCATCTTCGAGGGAACC 1350
          ||:::          :::|||
Db  347 AsnTyrProValGluHisProPheTyrArgAspValArgLeuPheArgLeuTyrGluGlyThr 366

Qy 1351 AATGAGAATTCTCCGGATGTACATCCGCC 1377
          ::: ||||||
Db  367 SerGlnIleGlnArgIleIleIleAla 375
```

RESULT 13
B87472
acyl-CoA dehydrogenase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87472
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:1259647
A;Accession: B87472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <STO>
A;Cross-references: UNIPROT:Q9A7C6; GB:AE005673; NID:gi13423230; PIDN:AAK23774.1; GSPDB:G
C;Genetics:
A;Gene: CC1798
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:

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Qy    1195  ATCGGAGGCAGCCATGGTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAG  1254
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Db     313  LeuGluAlaAlaAlaThrLysLeuPheAlaSerGluMetValGlyArgValAlaAspArg  332

Qy    1255  GCGCTGCAGATCCTCGGGGGCTTGGCGTACACAAGGGACTATCCGTACGAGCGCCATACTG  1314
            ||:::|||          |:::|||                |||:::
Db     333  AlaAlaValGlnValPheGlyGlyAlaGlyTyrValAlaAspTyrValIleGluArgLeuTyr  352

Qy    1315  CGTGACACCCGACCATCCTCCTCATCTTCGAGGAACCAATGAGATTCCGGATGTACATC  1374
            |||:::|||          |||||||          |:::|||
Db     353  ArgAspValArgIlePheArgIleTyrGlyIleValAlaSerGlnIleGlnLeuIleIle  372

Qy    1375  GCCCTGACGGGTCTGCAGCATGCCGGC  1401
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Db     373  AlaArgGluThrLeuLysArgGlyGly  381

RESULT 14
F84124

acyl-CoA dehydrogenase acdA [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84124
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <STO>
A;Cross-references: UNIPROT:Q9K6D1; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB075
C;Experimental source: strain C-125
C;Genetics:
A;Gene: acdA
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:                                  Length:          380
Score:                   7.77e-35           Matches:         156
Percent Similarity:      658.00             Conservative:    66
Best Local Similarity:   57.96%             Mismatches:      139
Query Match:             40.73%             Indels:          22
DB:                      14.61%             Gaps:            8
US-09-945-326-1 (1-2452) x F84124 (1-380)

Qy     250  GATGAACTTAATGAAATCAATCAGTTCTTCGGGACCCGTGGAAAAATTCTTCACTGAAGAG  309
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Db       7  AspGluGlnMetIleLysLysMet------------ValArgAspPheAlaGlyAsnGlu  23

Qy     310  GTG-----GACTCCCGAAAAATTGACCAGGAAGGGGAAAATCCCAGATGAAACTTTGGAG  363
            |||          :::          |||||:::|||          :::
Db      24  ValAlaProThrAlaGluGluArgAspGluGluGluAspGluArgPheAspAspPheAsp  43

Qy     364  AAATTGAAGAGCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAAGAATATGGTGGCCTGGGC  423
            |||:::||          |||:::               |||:::||
Db      44  GlnMetAlaGluLeuGlyLeuThrGlyIleLeuProTrpProGluGluGluTyrGlyIleGly  63

Qy     424  TTCTCCAACCATGTAC---TCAAGACTAGGGAGATCATCAGCATGGATGGGTCCATC  480
            :::          |||:::|||          |||
Db      64  AlaAspTyrValSerTyrValIleAlaValGluLeuSerArgValCysAlaSerThr  83

Qy     481  ACTGTGACCCTGGCCGCCGACCACGGGGATCATCCTGGCTGGCACT  540
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Db      84  GlyValThrLeuSerAlaHisSerLeuAlaSerTrpProValTyrLysPheGlyThr  103

Qy     541  GAGGAGCAGAAAGCCCAAATACTTGCCTAAACTGCGTCCGGGAGCACATTGCAGCCTTC  600
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Qy     601  TGCCTCACGGAGCCAGTGGGATGCAGCCGATGCAGCCGCCAATCCGGAGCGAGCCACTA  660
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Qy     721  CTGGCCAATATTTTACTGTGTTGCAAAGACTGAGTCGTTGATCTGATGGATCAGTG  780
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Db     162  IleAlaAspIleTyrIleValPheAlaValThrGlu-----------------  173

Qy     781  AAAGACAAA-----------ATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTC  828
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Db     174  ProGluLysArgHisLysGlyValSerAlaPheIleValGluAlaAspThrProGlyPhe  193

Qy     829  ACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCAT  888
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Qy     889  TTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAG  948
            |||||||||          |||               ||||||
Db     214  PheGluAspCysArgValProLysGluAsnLeuLeuGlyGluGlyLysAspGlyPheLys  233

Qy     949  GTGGGCCATGAACATCCTCAACGACGCCGGTTCAGCATGGCAGCCGTCTGGTCGGTGGGCTG  1008
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Db     234  IleAlaMetMetThrLeuAspGlyArgAsnGlyIleAlaAlaGlnAlaValGlyIle  253

Qy    1009  CTCAAGAGATTGATTGAATGAAATGACTGCTGAGTACGCCTGCACAAGGAAAACAGTTAACAAG  1068
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Qy    1069  AGGCTCAGTGAATTTGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTAC  1128
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            ||||||:::               :::
Db     312  TyrGlyLysGluSerAlaMetSerLysAlaAspPheAlaMetAspValThr  331

Qy    1249  AGTGAGGGCTGCAGATCCTCGGGGGCTTGGGCCGACATCCGTACCGAGCGGC  1308
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            :::||||||          |||
Db     352  TyrMetArgAspAlaLysIleThrGlnIleTyrGlnIleTyrGluGlyIleThrArgLeu  371

Qy    1369  TACATCGCC  1377
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Db     372  ValIleSer  374

RESULT 15
S55421

acyl-CoA dehydrogenase (EC 1.3.99.3) acdA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S55421; B69581
R;Glaser, P.; Danchin, A.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3:
A;Reference number: S55414
A;Accession: S55421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <GLA>
A;Cross-references: UNIPROT:P45867; EMBL:Z49782; NID:g853752; PIDN:CAA89868.1; PID:g85376
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fujita, M.; Fuma, S.; Galizzi, A.; Gallerc
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lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69581
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-379 <KUN>
A;Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PID:g2636254
A;Experimental source: strain 168
C;Genetics
A;Gene: acdA
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.:              1.77e-34        Length:         379
Score:                  652.50          Matches:        155
Percent Similarity:     58.42%          Conservative:   60
Best Local Similarity:  42.12%          Mismatches:     140
Query Match:            14.49%          Indels:         13
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US-09-945-326-1 (1-2452) x S55421 (1-379)

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Qy   457 ATCATCAGCATGATGGGTCCATCACTGTGACCCTGGCAGCGCCACCAGGCTATTGGCCTC 516
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Db    76 LeuSerLysValCysAlaSerThrGlyValThrLeuSerAlaHisIleSerLeuCysSer 95

Qy   517 AAGGGGATCATCTTGGCTGCCACTGAGGAGCAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCG 576
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Db    96 TrpProLeuPheAlaPheGlyThrGluGlnLysThrGluTyrLeuThrGlnLeuLeuAla 115

Qy   577 TCCGGGGAGCACATTGCAGCCTTCTCGCCTCACGGAGCCCAGTGGGAGCCGATGGCAGCC 636
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Db   116 LeuGlyGluLysIleGlyAlaPheAlaAlaLeuThrGlySerGlySerAspAlaGly 135

Qy   637 TCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCC 696
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Db   136 SerMetLysThrThrAlaGluArgIleGlyAsp------AspTyrValLeuAsnGlySer 153

Qy   697 AAGGTCTGATTACTAATGGAGGACTGGCCAATATTTTTACTGTGTTGCAAAGACTGAG 756
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Db   154 LysValPheIleThrAsnGlyGlyValAlaAspIleTyrIleValPheAlaValThr--- 172

Qy   757 GTCGTTGATTCTGATGGATCAGAGAAAGACAAA---ATCACAGCATTCATAGTAGAAAGA 813
         ||||| ||||||||||||||||              :::|||||||||||||||
Db   173 ------AspProGluLysLysLysGlyAlaValThrPheAlaPheIleValGluLysLys 188

Qy   814 GACTTTGGTGGAGTCACTAATGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAC 873
         |||||||||||  ||||:::||||||||||||||||||||||||
Db   189 AspPheGlyGlyPhePheThrGlyLysLysGluLysIleGlyLeuGlyIleArgSerPro 208

Qy   874 ACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTC 933
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Db   229 GlyGluGlyPheLysIleAlaMetLysThrLeuAspGlyGlyArgAsnGlyIleAlaAla 248

Qy   994 GTCGTGGCTGGCTGCTCAAGAGATTGAATGACTGCTGAGTACTACGCCTGCACAAGG 1053
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Db   249 GlnAlaValGlyIleAlaGlnGlnGlyAlaLeuAspAlaAlaLeuGlnTyrAlaLysGluArg 268

Qy  1054 AAACAGTTAACAAGAGGCTCAGTGAATTGATTGATTGAGAGAAATTTGCACTGATG 1113
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Db   367 GluIleGlnLeuArgLeuValIleSer 374

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Job time : 132.271 secs
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 2, 2005, 13:13:41 ; Search time 399.764 Seconds
(without alignments)
6281.796 Million cell updates/sec

Title: US-09-945-326-1
Perfect score: 4504
Sequence: 1 cgtgtgtgtgccctgcggc.........actgtaaaaaaaaaaaa 2452

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN_1_1_861 @runat_02052005_135410_22353 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3153	70.0	621	1	ACD9_HUMAN	Q9h845 homo sapien
2	2704	60.0	625	1	ACD9_MOUSE	Q8jzn5 mus musculu
3	2526	56.1	498	2	Q9H9W4	Q9h9w4 homo sapien
4	2374.5	52.7	622	2	Q6DDF2	Q6ddf2 xenopus lae
5	1739	38.6	343	2	Q9BUX5	Q9bux5 homo sapien
6	1365	30.3	655	1	ACDV_RAT	P45953 rattus norv
7	1360.5	30.2	659	2	Q7T2C2	Q7t2c2 brachydanio
8	1360	30.2	656	1	ACDV_MOUSE	P50544 mus musculu
9	1345	29.9	655	1	ACDV_BOVIN	P48818 bos taurus
10	1321	29.3	655	1	ACDV_HUMAN	P49748 homo sapien
11	1319	29.3	655	1	ACDV_MACFA	Q8hxy7 macaca fasc
12	1295.5	28.8	655	2	Q9V8T1	Q9v8t1 drosophila
13	1288	28.6	639	2	Q7Q868	Q7q868 anopheles g
14	1273.5	28.3	604	2	Q7Q870	Q7q870 anopheles g
15	1210.5	26.9	613	2	Q19057	Q19057 caenorhabdi
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17	895	19.9	589	2	Q67K07	Q67k07 symbiobacte
18	891.5	19.8	577	2	Q72KB1	Q72kb1 thermus the
19	845.5	18.8	594	2	Q631W4	Q631w4 bacillus ce
20	845.5	18.8	594	2	Q72Y79	Q72y79 bacillus ce
21	845.5	18.8	594	2	Q1XJ1	Q81xj1 bacillus an
22	845.5	18.8	594	2	Q6HBP9	Q6hbp9 bacillus th
23	845.5	18.8	600	2	Q815X2	Q815x2 bacillus ce
24	842.5	18.7	594	2	Q5F73	Q5f73 bacillus li
25	821	18.2	594	2	Q9K784	Q9k784 bacillus ha
26	819	18.2	172	2	Q9UNZ4	Q9unz4 homo sapien
27	815.5	18.1	594	2	O32176	O32176 bacillus su
28	789.5	17.5	594	2	Q8ENT4	Q8ent4 oceanobacil
29	751.5	16.7	569	2	Q738L4	Q738l4 bacillus ce
30	750.5	16.7	569	2	Q81DR7	Q81dr7 bacillus ce
31	749	16.6	569	2	Q6HJ21	Q6hj21 bacillus th
32	745.5	16.6	569	2	Q63BL2	Q63bl2 bacillus ce
33	742	16.5	569	2	Q81QR7	Q81qr7 bacillus an
34	737.5	16.4	571	2	Q65IW9	Q65iw9 bacillus li
35	734	16.3	169	2	Q9CZC5	Q9czc5 mus musculu
36	730.5	16.2	642	2	Q742M4	Q742m4 mycobacteri
37	719.5	16.0	382	2	Q8EM49	Q8em49 oceanobacil
38	713	15.8	386	2	Q7P5M8	Q7p5m8 fusobacteri
39	711.5	15.8	650	1	Y873_MYCTU	P63429 mycobacteri
40	711.5	15.8	650	1	Y897_MYCBO	P63430 mycobacteri
41	710	15.8	376	2	Q81JV7	Q81jv7 bacillus an
42	709.5	15.8	381	2	Q8R674	Q8r674 fusobacteri
43	709	15.7	158	2	Q7TSP3	Q7tsp3 rattus norv
44	705	15.7	376	2	Q72XA5	Q72xa5 bacillus ce
45	705	15.7	381	2	Q814S8	Q814s8 bacillus ce

ALIGNMENTS

RESULT 1
ACD9_HUMAN
ID   ACD9_HUMAN   STANDARD;   PRT;   621 AA.
AC   Q9H845; Q8WXX3;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
DE   (EC 1.3.99.-) (ACAD-9).
GN   Name=ACAD9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Dendritic cell;
RX   MEDLINE=22246103; PubMed=12359260; DOI=10.1016/S0006-291X(02)02336-7;
RA   Zhang J., Zhang W., Zou D., Chen G., Wan T., Zhang M., Cao X.;
RT   "Cloning and functional characterization of ACAD-9, a novel member of
RT   human acyl-CoA dehydrogenase family.";
RL   Biochem. Biophys. Res. Commun. 297:1033-1042(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura J., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung, and Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Has a dehydrogenase activity on palmitoyl-CoA (C16:0)
CC   and stearoyl-CoA (C18:0). It is three times more active on
CC   palmitoyl-CoA then on stearoyl-CoA. Has little activity on
CC   octanoyl-CoA (C8:0), butyryl-CoA (C4:0) or isovaleryl-CoA (C5:0).
CC   -!- COFACTOR: FAD (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed in most normal human
CC   tissues and cancer cell lines with high level of expression in
CC   heart, skeletal muscles, brain, kidney and liver.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   --
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF327351; AAL56011.1; -.
DR   EMBL; AK024012; BAB14775.1; -.
DR   EMBL; BC013354; AAH13354.1; -.
DR   EMBL; BC007970; AAH07970.1; -.
DR   PIR; JC7892; JC7892.
DR   HSSP; P15651; 1JQI.
DR   Genew; HGNC:21497; ACAD9.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.

DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Mitochondrion; Oxidoreductase; Transit peptide.
FT   TRANSIT   ?   ?   Mitochondrion (Potential).
FT   CHAIN   ?   621   Acyl-CoA dehydrogenase family member 9.
FT   ACT_SITE   426   426   Proton acceptor (By similarity).
FT   CONFLICT   397   397   A -> V (in Ref. 1).
SQ   SEQUENCE   621 AA;   68760 MW;   064BCE0378877F54 CRC64;

Alignment Scores:
Pred. No.:   Length: 621
Score: 4.28e-198   Matches: 621
Percent Similarity: 3153.00   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 70.00%   Gaps: 0
                                1

US-09-945-326-1 (1-2452) x ACD9_HUMAN (1-621)

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Qy    67 ATGAGCGGCTGCGGGTCTTCCTGCCACCACCAGGCTGCGGCTCGTGCCTGCGGGTCTG 126
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Db     1 MetSerGlyCysGlyLeuPheLeuPheArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy   127 GTGGTCTACCGCGAACCGGCGGTACTGCGCACCAGCCGCCTGTACAGGCTTTCGCC 186
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Db    21 ValValSerThrAlaAsnArgArgLeuArgThrSerProProValArgAlaPheAla 40

Qy   187 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTCCCATTCCAGAAGTAGC 246
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Qy   247 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCGTGGAAAAATTCTTCACTGAA 306
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Qy   307 GAGGTGGACTCCCGAGAAAATTGACCAGGAGGGAAAATCCCAGATGAAACTTTGGAGAAA 366
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Db    81 GluValAspSerArgGlyIleAspGlnIleAspLeuProAspGluThrLeuGluGlyLys 100

Qy   367 TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAAGAAGAAATATGGTGGCCTGGGCTTC 426
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Db   101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluGlyGlyLeuGlyLeuGlyPhe 120

Qy   427 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCACTGTG 486
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Db   121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy   487 ACCCTGGCAGCGCACCAGGGTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG 546
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrLeuAlaAlaHisGlnGlyIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160

Qy   547 CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCACATTGCAGCCTTCTGCCTC 606
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Db   161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180

Qy   607 ACGGAGCCCAGTGGGAGCCGATGGGAGCTCAATCCGAGCAGAGCCACACTAAGTGAA 666
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy   667 GACAAGAAGCACTACATCCTCAATGCCTTGGATTACTAATGGAGGACTGGCC 726
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Db   201 AspLysLysHisTyrIleLeuAsnGlySerLysSerValTrpIleThrAsnGlyGlyLeuAla 220

Qy   727 AATATTTTACTGTGTTGCAAAGACTGAGTCGTTGATTCTGATGGATCAGTGAAAGAC 786
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Db   221 AsnIlePheThrValPheAlaLysThrGluValLeuAspSerLeuIleLeuMetAspGlnTrpLysAspGly 240

Qy   787 AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGAAACCCGAA 846
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Db                                  621 Cys 621

RESULT 2
ACD9_MOUSE
ID   ACD9_MOUSE     STANDARD;      PRT;     625 AA.
AC   Q8JZN5; Q8BK76; Q8COB5;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
DE   (EC 1.3.99.-) (ACAD-9).
GN   Name=Acad9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
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Qy   847  GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA     906
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Db   261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle     280

Qy   907  CCTGTGGAAAACATCCTTGAGAGAGTCGGAGATGGTTAAGGTGCCATGAAACATCCTC     966
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Db   281  ProValGluAsnIleLeuGluGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu     300

Qy   967  AACAGCGGCCGGTTCAGCATGGGCAGCGTGCTGTGGCTGGGCGTGGCCGTGGTGGCCGCC     1026
                  ||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu     320

Qy   1027 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTAACAAGAGGCTCAGTGAATTTGGA     1086
                  || || ||||||||| |||||||||||||||||||||||||||||||||||||
Db   321  MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgGlySerGluPheGly     340

Qy   1087 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCCTTACGTCATGGAGAGTATGACC     1146
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Db   341  LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaLeuArgHisGlyGluTyrMetThr     360

Qy   1147 TACCTCCACAGGAGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCC     1206
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Db   361  TyrLeuThrAlaGlyMetLeuAspGlnProGlyPhePheProAspCysSerIleGluAlaAla     380

Qy   1207 ATGGTGAAGGTGTTCAGCTCCGAGGCCGCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC     1266
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Db   401  LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg     420

Qy   1327 ATCCTCCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACTCACCCGACGGGT     1386
                  ||||||| ||||||||||||| || ||||||||| || |||||||| ||| ||||||
Db   421  IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly     440

Qy   1387 CTGCAGCATCCCGGCCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG     1446
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Db   441  LeuGlnHisAlaGlyAlaGlyProSerLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal     460

Qy   1447 AGCACAGTGCATGGAGGATACCGGTTGGCCGGAGGCTTCGGACTCCCTGGGCCGAACTGTGGAC     1506
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Db   461  SerThrValMetAspThrArgLeuAlaGlyGlyPheArgLeuProGlyArgThrValAsp     480

Qy   1507 CTGGGGGCTGACAGGCAACCAATGAGTTGTGCACCCAGTCTTGCGACAGTGCCAACAAG     1566
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Qy   1567 TTTGAGGAGAACACCTACTGCTTCGGCGGACCGTGGAGACACTGCTCCGGTTTGGC     1626
                  ||||||| ||||||| ||||| ||||||| ||| |||||||| ||||||||||
Db   501  PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly     520

Qy   1627 AAGACCATCATGGAGGAGGAGCTGTACTGAAGCCGGGTGCCAACATCCTCATCAACCTG     1686
                  |||||||||||||||||||| ||||| |||||||| |||||||||||||| ||||
Db   521  LysThrIleMetGluGluGluLeuTyrLysAlaGlyValAlaAsnIleLeuIleAsnLeu     540

Qy   1687 TATGGCATGACGGCCGTGCTCTCGCGGGCCCAGCCGCCTCCATCCGCATGGCTCCGCAAC     1746
                  |||||||| || |||||||||||| || ||||| |||||| ||||||||||||||||
Db   541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgIleArgIleGlyLeuArgAsn     560

Qy   1747 CACGACCACGAGGTTCTTCTGGCCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC     1806
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Db   561  HisAspHisGluValLeuLeuAlaGlnHisLeuLeuArgAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu     580

Qy   1807 TTCAGCCTCTCTCAGCTGACAAGTATGCTTCCAGAAAACCTAGATGAGCAGATTAAGAAA     1866
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Db   581  PheSerLeuSerGlnLeuThrSerMetLeuProGluAsnLeuAspGluGlnIleLysLys     600

Qy   1867 GTGTTCCCAGAGATCCTTGAGAAGGGAGCCTATATCTGTGCCCACCCTCTGGACAGGACA     1926
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Db   601  ValSerGlnIleLeuGluLysGlyAlaTyrIleCysAlaHisProLeuAspArgThr     620

Qy   1927 TGC 1929
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RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC  -!- FUNCTION: Has a dehydrogenase activity on palmitoyl-CoA (C16:0)
CC      and stearoyl-CoA (C18:0). It is three times more active on
CC      palmitoyl-CoA then on stearoyl-CoA. Has little activity on
CC      octanoyl-CoA (C8:0), butyryl-CoA (C4:0) or isovaleryl-CoA (5:0)
CC      (By similarity).
CC  -!- COFACTOR: FAD (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC  -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC  --------------------------------------------------------------------------
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  --------------------------------------------------------------------------
DR  EMBL; AK031820; BAC27565.1; -.
DR  EMBL; AK075984; BAC36096.1; -.
DR  EMBL; BC031137; AAH31137.1; -.
DR  EMBL; BC032213; AAH32213.1; -.
DR  EMBL; BC033277; AAH33277.1; -.
DR  PIR; PT0697; PT0697.
DR  PIR; PT0721; PT0721.
DR  HSSP; P15651; 1JQI.
DR  MGD; MGI:1914272; Acad9.
DR  InterPro; IPR006089; Acyl-CoA dh.
DR  InterPro; IPR006090; Acyl-CoA_dh_C.
DR  InterPro; IPR006091; Acyl-CoA dh_M.
DR  InterPro; IPR006092; Acyl-CoA dh_N.
DR  InterPro; IPR009100; AcylCoA_denyd_NM.
DR  InterPro; IPR009075; AcylCoADH_C_like.
DR  Pfam; PF00441; Acyl-CoA dh; 1.
DR  Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR  Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR  PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR  PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW  FAD; Flavoprotein; Mitochondrion; Oxidoreductase; Transit peptide.
FT  TRANSIT       1       ?      Mitochondrion (Potential).
FT  CHAIN         ?      625     Acyl-CoA dehydrogenase family member 9.
FT  ACT_SITE    430      430     Proton acceptor (By similarity).
FT  CONFLICT     15       15     A -> G (in Ref. 1; BAC27565).
FT  CONFLICT     53       53     K -> E (in Ref. 1).
FT  CONFLICT    163      163     D -> E (in Ref. 1).
FT  CONFLICT    540      540     I -> V (in Ref. 1; BAC27565).
SQ  SEQUENCE    625 AA;  68707 MW;  4F06FFBFD82F022 CRC64;

Alignment Scores:
Pred. No.:
Score:                   1.21e-168          Length:         625
Percent Similarity:      91.81%             Matches:        2704.00
Best Local Similarity:   85.71%             Conservative:   38
Query Match:             60.04%             Mismatches:     47
DB:                                         Indels:         4
                                            Gaps:           1

US-09-945-326-1 (1-2452) x ACD9_MOUSE (1-625)

Qy   67 ATGAGCGGCTGCGGGGTCGCGGGTCTTCCTCGGC----------ACCACGGCTGCGGCTCGTGCC 114
            ||||||||   || ||    ||| |||||||||||         ||||||||||||| |||||
Db    1 MetSerGlyCysValLeuLeuSerArgValAlaGlyAlaThrAlaAlaAlaAlaAlaAlaArgAla 20

Qy  115 TGCCCGGGGTCTGGTGGTCTCTACCGGAACCGGCGACTACGCCTGCGCACCAGCCCGCCTGTA 174
            |||| ||    |||| ||    |||| |||| ||||||
Db   21 SerArgValLeuArgValGluPheThrAlaArgArgProLeuHisThrSerLeuGlnSer 40

Qy  175 CGAGCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGAAGAGTTTTCCCATTT 234
            ||||    |    || |||||||||||          ::: || || ||
Db   41 CysSerPheAlaLysGluLeuPheLeuGlyLysAsnIleLysGlnIleLysGlyValPheProPhe 60

Qy  235 CCAGAAGTTAGCCAAGATGAACTAATGAAATCAATCAGTTCTTGGACCCGTGGAAAAA 294
            ||||||||||||||||||||||  :::||||||| ::::|||||||||||
Db   61 ProGluValSerGlnHisGluLeuSerGluIleLeuAsnGlnPheValGlyProLeuGluGluLys 80

Qy  295 TTCTTCACTGAAGAGAGTGGACTCCCGAAAAATTGACCAGGAGGAAGGAAAATCCCAGATGAA 354
            ||||||||||||||||||||  :: :: ||||||||||||||||||
Db   81 PhePheThrGluGluSerGlyLeuProLysAsnLeuAspGlnGluGlyLysIleProValAsp 100

Qy  355 ACTTGGAGAAATTGAAGAGCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAAATATGGT 414
            |||||||||||||||||||||||||||||||| :::||||||||||||
Db  101 ThrLeuGluLysLeuLysSerLeuGlyLeuPheGlyIleValProGluGluTyrGly 120

Qy  415 GGCCTGGCTTCCACACCATGTACTCAAGACTGACTAGGGGGAGATCATCAGCATGGATGGG 474
            ||||||| ||      :::||||||||| |||||||||
Db  121 GlyLeuGlyLeuSerAsnThrMetTyrAlaArgLeuGlyGluIleIleSerLeuAspAla 140

Qy  475 TCCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCT 534
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  141 SerIleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuVal 160

Qy  535 GGCACTGAGGAGCAGAAAGCCAAAATACTTGCCTAAACTGGGCTCCGGGGAGCACATTGCA 594
            |||      :::|||||||||||||||||||| ::: ::|||||||||||||
Db  161 GlyAlaGluGluGlnLysAlaLysIleLeuAlaTyrLeuProLysSerGlySerGlyGluHisIleAla 180

Qy  595 GCCTTCTGCCTCACGGAGCCCAGTGAGGACGATGCAGCCTCAATCCGGAGCAGAGCC 654
            ||||||||||||||||||||||||||||||||| :::|||||||||||||
Db  181 AlaPheCysLeuThrGluProAlaSerGlyAlaAspAlaAlaSerIleArgThrArgAla 200

Qy  655 ACACTAAGTGAAGACAAGAAGCACTACATCCTCCAATGGCTCCAAGGTCTGATTACTAAT 714
            ||| :::||||||||||||||||||||||||||||||| || ||||||||||
Db  201 ThrLeuSerGluAspLysLysHisTyrPheIleLeuAsnGlySerLysValTrpIleThrAsn 220

Qy  715 GGAGGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTGTCGTTGATTCTGATGGA 774
            |||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  221 GlyGlyLeuAlaAsnIlePheThrValPheAlaLysThrGluValSerLeuIleLeuMetGly 240

Qy  775 TCAGTGAAAGACAACAAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGGAGTCACTAAT 834
            ||| :::||||||||||||||||||||||||| :::|||||||||||||
Db  241 SerLysThrAspLysMetThrAlaPheIleValGluArgAspPheGlyGlyIleThrAsn 260

Qy  835 GGGAAACCCGAAGATAAATTAGGCATTCGGGGGCTCCAACACTTGTGAAGTCCATTTTGAA 894
            |||||||||| |||||||||||||||||||||||| || ::: ::||||||||
Db  261 GlyLysProGluAspLysLeuGlyIleLeuArgGlySerAsnThrCysGluValHisPheGlu 280

Qy  895 AACACCAAGATACCTGTGGAAAACATCCTTGGAGAGTCCGAGATGGGTGGTTAAGGTGGCC 954
            |||||||| ||||| :::||||||||||||||||||||||||| ||||||||||||
Db  281 AsnThrArgValProValGluAsnValLeuGlyGluValLeuGlyGlyPheLysValAla 300

Qy  955 ATGAACATCCTCAACAGCGGCCGGTTCAGCATGGAGAGTGGTTCAGCTTCAGCTTCAAG 1014
            |||||||||||  :::||||||||||||||||||||||||| :::||||||||||||
Db  301 MetAsnIleLeuAsnSerGlyArgPheSerMetGlySerAlaValAlaGlyMetLeuLys 320

Qy 1015 AGATTGATTGAAATGACTGCTGAGTACGGCTCGACCAAGGAAACAGTTAACAAGAGGCTC 1074
            :::|||||||||||||||| ||| ::: :::||||||||||||
Db  321 LysLeuIleGluLeuMetThrSerGlyMetLeuAspGlnProGlyPheProAspCysSer 340

Qy 1075 AGTGAATTTGGATTGATTCAGGAGAAATTTGCACTGATGCTCAGAAGGCTTACGTCATG 1134
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  341 SerGluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMet 360

Qy 1135 GAGAGTATGACCTACCTCACCAGAGGGATGCTGACCAACCTGGCTTCCGACTGCTCC 1194
            ||||   :::||||||||||||||||||||
Db  361 GluSerMetAlaTyrLeuThrSerGlyMetLeuAspGlnProGlyPheProAspCysSer 380

Qy 1195 ATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCGCAGTGTGTGAGTGAG 1254
            ||||||| ||    |||| || ||    ||||| |||||
Db  381 IleGluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGlu 400

Qy 1255 GCGCTGCAGATCCTCGGGGGCTTGGGCTCACAAGGGACTATCCGTACGAGCGCCATACTG 1314
            ||||||||||||||  ||| :::|||||||||||||
Db  401 AlaLeuGlnIleLeuGlyGlySerGlyTyrMetLysAspTyrProTyrGluArgMetLeu 420

Qy 1315 CGTGACACCCGCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATC 1374
            |||||||| :::|||||||||||||||||||||||||| :::||||||||||||||
Db  421 ArgAspAlaArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgLeuPheIle 440
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Qy   1375  GCCCTGACGGGTCTGCAGCATGCCGGCCCATCCTGACTACCAGATCCATGAGCTTAAA  1434
                 ||||||||||||||||| ||||||||||||||||| :::|||||||||||||||
Db    441  AlaLeuThrGlyLeuGlnHisAlaGlyTyrArgIleLeuThrSerArgIleLysGluLeuLys  460

Qy   1435  CAGGGCAAAGTGAGCACAGTCATGATGAACCGTTGGCCGGAGGCCTTCGGGACTCCCTGGGC  1494
                 ||:::|||||||||||||||||::|||||||||||||||||||||||||||||||||
Db    461  SerGlyAsnValThrThrValMetGluThrIleGlyTrpIleGlyArgLysLeuArgAspSerLeuGly  480

Qy   1495  CGAACTGTGGACCTGGGGCTGACAGCAACCATGAGTTGTGCACCCAGTCTTGCGGAC  1554
                 ||||||||||||||||||| ||||::|| |||||||||||||||
Db    481  ArgThrValAspLeuGlyLeuThrGlyLeuThrArgAspLeuGluGlyValValHisProSerLeuGlyAsp  500

Qy   1555  AGTGCCAACAAGTTTGAGGAGAACACCTACTGCTTCGGGCACCGTGGAGACACTGCTG  1614
                 ||:||||||||    :::||||||  |||||||||||||||||||||||||
Db    501  SerAlaAsnLysLeuGluGluAsnThrTyrPheGlyArgThrValGluThrLeuLeu  520

Qy   1615  CTCCGCTTTGGCAAGACCATCATGAGGAGGACAGCAGTTGGTACTGAAGCGGGTGGCCAACATC  1674
                 ||||||||||||||::|||||||||||||||||||||||||||||||||||||||
Db    521  LeuArgPheGlyLysAsnIleValGluGlnLeuValLeuLysArgValAlaAsnIle  540

Qy   1675  CTCATCAACCTGTATGGCATGACGGCCGTGCTGTCTCGCGGGCCAGCCGCCTCCATCCGCATT  1734
                 |||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db    541  LeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgArgAlaSerArgSerIleArgIle  560

Qy   1735  GGGCTCCGCAACCACGACGAGTTCTCTTGGCCAACAACCTTCTGCCGTGGAAGCTTAC  1794
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561  GlyLeuArgAsnHisAspGluPheSerTrpProThrThrPheCysValGluAlaTyr  580

Qy   1795  TTGCAGAATCTTCTTCAGCCTCTCTCAGCTGACAAGTATGCTCCAGAAAACCTAGATGAG  1854
                 ||||||||||||||||||||||||||||||||||||::|||||||||||||||||
Db    581  PheGlnAsnLeuLeuSerLeuSerGlnLeuSerAlaAspLysAsnLeuAspGlu  600

Qy   1855  CAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGGAGAGCCTATATCTGTGCCACCCT  1914
                 |||||||||::|||||||||||||||||||||||||||||||||||||||||||
Db    601  GlnIleLysLysValSerValSerArgGlnIleLeuGluLysGluArgAlaTyrIleLeuCysAlaHisPro  620

Qy   1915  CTGGACAGG  1923
                 ||||||||
Db    621  LeuAspArg  623
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RESULT 3
Q9H9W4

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ID   Q9H9W4;           PRELIMINARY;       PRT;      498 AA.
AC   Q9H9W4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ12506.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita S.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; AK022568; BAB14104.1; -.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR005829; Sug_transporter.
DR   Pfam; PF00441; Acyl-CoA_dh;_1.
DR   Pfam; PF02770; Acyl-CoA_dh_M;_1.
DR   Pfam; PF02771; Acyl-CoA_dh_N;_1.
DR   PROSITE; PS00072; ACYL_COA_DH_1;_1.
DR   PROSITE; PS00073; ACYL_COA_DH_2;_1.
DR   PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE   498 AA;   55083 MW;  A57B7121B8FB1310 CRC64;
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Alignment Scores:

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Pred. No.:                        1
Score:                            5.25e-157      Length:          498
Percent Similarity:               2526.00        Matches:         498
Best Local Similarity:            100.00%        Conservative:      0
Query Match:                      100.00%        Mismatches:        0
DB:                               56.08%         Indels:            0
                                  2              Gaps:              0
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US-09-945-326-1 (1-2452) x Q9H9W4 (1-498)

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Qy    436  ATGTACTCAAGACTAGGGGAGATCATCAGCATCAGCATGGGTCCATCACTGTGACCCTGCA  495
                1  MetTyrSerArgLeuGlyGluIleIleSerIleSerMetGlyGlySerIleThrValThrLeuA  20

Qy    496  GGGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGGAGAAAGCC  555
               21  AlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuLeuAlaGlyThrGluGluGlnLysAla  40

Qy    556  AAATACTGCCTAAACTGGCGTCCGGGAGCACATTGCAGCCTTCTGCCTCTCACGGAGCCA  615
               41  LysTyrLeuProLysLeuAlaSerGlyValGluHisIleAlaAlaPheCysLeuThrGluPro  60

Qy    616  GCCAGTGGGAGCCGATGCCAGCCTCAATCCGGAGCAGAGCCACCAATAAGTGAAGACAAGAAG  675
               61  AlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGluLeuSerGlyLys  80

Qy    676  CACTACATCCCTCAATGGCTCCAAGGTCTGATTACTAATGAGGACTGGCCAATATTTTT  735
               81  HisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAlaAsnIlePhe  100

Qy    736  ACTGTGTTTGCAAAGACTGAGGTCGTTGATTCTGATCAGTCAGTGAAAGACAAAATCACA  795
              101  ThrValPheAlaLysThrGluValValAspSerAspGlnSerValLysAspLysIleThr  120

Qy    796  GCATTCATAGTAGAAAGAGACTTTGTGGAGTCACTAATGGGAAATGCCGAAGATAATTA  855
              121  AlaPheIleValGluArgAspPheGlyValThrAsnGlyLysAlaGluAspAsnLysLeu  140
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ID   Q6DDF2      PRELIMINARY;      PRT;   622 AA.
AC   Q6DDF2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Acad9-prov protein.
GN   Name=acad9-prov;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocytes;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocytes;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocytes;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; BC077618; AAH77618.1; -.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE 622 AA;  68429 MW;  1BA5F489FF08A9C9 CRC64;
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Alignment Scores:
Pred. No.:                             622
Score:                                 453
Alignment Scores:          4.93e-147    Length:
Score:                     2374.50      Matches:
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Qy    856 GGCATTCGGGGCTCCAACACTTCTGAAGTCCATTTGAAAACACCAGATACCTGTGGAA 915
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Db    141 GlyIleArgGlySerAsnThrSerGluValHisPheGluGluThrLysIleProValGlu 160

Qy    916 AACATCCTTGGAGAGGTCGGAGATGGGGTTTAAGGTGCCATGAACATCCTCAACAGCGGC 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 AsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeuAsnSerGly 180

Qy    976 CGGTTCAGCATGGCAGCGTCGTGGCTGGGCGTGCTCAAGAGATTGAAATGACTGCT 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuMetThrAla 200

Qy   1036 GAGTACGGCCTGCACAAGGAAACAGTTAACACAGAGGCTCAGTGAATTGATTGATTCAG 1095
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Db    201 GluTyrAlaCysThrArgLysThrArgLysGlnPheAsnLysArgLeuSerGluPheLeuLeuGln 220

Qy   1096 GAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACA 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrTyrLeuThr 240

Qy   1156 GCAGGGATGCTGACCAACCTGGCTTCCGCACTGCTTCCATCGAGCAGCCATGGTGAAG 1215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AlaGlyMetLeuAspGlnProGlyPhePheProAspCysSerSerIleGluAlaAlaMetValLys 260

Qy   1216 GTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCCGGGGC 1275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 ValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIleLeuLeuGlyGly 280

Qy   1276 TTGGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGGCATCCTCTC 1335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 LeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArgIleLeuLeuLeu 300

Qy   1336 ATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCAT 1395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IlePheGluGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyLeuGlnHis 320

Qy   1396 GCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTC 1455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 AlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysValSerThrVal 340

Qy   1456 ATGGATACCGTTGGCCGGAGGCTTCGGAGCTCCCTGGGCCGAACTGTGACCTGGGGCTG 1515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 MetAspThrValGlyArgArgLeuArgSerLeuGlyArgThrValThrTrpGlyLeu 360

Qy   1516 ACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGGGCAACAGTGCCAACAAGTTTGAGGAG 1575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu 380

Qy   1576 AACACCTACTGCTTCGGGCGACCGTGGAGACACTGCTGCTCCGCTTTGGCCAAGACCATC 1635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 AsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGlyLysThrIle 400

Qy   1636 ATGGAGGAGCAGCTGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATG 1695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 MetGluGluGlnLeuTyrArgValAlaAsnIleLeuIleAsnLeuTyrGlyMet 420

Qy   1696 ACGGCCGTGCTGTCCGCGGGCCAGGCCGCCTCCATCGGCCATTGGGCTCCGCAACCACCAC 1755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsnHisHis 440

Qy   1756 GAGGTTCTTTGGCCAACACCTTCTGCGTGGAAGAGCTTACTTGCAGAATCTCTTCAGCCTC 1815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 GluValLeuLeuAlaAsnThrPheCysValGluAspLeuAsnLeuPheSerLeu 460

Qy   1816 TCTCCAGCTGGACAAGTATGCTCCAGAAAAACCTAGTAGCAGATTAAGAAAGTGTCCCAG 1875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 SerGlnLeuAspLysSerTyrAlaProGluAspGluGlnIleLysLysLysValSerGln 480

Qy   1876 CAGATCCTTGAGAAGCAGAGCCTATATCTGTGCCCACCCTCTGGACAGGACATGC 1929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThrCys 498
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```
RESULT 4
```

Wed May 11 06:57:40 2005

Percent Similarity:	85.41%	Conservative:	74
Best Local Similarity:	73.42%	Mismatches:	87
Query Similarity:	52.72%	Indels:	3
DB:	2	Gaps:	1

US-09-945-326-1 (1-2452) x Q6DF2 (1-622)

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Qy     76  TGCGGGCTCTTCCTCGCCACACGGCTCGCCTCGCCTCGCGGGGTCTCGTGGTCTCT  135
               |||||||    ||   |||        |||||  ||    || ||||||
Db      8  CysGly--------ArgAlaAlaSerLeuThrArgValTrpAlaGlyProAlaGlyPro  24

Qy    136  ACCGGAACCGGCGGCTACTCGCCACCAGCCCGCCTGTACGAGCCCTTCGCCAAAGAGCTT  195
               ||||                   ||||         |||||||||
Db     25  GluLeuPheProArgSerPheThrCysSerProHisArgLeuAlaTyrAlaLysGluLeu  44

Qy    196  TTCCTAGGCAAAATCAAGAGACAAGAAGAGTTTCCATTTCCAGAGAGTTAGCCAAGATGAA  255
               ||||||    ||:::|          ||:|:|:||||
Db     45  PheLeuGlySerIleLeuArgLysAspGluValPheProGluIleSerLysGluGlu  64

Qy    256  CTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAGAGGTGGAC  315
               :||   ||||||            |||||||||       ||:::|
Db     65  LeuGluGluGlnPheAlaValAlaProValGlyLysPhePheAsnGluGluValAlaAsp  84

Qy    316  TCCCGAAAAATTGACCAGGAGGGAAAACTTTGGAGAAATTTGAAGAGC  375
               ||:: |||||||       |||||||       ||:::
Db     85  SerLysLeuIleAspGlnThrAlaLysIleProGluThrLeuAspLysGlyLeuLysAsn  104

Qy    376  CTAGGGCTTTTTGGGCTGCAAGTCCAGAGAATATGTGGCCTGGCCTTCTCCAACACC  435
               ||||||||||:::||||||                |||||:||
Db    105  LeuGlyLeuPheGlyLeuGlnIleProGluGluTyrGlyGlyLeuGlyLeuSerAsnThr  124

Qy    436  ATGTACTCAAGACTAGGGGAGATCATCAGCATGGTCCATCACTGTGACCCTGGCA  495
               |||||||||||||        |||        |||||
Db    125  MetTyrAlaArgLeuGlyGluIleIleSerLeuAspGlyAlaIleAlaValThrLeuAla  144

Qy    496  GCGCCACCAGGCTATTGGCCTCAAGGGAGCATCTTGGCTGCTGCACTGAGGAGCAGAAAGCC  555
               |||||:::||||||         |::||
Db    145  AlaHisGlnAlaIleGlyLeuLeuLysGlyIleIleLeuAlaGlyAsnAspGluGlnGlnLysAla  164

Qy    556  AAAATACTTGCCTAAACTGCCTCCGGGGAGCACATTGCAGCCTTCGCCCTTGCTCCAGGAGCCA  615
               ||||:::|||         ||:|||          ||||:||
Db    165  LysTyrLeuProLysGlyLeuAlaSerGlyGluHisIleAlaAlaPheCysLeuThrGluPro  184

Qy    616  GCCAGTGGAGGCGATGGACAGCCTCAATCCGGAGCAGAGCCACTAAGTGAGAACAAGAAG  675
               |||||||:|||||                 |||||:|:
Db    185  GlySerGlySerAspAlaAlaSerIleGlnSerArgAlaThrLeuProLeuProAspGlyLys  204

Qy    676  CACTACTACCTCCAATGGCTCGAAGGTCTCGGATTACTAATGGAGAGGACTGGCCAATATTTT  735
               ||||:::||||||||         |||||:||
Db    205  HisPheLeuLeuAsnGlySerLysTrpIleSerTrpIleSerAsnGlyGlyValIleLeuAlaAspIlePhe  224

Qy    736  ACTGTGTTTGCAAAGACTGAGGTCGTTGATGATGATGAGTCAGTGAAAGAACAAAATCACA  795
               |||||||:::|||||        |||||:|:
Db    225  ThrValPheAlaArgThrGluValValAspAspAspGlyValThrLysLysAspLysIleSer  244

Qy    796  GCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCGAAGATAAATTA  855
               |||||||||||||||         |||||:||:||
Db    245  AlaPheIleValGluArgAspPheGlyGlyValThrHisGlyAsnArgThrArgLysLeuAsnGlyLeuProAspLysLeu  264

Qy    856  GGGCCATTCGGGGCTCCAACACTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAA  915
               ||||||||:::||||||         ||:::|
Db    265  GlyIleLeuArgGlySerAsnThrCysGluLeuHisPheGluGlnAsnThrLysValProValGlu  284

Qy    916  AACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACGACGGC  975
               ||:::||||||||||         |||:|:|
Db    285  AsnValIleGlyValGlyGlyGlyGlyGlyPheLysGlyValAlaAlaMetAsnIleLeuAsnSerGly  304

Qy    976  CGGTTCAGCATGGGCAGCGTGTGCTGGGCTGTGCTCAAGAGATTGATTGAAATGACTGCT  1035
               |||||||||||||         ||:::|:|
Db    305  ArgPheSerMetGlySerAlaSerAlaGlyIleIleLysLeuLysGluIleGluMetThrAla  324

Qy   1036  GAGTACGCCTGCACAAGGAAACAGTTTAACAGAAGGCTCAGTGAGTTGATTGATTCAG  1095
               ||||||||||||         |||||||
```

```
Db    325  GluTyrAlaCysThrArgLysGlnPheAsnLysLysLeuSerAspPheGlnLeuIleGln  344

Qy   1096  GAGAAATTGCACTGATGGCTCAGAAGGCTTAGTCATGGAGAGTATGACCTACCTCACA  1155
               ||||||||||||||:::||                |||||||||
Db    345  GluLysPheAlaLeuMetAlaGlnLysAlaPheValMetGluSerMetAlaTyrLeuThr  364

Qy   1156  GCAGGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATGAGGCAGCCATGGTGAAG  1215
               ||||||||||||:::|||                |||||||||
Db    365  AlaGlyMetMetAspArgProGlyLeuProAspCysSerValAlaAlaMetValSys  384

Qy   1216  GTGTTCAGCTCCGAGGCCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGC  1275
               ||||||||||||:::||                |||||||
Db    385  ValPheSerSerGluGlyLeuAlaTrpLeuCysValSerGluAlaLeuGlnIleLeuGlyGly  404

Qy   1276  TTGGGCTACACAAGGGACTATCCGTACAGACGCGCGATACTGCGTGACACCGGCATCCTCTC  1335
               ||||||||||||:::|||                |||||:|:
Db    405  LeuGlyTyrMetLysAspTyrProTyrGluArgTyrLeuArgAspAspSerArgIleLeuLeu  424

Qy   1336  ATCTTCGAGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCAT  1395
               |||||||||:::||                |||||:||
Db    425  IlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyMetGlnHis  444

Qy   1396  GCCGGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCAGTC  1455
               ||||||||||||:: |||                |||||||||
Db    445  AlaGlyLysIleLeuThrGlyIleLeuGlumetLysGlyAsnValGlyValAla  464

Qy   1456  ATGGATACCGTTGGCCCGAGGCTTCGGGGACCTCCCTGGGCCGAACTGTGGACCTGGGGCTG  1515
               ||:::||                |||||:|:
Db    465  MetGluLeuPhePheLysLeuArgAspSerMetGlyArgAsnValAsnLeuGlyLeu  484

Qy   1516  ACAGGCAACCATGTGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAGTTGAGGAG  1575
               ||||||||||||:::||:|                |||||:|:
Db    485  ThrGlyAsnGlyGlyValIleHisProSerLeuGluSerValGlyLeuGluGlu  504

Qy   1576  AACACCTACTGCTTCGGCGACCGTGGAGACACTGCTTCTCCGCTTTGGCAAGACCATC  1635
               ||||||||||||||         |||||:|:
Db    505  AsnValTyrTyrPheGlyThrThrValGluSerLeuIleLeuTyrArgPheGlyLysThrIle  524

Qy   1636  ATGGAGGAGCAGCTGGTACTGGAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATG  1695
               ||||||||||||||:::||                |||||||
Db    525  ValGluGluGlnLeuGluLeuLysLysArgValAlaAlaAspValIleIleLeuAsnLeuTyrAlaMet  544

Qy   1696  ACGGCCGTGTCGTGCGGGGCCAGCCGCCTCCGCCAATCCGGCATTGGGCTCCGCAACGACCAC  1755
               ||||||||||||:::|                |||||:|:
Db    545  ThrAlaValIleSerArgAlaSerArgArgSerValGlyLeuProAsnHisAspHis  564

Qy   1756  GAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCTGGAAGATCTCTTCAGCCTC  1815
               |||||||||:::|:|                |||||||
Db    565  AspValLeuLeuLysAlaAsnMetPheCysSerGluValTyrPheLysAspAsnTyrThrLeu  584

Qy   1816  TCTCAGCTGGACAAGTATGCTCCAGAAAACTAGATGAGCAGATTAAGAAAGTGTCCCAG  1875
               ||:::||                |||||:|:
Db    585  AlaGlnLeuGlyLysHisSerProGluAsnGlnAsnAspAspSerIleArgLysIleAlaGlyGly  604

Qy   1876  CAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCTCTGGACACGACA  1926
               ||||||||||:::||||                |||||||||
Db    605  HisIleLeuGluLysArgGlyTyrThrCysSerHisProLeuAspArgThr  621
```

RESULT 5

Q9BUX5

ID	Q9BUX5	PRELIMINARY;	PRT;	343 AA.

AC   Q9BUX5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ACAD9 protein (Fragment).
GN   Name=ACAD9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.

```
Db   101 AlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeu 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261 CAGATCCTCGGGGCTGGGCTACACAGGACTATCCTGACGAGCCGCCATACTGCCTGAC 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GlnIleLeuGlyAlaGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAsp 140

Qy  1321 ACCCGACCATCCTCCATCTTCCGAGGAACCAATGAGATTCTCCGGATGTACATCGCCCTG 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeu 160

Qy  1381 ACGGGTCTGCAGCATGCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCC 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 ThrGlyLeuGlnHisAlaAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAla 180

Qy  1441 AAAGTGAGCACAGTCACATGGATACCGTTGGCGGAGCTTCGGGAGCTCCCGGCCGAACT 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LysValSerThrValMetAspThrValGlyArgArgLeuArgAspSerArgLeuGlyArgThr 200

Qy  1501 GTGGACCTGGGCTGACAGGCAACCATGAGTGTGCACCCCAGTCTGCGGACAGTGCC 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 ValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAla 220

Qy  1561 AACAAGTTGAGGAGAACACTACTGCTTCCGGCACCGTGGAGACACTGCTGTCCGC 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArg 240

Qy  1621 TTTGGAAGACCATCATGAGGAGCAGCTGTGTACTGAAGCGGTGGCCAACATCCTCATC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PheGlyLysThrIleMetGluGluGlnLeuGluValLeuLysArgValAlaAsnIleLeuIle 260

Qy  1681 AACCTGTATGGCATGACGGCCGTGCTGTCCGCGGGACCCAGCCGCTCCATCCGCATTGGGGTC 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnLeuTyrGlyMetThrAlaValLeuSerAlaValLeuSerArgAlaSerArgIleGlyGlyLeu 280

Qy  1741 CGCAACCACGACCACGAGGTTCTCTTGGCCAACACCTTCTCGTGGAAGCTTACTTGCAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGlnAlaTyrLeuGln 300

Qy  1801 AATCTCTTCAGCCTTCTCAGCTGACACAGTATGCTCCAGAAAACTAGATGAGCGAGCAGATT 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleIle 320

Qy  1861 AAGAAAGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCCTGGAC 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 LysLysValSerGlnGlnIleLeuGluLysAlaSerLeuTyrIleCysAlaHisProLeuAsp 340

Qy  1921 AGGACATGC 1929
         |||||||||
Db   341 ArgThrCys 343
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RESULT 6
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ACDV_RAT
ID   ACDV_RAT        STANDARD;      PRT;   655 AA.
AC   P45953;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD).
GN   Name=Acadvl; Synonyms=Vlcad;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=Wistar; TISSUE=liver;
RX   MEDLINE=94308174; PubMed=8034667;
RA   Aoyama T., Ueno I., Kamijo T., Hashimoto T.;
RT   "Rat very-long-chain acyl-CoA dehydrogenase, a novel mitochondrial
RT   acyl-CoA dehydrogenase gene product, is a rate-limiting enzyme in
RT   long-chain fatty acid beta-oxidation system. cDNA and deduced amino
```

RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC001817; AAH01817.2; -.
DR   HSSP; P15651; 1JQI.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA dh.
DR   InterPro; IPR006090; Acyl-CoA dh_C.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR005829; Sug_transporter.
DR   Pfam; PF00441; Acyl-CoA dh; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
DR   PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
FT   NON_TER   1
SQ   SEQUENCE 343 AA; 38569 MW; 10E178193774SC00 CRC64;

Alignment Scores:
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Pred. No.:            1.9e-105          Length:        343
Score:                1739.00           Matches:       343
Percent Similarity:   100.00%           Conservative:    0
Best Local Similarity:100.00%           Mismatches:      0
Query Match:          38.61%            Indels:          0
DB:                                     Gaps:            0
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US-09-945-326-1 (1-2452) x Q9BUX5 (1-343)

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Qy   901 AAGATACCTGGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAAC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 LysIleProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsn 20

Qy   961 ATCCTCCAACAGCGGCCGGTTCAGCATGGGCAGCCGTCGTGCTGCTTCAAGAGATTG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 IleLeuAsnSerGlyArgGlyPheSerMetGlySerValValAlaAlaValLeuLeuLysArgLeu 40

Qy  1021 ATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAAACAGTTTAACAAGAGGCTCAGTGAA 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 IleGluMetThrAlaGluTyrAlaCysThrArgLysThrArgLysGlnPheAsnLysArgLeuSerGlu 60

Qy  1081 TTTGGATTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGT 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PheGlyLeuIleGlnGluLysLeuHisPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSer 80

Qy  1141 ATGACCTACCTCACAGACAGGAGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAG 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 MetThrTyrLeuThrAlaGlyMetLeuAspThrProGlyPheProAspCysSerIleGlu 100

Qy  1201 GCAGCCATGTGAAGGTGTTCAGCTCCGAGGCCGCCTGCCAGTGTGTGAGTGAGGCGCTG 1260
```

```
RT   acid sequence and distinct specificities of the cDNA-expressed
RT   protein.";
RL   J. Biol. Chem. 269:19008-19094(1994).
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; D30647; BAA06331.1; -.
DR   PIR; A54872; A54872.
DR   HSSP; Q06319; 1BUC.
DR   RGD; 2014; Acadvl.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   Direct protein sequencing; FAD; Fatty acid metabolism; Flavoprotein;
KW   Mitochondrion; Oxidoreductase; Transit peptide.
FT   TRANSIT       1     40       Mitochondrion.
FT   CHAIN        41    655       Acyl-CoA dehydrogenase, very-long-chain
FT                                specific.
FT   DOMAIN       41    482       Catalytic.
SQ   SEQUENCE   655 AA;  70749 MW;  E808EDEB0E4595D7 CRC64;
```

Alignment Scores:
```
Pred. No.:                  980
Score:                   1365.00
Percent Similarity:       62.77%
Best Local Similarity:    46.05%
Query Match:              30.31%
DB:                           1
```

```
Length:        655
Matches:       303
Conservative:  110
Mismatches:    202
Indels:         43
Gaps:           13
```

US-09-945-326-1 (1-2452) x ACDV_RAT (1-655)

```
Qy    30 GGGAGACTGGCTGAGGCTGGGG--AACATCGGCAGCATGAGCCGGCTGCGGGCTCTT 86
          ::    |||||||||||||||||     :: ||||||||||||||||||||||
Db    11 GlyArgGlnLeuLeuArgLeuGlyAlaValGlyMetAlaArgSerAlaAlaLeuGlnGlyGln 30

Qy    87 CCTGCCGCCACCGCGGCTCGGCGCCGGGGTCGTGGTGTCTCTCACCGCGGAACCG 146
          |||  |||||||||||   :||||||||||                   ||   ::
Db    31 Pro-ArgProThrSerAlaGlnArg---------------LeuTyrAlaSerGluAlaThrGl 46

Qy   147 GCGGCTACTCGCGC--------------------------ACCAGCCCGCCTGT 173
          ::|:||  |||||
Db   147 nAlaValLeuGlyLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl 66

Qy   174 ACGAGCT--------TTCCGCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGA 221
          ||:|||           :||||||||||||||||||  |||||:||||||||||
Db    66 aArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGl 86
```

```
Qy   222 AGTTTCCATTCAGAAGTTAGCCAAGATGAACTAATGAA---------------AT 266
          :||||||||||::||  ||
Db    86                                       nValPheProTyrProSerVal 102
                                                 LeuAsnGluGlnThrGlnPheLe
```

```
Qy   267 CAATCAGTTCTTGGACCCCGTGGAAAATTCTTCACTGAGAGGTGACTCCGAAAAT 326
          ||   :: ||||||||||    :: |||||  ||||||||||
Db   102 uLysGluLeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaAlaLysAs 122
```

```
Qy   327 TGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTT 386
          |||    : ::::||||||     :::::|||||||||||||||
Db   122 nAspSerLeuGluLysValGlyValGlyAspThrLeuGlnLysGlyLeuLysGlyLeuGlyLeuLysGlyLeuAlaPh 142
```

```
Qy   387 TGGGCTGCAAGTCCAGAGAATATGGTGGCCCTTCGCCAACACCATGTACTCAAG 446
          |||||||||||    :||||||||||||||||||||||||||||||||||
Db   142 eGlyLeuGlnValProSerGluGlyLeuGlyLeuGlySerAsnThrGlnTyrAlaAr 162
```

```
Qy   447 ACTAGGGGAGATCATCAGCATG--GATGGGTCCATCACTGTGACCCTGGCAGCGCACCA 503
          ||||||||||||||||||||    :::|||||||||||||||||||||
Db   162 gLeuAlaGluIleValGlyMetHisAspLeuGlyMetHisLeuGlyValThrLeuGlyAlaHisGl 182
```

```
Qy   504 GGCTATTGGCCTCAAGGGGATCATCTTGGCTGCACTGAGGAGCAGAAAGCCAAATACTT 563
          ||||||||||||  :: |||||||||||||||||||||||||||||||||||
Db   182 nSerIleGlyPheLysGlyIleIleLeuLeuAlaLeuArgSerArgLysProLysTyrLe 202
```

```
Qy   564 GCCTAAACTGGCGTCCGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCAGCCAGTGG 623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202 uProArgValAlaSerGlyLnAlaLeuAlaLeuAlaPheCysLeuThrGluProSerSerGl 222
```

```
Qy   624 GAGGCGATGCAGCCTCAATCCGGAGCAGAGCACAAGTGAAGACAAGAGCACTACAT 683
          |||   :: ||||||||||||||||||||||||||||||||||||||||
Db   222 ySerAspValAlaSerIleArgSerAlaValProSerAlaGlyLysTyrTyrTh 242
```

```
Qy   684 CCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGATCTGGCCAATATTTTACTGTGTT 743
          |||||||||||||||  :: |||||||||||||||||||||||||||||
Db   242 rLeuAsnGlySerLysValTrpIleSerAsnGlyGlyLeuAspAspIlePheThrValPh 262
```

```
Qy   744 TGCAAAGACTGAGGTCGTTGAT---TCTGATGATCAGTGAAAAGACAAAATCACAGCATT 800
          |||||||||||||||||||||      ::  ||||||||||||||
Db   262 eAlaLysThrGluValValAspSerAspAspGlnAlaLysAspArgAlaValIleThrAlaPh 282
```

```
Qy   801 CATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGCATAATGGAAATAAATAGGCAT 860
          |:|| |||||||||||||    ||||||||||||||||
Db   282 eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysProGlyLysMetGlyIl 302
```

```
Qy   861 TCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAACAT 920
          |:::  ||||  :: |||||||||||||||||||||||||||
Db   302 eLysAlaSerAsnThrSerGluValTyrPheAspGlyValValProAlaGluAsnVa 322
```

```
Qy   921 CCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTT 980
          |||||||||||||    ||||||||||||||||||||||||||||
Db   322 lLeuGlyGluValGlyAspGlyPheLysGlyValAlaArgSerAlaAspGlyArgPh 342
```

```
Qy   981 CAGCATGGTGGACCGGCAGCGTCGTGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTA 1040
          :::|||||||||||||||||||||||||||||||||  :: :::::||||||||
Db   342 eGlyMetAlaAlaThrLeuLeuGlyThrMetLysMetLysAlaIleIleAlaValAlaAspHi 362
```

```
Qy  1041 CGGCTTGCACAAGGAAACAGTTAACAAGAGGCTCAGTGAATTTGATTCAGGAGAA 1100
          :|| |||||||||||||||||||||||||||||||||||||  |||||||||||
Db   362 sAlaThrAsnArgThrGlnPheGlyTyrAspLysLysHisAsnPheGlyValIlleGlnGluLLy 382
```

```
Qy  1101 ATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGGATGACCTACCTCACCAGCAGG 1160
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   382 sLeuAlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAl 402
```

```
Qy  1161 GATGCATGGTGACCAACCTGGCTTCCCCGACTGCTCCATCGAGGCAGCCATGGTGAAGGTGTT 1220
          :::||||||||||   ||||||||||||||||||||||||||||||||||
Db   402 aAsnMetAspGln---GlyPheLysAspPheGlnIleGlnIleGluAlaAlaAlaIleSerLysIllePh 421
```

```
Qy  1221 CAGCTCCAAAGAGCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTGCAGAAAATCAAGAAGAAAGA 1280
          :::||||||||||||||||||||||||||||||||||||||||
Db   421 eGlySerGluAlaAlaTrpLysValThrArgLysValThrAspGluCysIleGlnIleMetGlyGlyMetGl 441
```

```
Qy   1281 CTACACAAGGGACTATCCGTACGAGCGCCATACTGCCGTGACACCCGGATCCTCCTCATCTT 1340
          ||::  :::::::   |||||||||||  ||||||||||||||||||||||||||
Db    441 yPheMetLysGlyuProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePh 461

Qy   1341 CGAGGGAACCAATGAGATTCCGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGG 1400
          ||::|||||||||  |||||||||||||::|||||||:::||||::|||
Db    461 eGluGlyThrAsnAspIleuPheLeuArgeuPheValAlaLeuGlnLeuGlyCysMetAspLysGl 481

Qy   1401 CCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG-----GCCAAAGTGAGCACACAGT 1454
          |:::   ||||||                      :::  ||||||   |||
Db    481 yLysGluLeuThrGlyLeuGlyAsnAlaLeuuLysAsnProLeuGlyAsnValGlyLeuLe 501

Qy   1455 CATGGATACCGGTTGGCCGGAGGCTTCGGACATCCCTGGGCCGCGAACCTGTGGACCTGGGCT 1514
          :::::::|||||||                     ||      ||
Db    501 uIleGlyGluAlaSerLysGlnLeuuArgArgThrGlyIleGlySerGlyLeuSerLe 521

Qy   1515 GACAGGCAACCAATGAGAGTTGTGCACCCAGTTCTTCGCGGACAGCTGCACAAGTTTGAGGA 1574
          ||||||||||||||                :::|||
Db    521 uSer-------GlyIleuValHisProGluLeuSerArgSerGlyGluLeuAlaValGl 538

Qy   1575 GAACACCTACTGCTTCGGCCGGACCGTGGAGACACTCGTGCTCCGCTTTGGCAAGACCAT 1634
          ||                    |||||:::|||||||
Db    538 nAlaLeuGluGlnPheAlaThrValValGlyGlyuLeuMetLysHisLysLysGlyIl 558

Qy   1635 CATGGAGGAGCAGCTGGTACTGGAAGCGGTGGCCAACATCCTCATCAACCTGTATGGCAT 1694
          |:::           ||||||    :::::||||||
Db    558 eValAsnGluGlnPheLeuLeuGlnArgLeuuIleArgAspGlyAlaAlaAspLeuTyrTyrAlaMe 578

Qy   1695 GACGGCCGTGCTGTCGCGGGCCAGCCGCTCCATCCGCATTGGGCTCCGCAACCACGACCA 1754
          |||||||    :::        ||||||||||::::
Db    578 tValValLeuSerArgLeuSerArgSerLeuuSerGlyGluGlyTyrProThrAlaGlnHi 598

Qy   1755 CGAGGTTCTTGGCCAACACCTTCTGCGTGGAAGCT------------TACTTGCAGAATCT 1805
          ||||||                              :::|||||
Db    598 sGluLysMetLeuCysAspSerTrpCysIleuGluAlaAlaThrArgIleArgGluAsnMe 618

Qy   1806 CTTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAA 1865
          |||||                    :::       |||        :::
Db    618 tAlaSerLeuGlnSerProGln------GlnGlnLeuPheArgAsnPheArgSe 636

Qy   1866 AGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTG 1917
          :::|||||   ::::::     |||||
Db    636 rIleSerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu 653
```

RESULT 7

Q7T2C2
ID   Q7T2C2;   PRELIMINARY;   PRT;   659 AA.
AC   Q7T2C2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Acyl-Coenzyme A dehydrogenase, very long chain.
GN   ORFNames=zgc:64067;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; BC054606; AAH54606.1; -.
DR   HSSP; Q06319; 1BUC.
DR   ZFIN; ZDB-GENE-030131-899; zgc:64067.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh_1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE   659 AA; 71111 MW; C12D31F27C92F71F CRC64;

Alignment Scores:
Pred. No.:   Length: 659
Score: 1.62e-80   Matches: 285
Percent Similarity: 63.62%   Conservative: 105
Best Local Similarity: 46.49%   Mismatches: 204
Query Match: 30.21%   Indels: 19
DB: 2   Gaps: 8

US-09-945-326-1 (1-2452) x Q7T2C2 (1-659)

```
Qy    94 ACCACGGCTGCGGCTGCGTCGTCGTGCCTGCCGCGGGTCTGGTGGTCTCTACCGCGAACCGGCGGCGGCTA 153
         |||||||||  |||                     :::      ||||||||||||||
Db    59 ThrThrAlaThrAlaGluThrValAspLysAlaValValSerValGluSer--------- 75

Qy   154 CTCGGCACCAGCCCGCCGCTGTACAGCCTTTCGGCCAAAGAGCTTTCCTAGGCAAAATCAAG 213
         |||||||||||                    :::||:::||||||
Db    76 ------------------LysSerPheAlaValAlaAsnMetPheLysGlyInIleSer 88

Qy   214 AAGAAGAAGTTTCCCATTTCCAGAAGTAGCGAAGATGAACTTAATGAA---ATCAAT 270
         :::|||||||||||:::|||            :::     :::
Db    89 ThrSerGlnValPheProTyrProSerValLeuAsnGluGlnSerGlnPheLeuArg 108

Qy   271 CAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGACTCCCGAAAAATTGAC 330
         |||            |||||||||||||||
Db   109 GluLeuValGlyProCysSerLysPheGluPheGluGluValAsnAspProMetLysAsnAsp 128

Qy   331 CAGGAAGGGAGAAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGG 390
         |||||||||            |||||||||||
Db   129 AlaLeuGluLysValGluHisThrLeuGlnLeuGluLysGlyLeuGlyAlaPheGlyV 148

Qy   391 CTGCAAGTCCAGAAGAATATGGGCCTGGGCTTCTCCAACAACATGTACTCAAGACTA 450
         ||||||||                :::|||:::||:::||||
Db   149 LeuGlnValProAlaAspLeuGlyValGlyValAlaGlyuLeuThrArgAsnThrArgAsnThryrAlaArgLeu 168

Qy   451 GGGGAGATCATCAGCATG---GATGGGTCCCATCACTGTGACCCTGGCAGCGCACCAGGCT 507
         ||:::     :::      |||                |||:::|||
Db   169 ValGluIleValGlyMetHisAspLeuGlyValGlyIleThrLeuGlyuValGlyAlaHisGlnSer 188
```

Qy 508 ATTGGCCTCAAGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTGCCT 567
         ||| || || :::|||||||| ||| ||| ||||||||||
Db 189 IleGlyPheLysGlyIleLeuLeuPheGlyAsnProGlnLysGluLysTyrLeuPro 208

Qy 568 AAACTGGCTCCGGGAGCACATTGAGCTTCTGCTCACGGAGCCAGCCAGTGGGGAGC 627
         ||||| |||||||| |||| |||||||||||||||||
Db 209 LysLeuAlaThrGlyGluAsnIleAlaAlaPheCysLeuThrGluProAlaSerGlySer 228

Qy 628 GATGCAGCCTCAATCCGGAGCAGCGAGAGCCACACTAAGTGAAGACAAGAAGCACTACATCCTC 687
         |||||||||||:::|| || ||| ::::::||| :::
Db 229 AspAlaAlaSerIleLysThrThrAlaValArgSerProCysGlnThrTyrThrMet 248

Qy 688 AATGGCTTCCAAGGTCGGATTACTAATGGAGGACTGGCCAATATTTTACTGTGTTGCA 747
         |||||||| || |:::|||||||| ||||
Db 249 AsnGlySerLysIleTrpIleSerGluAsnGlyGlyThrAlaGluIlePheThrValPheAla 268

Qy 748 AAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATA 804
         ||||| |||| ::: |||||||||||||||||
Db 269 LysThrProValLysAspGluLysSerThrGlyLeuMetLysAspLysIleThrAlaPheIle 288

Qy 805 GTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAAGATAAATTAGGCATTCGG 864
         ||| ||||||| ||||||:::||||:::||||
Db 289 ValGluArgSerPheGlyGlyValSerSerGlyLysProProGluLysLysMetGlyIleLeuLys 308

Qy 865 GGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTT 924
         |||||||||||||:::|||| ::::||| :::|||
Db 309 AlaSerAsnThrAlaCluValTyrPheGluAsnValArgValProAlaAspCysValLeu 328

Qy 925 GGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGC 984
         ||||||||| |||:::||||||||||||||
Db 329 GlyGluValGlyGlyAspGlyLeuLysValAlaMetAsnIleLeuAsnAsnGlyArgPheGly 348

Qy 985 ATGGGGCAGCGTCGTGCGTGGCCGTCTCAAGAGATGATTGAAATGACTGCTGAGTACGCC 1044
         ||| ::: |||||||| :::||||||||||
Db 349 MetAlaAlaAlaLeuSerGlyThrMetLysGlyValIleThrLysValAlaValAspHisAla 368

Qy 1045 TGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTT 1104
         ||| ::: |||||| ||||:::||||
Db 369 AlaAsnArgThrGlnPheGlyIleHisAsnTyrGlyLeuAlaIleGlnGluGluLysMet 388

Qy 1105 GCACTGATGGTCAGAAGGCTTCAGTCGTCATGGAGAGTATGACCTACCTCACAGCAGGGATG 1164
         || :::|||||||||||||||||| :::||||
Db 389 AlaArgMetAlaMetAlaLeuGlnTyrValThrGluSerMetAlaTyrMetValSerGlyAsn 408

Qy 1165 CTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGCAGCCATGTGAAGGTGTTCAGC 1224
         |:::|||||||||||| :::|||||
Db 409 MetAspSer---GlyAlaThrGluProGlnIleGluAlaAlaIleSerLysIlePheAla 427

Qy 1225 TCCGGAGGCGGCCTGCAGTGTGTGAGTAGTGAGCGCGTCGAGATCCTCGGGGCTTGGCTAC 1284
         |||||||||||||||||||| :::||||||||
Db 428 SerGluAlaAlaTrpLeuvalThrArgpleuvalValCysIleGlnValMetGlyGlyMetGlyPhe 447

Qy 1285 ACAAGGGACTATCCGTACAGGCCTACGACTACTGCGTGCACACCCGGCATCCTCCTACCTCCGAG 1344
         || ::: ||||||||||||||||||||
Db 448 MetLysAspAlaGlyValGlnLysGluArgGluValArgAspLeuProAlaArgIlePheGlu 467

Qy 1345 GGAACCAATGAAGATGAGATTCCGGAGGCTTCGGACTACGTCGACCATGCCGGCCGC 1404
         ||||||||||::: |||||||||||||||
Db 468 GlyThrAsnAspGluIleGluLeuPheValAlaLeuPheValLeuAsnGlyAlaGlyAsn 487

Qy 1405 ATCCTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGGCACAGTCATG 1458
         |||||||||||||||:::   :::
Db 488 GlnLeuLysSerLeuGlnLysAlaLeuLysAlaAsnProLeuGlyAsnAlaGlyMetLeuAla 507

Qy 1459 GATACCGTTGCCGGAGGCTTCGGGGACTCCTGGGCCGAACTGTGAACTGGGGTGACA 1518
         |||:::|| ||||||||||||||||||
Db 508 GlyGluIleThrLysAspAlaArgAlaLeuArgAlaGly------LeuGlySerGlyLeuThr 525

Qy 1519 GGCAACCATGAGTGTGCACCCCAGTCTTGCGGACAGTCTGCCAACAAGTTTGAGGAGAAC 1578
         |||||||||| :::|||||||||||||||
Db 526 ---LeuGlnGlyThrValHisProGluLeuAsnHisSerGlyGluLeuThrVallysAla 544

Qy 1579 ACCTACTGCTTCGGCCCGGACCGTGGAGACACTGCTGCTCCCCGCTTTGCCAAGACCATCATG 1638

Db
         |||||||
         545 IleGluGlnPheGlyAlaValIleGluGluLeuLeuGluLeuLysGlyIleLysLysIleIle 564

Qy 1639 GAGGAGCAGTCGGTACTGGAAGCGGGGTGGCCAACATCCTCATCAACCTGTATGGCCATGACG 1698
         :::|||||| ||||||||||:::||||||
Db 565 AspGluGlnPheValLeuLysAlaArgValAlaAspCysAlaIleSerAspTyrAlaMetVal 584

Qy 1699 GCCGTCGTGCCGGCGCCAGCCGCTCCATCCGCCATTGGGCTCGGCAACCAGCCACCACCAGAG 1758

Db 585 ValValLeuSerArgAlaSerArgSerLeuAsnGlnHisGlyHisSerAlaGlnHisGlu 604

Qy 1759 GTTCTCTTGGCCAACACCTTCTGCGTGCACTGCGTGGAAGATCCTCTTCAGCCTCTCT 1818
         :::|| ||||||||||||||| |||
Db 605 LysMetLeuCysGluThrTrpCysThrGluAlaHisAlaArgValMetGlnAspIleLys 624

Qy 1819 CAGTCGACAAGTAATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGCCCAGCAG 1878
         ||| :::   :::||||||||||||
Db 625 PheLeuArgSerGlyThrSerLysGlnThrPheLysAsnLeuArgAlaIleSerArgAlaAla 644

Qy 1879 ATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCCTG 1917
         :::|| ||||||||||
Db 645 ValValGluAsnGlyGlyValValAlaProHisProLeu 657

RESULT 8
ACDV_MOUSE
ID   ACDV_MOUSE   STANDARD;   PRT;   656 AA.
AC   P50544; O35289; O55113;
DT   01-OCT-1996 (Rel. 34, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD) (MVLCAD).
GN   Name=Acadvl; Synonyms=Vlcad;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Blood;
RA   Andresen B.S., Lund H., Bross P., Gregersen N.;
RT   "Mouse very-long-chain acyl-CoA dehydrogenase (VLCAD) gene.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RA   Andresen B., Lund H., Bross P., Corydon M., Gregersen N.;
RT   "Cloning and characterization of mouse very-long-chain acyl-CoA
RT   dehydrogenase.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., McEwan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 84-656 FROM N.A.
RC STRAIN=ICR; TISSUE=Liver;
RX MEDLINE=9345418; PubMed=9680378;
RA Cox K.B., Johnson K.R., Wood P.A.;
RT "Chromosomal locations of the mouse fatty acid oxidation genes Cpt1a,
RT Cpt1b, Cpt2, Acadvl, and metabolically related Crat gene.";
RL Mamm. Genome 9:608-610(1998).
RN [5]
RP SEQUENCE OF 339-656 FROM N.A.
RA Rao G., Krimer D., Krasikov T., Austin C., Skoultchi A.I.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC   fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC   ETF.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC   step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC   of different substrate specificities are present in mammalian
CC   tissues.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC --
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CC or send an email to license@isb-sib.ch).
CC --
DR EMBL; Y11770; CAA72435.1; -.
DR EMBL; Z71189; CAA94919.2; -.
DR EMBL; BC026559; AAH26559.1; -.
DR EMBL; AF017176; AAC31642.1; -.
DR EMBL; U41497; AAA85185.1; -.
DR HSSP; Q06319; 1BUC.
DR SWISS-2DPAGE; P50544; MOUSE.
DR MGD; MGI:895149; Acadvl.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh_C.
DR InterPro; IPR006091; Acyl-CoA dh_M.
DR InterPro; IPR006092; Acyl-CoA dh_N.
DR InterPro; IPR009100; AcylCoA dehyd_NM.
DR InterPro; IPR009075; AcylCoADH_C_like.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR Pfam; PF02770; Acyl-CoA dh_M; 1.
DR Pfam; PF02771; Acyl-CoA dh_N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW Oxidoreductase; Transit peptide.
FT TRANSIT   1   41   Mitochondrion (By similarity).
FT CHAIN   42   656   Acyl-CoA dehydrogenase, very-long-chain
FT   specific.
FT DOMAIN   42   483   Catalytic.
FT CONFLICT   339   339   NNG -> GTR (in Ref. 5).
FT CONFLICT   423   423   C -> W (in Ref. 5).
FT CONFLICT   427   427   A -> G (in Ref. 5).
FT CONFLICT   441   441   M -> I (in Ref. 5).
FT CONFLICT   507   507   G -> A (in Ref. 5).
FT CONFLICT   532   532   R -> P (in Ref. 5).
FT CONFLICT   567   567   Q -> K (in Ref. 5).
FT CONFLICT   570   571   AD -> GG (in Ref. 5).
FT CONFLICT   573   573   A -> P (in Ref. 5).
FT CONFLICT   593   593   G -> A (in Ref. 5).
FT CONFLICT   596   596   T -> A (in Ref. 5).
FT CONFLICT   612   612   A -> P (in Ref. 5).
FT CONFLICT   628   628   H -> Q (in Ref. 4).

SQ SEQUENCE   656 AA; 70875 MW; A011OCA5C6CF4F89 CRC64;

Alignment Scores:
Pred. No.:
Score: 1.74e-80
Percent Similarity: 66.05%
Best Local Similarity: 48.24%
Query Match: 30.20%
DB:

Length: 656
Matches: 287
Conservative: 106
Mismatches: 184
Indels: 18
Gaps: 9

US-09-945-326-1 (1-2452) x ACDV_MOUSE (1-656)

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Qy   169 CCTGTACGAGCT---------------TTCGCCAAAGAGCTTTCCTAGGCAAAATCAAGAAG 216
             ||                       ||||||||||   ::||||
Db    66 ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlnLeuThrIle 85

Qy   217 AAAGAAGTTTCCCATTTCCAGAGAGTT---AGCCAAGATGAACTTAATGAAATCAATCAG 273
             ::||||||||||||::|||   ||||||||         ::|   ||:
Db    86 AspGlnValPheProTyrProSerValLeuSerGluGlnLeuLysGlu 105

Qy   274 TTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAG 333
             |||||||          ::|||||   ||||||||
Db   106 LeuValGlyProValAlaArgPheGluPheGluValAlaAsnAspProAlaLysAsnAspAla 125

Qy   334 GAAGGGAAAATCCCAGTAGAAACTTTGGAGAAATTGAAGAGCCTAGGCTTTTGGGCTG 393
             ||||:::          |||:||||||
Db   126 LeuGluLysValGluAspAspThrLeuGlnGlyLeuGlyLeuLysGluLeuGlyGlyAlaPheGlyLeu 145

Qy   394 CAAGTCCCAGAAGAATATGGTGGCCTGGCGTTCTCCAACACCATGTACTCAAGACTAGGG 453
             ||||||||||||||          :::||||||||
Db   146 GlnValProSerGluLeuGlyLeuGlyLeuSerAsnThrGlnTyrAlaArgLeuLeuA 165

Qy   454 GAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGCAGCGCACCAGGCTATT 510
             |||||||          :::|||:||||||
Db   166 GluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSerIle 185

Qy   511 GGCCTCAAGGGGGATCATCTTGGCTGCACTGAGGAGCCAGAAGCCAAATACTTGCCTAAA 570
             ||||||::::         ||||||||
Db   186 GlyPheLysGlyIleLeuLeuTyrGlyThrGlyGlyIleAlaGlnLysArgGluLysTyrLeuProArg 205

Qy   571 CTGGGCGTCCGGGAGCACCATTGCAGCCTTCTGCCTCACGGAGCCCAGCCCAGTGGGAGCGAT 630
             :::||||||||||||          :::|||||||
Db   206 ValAlaSerGlyLeuAlaLeuAlaLeuAlaPheCysLeuThrGluProSerGlySerAsp 225

Qy   631 GCAGGCTCAATCCGGAGCAGCAGCCACCTAAGTGAAGACGAAGACAAGAGCACTACCATCCTCAAT 690
             ||||||||||:::         ||||||||
Db   226 ValAlaSerIleArgSerSerAlaIleProSerProCysGlyLysTyrThrLeuAsn 245

Qy   691 GGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAG 750
             ||||||||||:::         |||::|||||||
Db   246 GlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAsnIlePhePheThrValPheAlaLys 265

Qy   751 ACTGAGGTCGTTGAT---TCTGATGCAGTAGAAGACAAAATCACAGATTCATAGTA 807
             ||:::         ||||||||
Db   266 ThrProIleLysAspAlaThrGlyAlaIleArgValLysGluLysIleThrAlaPheValVal 285

Qy   808 GAAAGAGACTTGGTGGAGTCACTAATGGAAACCCGAGAGATAATTAGGCATTCGGGGGC 867
             ||||||||||:::         ||||||||
Db   286 GluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIleLysLysAla 305

Qy   868 TCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGA 927
             ||||||||||:::|:||:         ||:||||||
Db   306 SerAsnThrSerGluValTyrPheAspGlyValTyrPheLysValProSerGluAsnValLeuGly 325

Qy   928 GAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGCCGTTCAGCATG 987
             ||||||||||||||:::         ||||||||
Db   326 GluValGlyAspGlyPheLysValAlaValAlaValAsnIleLeuAsnArgArgPheGlyMet 345

Qy   988 GGCAGGCGTCGTGGCCTGGCGTGCTCAAGAGATTGAAATGACTGCTGCTAGTACGGCGCCTGC 1047
             ::|||         :::||||||
Db   346 AlaAlaThrLeuAlaLeuGlyThrMetLysSerLeuIleAlaLysValAspHisHisAlaThr 365

Qy  1048 ACAAGGAAAACAGTTTAACAGAGAGGCTCAGTGAATTTGATTGATTCAGGAGAAATTTGCA 1107
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OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Liu W., Zhu H., Sun X.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U30817; AAA74051.1; -.
DR   HSSP; Q06319; 1BUC.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW   Oxidoreductase; Transit peptide.
FT   TRANSIT       1     40       Mitochondrion (By similarity).
FT   CHAIN        41    655       Acyl-CoA dehydrogenase, very-long-chain
FT                                specific.
FT   DOMAIN       41    482       Catalytic.
SQ   SEQUENCE   655 AA;  70520 MW;  F9DC6285023CFC0 CRC64;
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Alignment Scores:
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Pred. No.:                                 Length:           655
Score:                         1.68e-79    Matches:          285
Percent Similarity:            1345.00     Conservative:     110
Best Local Similarity:         65.51%      Mismatches:       194
Query Match:                   47.26%      Indels:           14
DB:                            29.86%      Gaps:             9
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US-09-945-326-1 (1-2452) x ACDV_BOVIN (1-655)

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Qy   133  TCTACCGGCGAACCGGCGGGCTACTGCCGCACCAGCCCGCCTGTACGAGCTTTCGCCAAAGAG  192
          |||||:::   ||||||     :::::|||||||||     ||||  :::|||||||
Db    57  SerGluAlaSerThrArgGluArgGluAlaAsnSerValSerLysSerPheAlaValGly   76

Qy   193  CTTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTCCATTTCCAGAAGTT---AGCCAA  249
          ::|||||||:||||||:||||||:|||||||   :::::||  ::::::
Db    77  ThrPheLysGlyGlnLeuThrThrAspPheGlnValPheProSerValLeuAsnGlu   96

Qy   250  GATGAACTTAATGAAATCAATCAGTTCTTCGGACCCGTGAAAAATTCTTCACTGAGGAG  309
          |:||||:: |||:| ||||||:::|||||     ||||||     :|||||  ||||||
Db    97  AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPheGluGluGluVal  116

Qy   310  GTGGGACTCCCGAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTCGAGAAATTG  369
          :::::  :::|||   :::    ||   |||  :::   :::::       ||:::::|||
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RESULT 9
ACDV_BOVIN
ID   ACDV_BOVIN     STANDARD;     PRT;    655 AA.
AC   P48818;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD).
GN   Name=ACADVL; Synonyms=VLCAD;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
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Db   366  AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeuAla  385
Qy  1108  CTGATGGCTCAGAAGGCTTACGTCAGGAGTATGACCTACCTCCACAGCAGGATGTCTG  1167
Db   386  ArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsnMet  405
Qy  1168  GACCAACCTGGCTTTCCCGACTGCTCCATCGAGCAGCCAGCCATGGTCAGCTGTTCAGCTCC  1227
Db   406  AspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePheCysSer  424
Qy  1228  GAGGCGCCTGGCAGTGTGTGAGTGAGGCGCTCGAGATCCTCCGGGGGCTTGGGCTACACA  1287
Db   425  GluAlaAlaAlaTrpLysValAlaAlaAspGluCysIleGlnIleMetGlyGlyMetGlyPheMet  444
Qy  1288  AGGGACTATCCTACGACGGGCATACTGCGTGACACCCGACATCCTCCTCATCTTCGAGGGA  1347
Db   445  LysGluProGlyValGluArgValLeuArgArgIleArgIlePheGluGluGly  464
Qy  1348  ACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCCAGCATGCCCGGCCCGCATC  1407
Db   465  AlaAsnAspIleLeuArgLeuProPheValAlaLeuGlnGlyCysMetAspLysLysGlyLysGlyGlu  484
Qy  1408  CTGACTACCAGGATCCATGAGCTTAAACAG-----GCCAAAGTGAGCACAGTCATGGAT  1461
Db   485  LeuThrGlyLeuGlyAsnAlaLeuLysAsnProHisGluValAsnValGlyLeuLeuMetGly  504
Qy  1462  ACGGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGACCTGGGGCTGACAGGC  1521
Db   505  GluAlaGlyLysGlnLeuLeuArgArgThrGlyIleLeuGlySerGlyLeuSerGluSer---  523
Qy  1522  AACCATGGAGTTGTGCACCCCAGTCTGCCGGACAGTGCCAACAAGTTGGAGGAGAACACC  1581
Db   524  -----GlyIleValHisProGluLeuSerArgSerGlyLeuLeuAlaValGlnAlaLeu  541
Qy  1582  TACTGCTTCGGCGACCGTGGAGACACTGCTGCTCCGCTTTGGCAAGACCATCATGGAG  1641
Db   542  AspGlnPheAlaThrValValGluAlaLysLysLeuValLysHisLysLysGlyIleValAsn  561
Qy  1642  GAGCAGCTGTGGTACTGGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACCGGCC  1701
Db   562  GluGlnPheLeuLeuGlnAsnArgLeuAlaLeuIleAspGlyAlaIleAlaIleAspProLeuTyrArgAlaMetValVal  581
Qy  1702  GTGCTGTCCGCGGAGGCTTCGCGGGCCCAGCCGCCCATTCGGCCCAACCAGCCACGAGGTT  1761
Db   582  ValLeuSerArgAlaSerArgLeuSerGluLeuSerGluGlyTyrProThrAlaGlnHisGluLys  601
Qy  1762  CTCTTGGCCCAACACCTTCTGCGTGGAAGCT--------TACTTCGAGAATCTCTTCAGC  1812
Db   602  MetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetCAlaSer  621
Qy  1813  CTCTCTCAGCTGGACAAGATGTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCC  1872
Db   622  LeuGlnSerProGlnHis-----GlnGluLeuPheArgAsnPheArgSerIleSer  639
Qy  1873  CAGCAGATCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTG  1917
Db   640  LysAlaMetValGluAsnGlyGlyLeuValThrGlyAsnProLeu  654
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RESULT 10
ACDV_HUMAN
ID   ACDV_HUMAN   STANDARD;   PRT;   655 AA.
AC   P49748; O76056; Q8WUL0;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD).
GN   Name=ACADVL; Synonyms=VLCAD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=96397809; PubMed=7668252;
RA   Aoyama T., Souri M., Ueno I., Kamijo T., Yamaguchi S., Rhead W.J.,
RA   Tanaka K., Hashimoto T.;
RT   "Cloning of human very-long-chain acyl-coenzyme A dehydrogenase and
RT   molecular characterization of its deficiency in two patients.";
RL   Am. J. Hum. Genet. 57:273-283(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND VARIANTS.
RC   TISSUE=Placenta;
RX   MEDLINE=96254975; PubMed=8845838; DOI=10.1093/hmg/5.4.461;
RA   Andresen B.S., Bross P., Vianey-Saban C., Divry P., Zabot M.-T.,
RA   Roe C.R., Nada M.A., Byskov A., Kruse T.A., Neve S., Kristiansen K.,
RA   Knudsen I., Corydon M.J., Gregersen N.;
RT   "Cloning and characterization of human very-long-chain acyl-CoA
RT   dehydrogenase cDNA, chromosomal assignment of the gene and
RT   identification in four patients of nine different mutations within the
RT   VLCAD gene.";
RL   Hum. Mol. Genet. 5:461-472(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).

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RC   TISSUE=Peripheral blood;
RX   MEDLINE=9125338; PubMed=8554625;
RA   Orii K.O., Aoyama T., Souri M., Orii K.E., Kondo N., Orii T.,
RA   Hashimoto T.;
RT   "Genomic DNA organization of human mitochondrial very-long-chain acyl-
RT   CoA dehydrogenase and mutation analysis.";
RL   Biochem. Biophys. Res. Commun. 217:987-992(1995).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Liver, Lung, and Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=95286809; PubMed=7769092;
RA   Aoyama T., Souri M., Ushikubo S., Kamijo T., Yamaguchi S.,
RA   Kelley R.I., Rhead W.J., Uetake K., Tanaka K., Hashimoto T.;
RT   "Purification of human very-long-chain acyl-coenzyme A dehydrogenase
RT   and characterization of its deficiency in seven patients.";
RL   J. Clin. Invest. 95:2465-2473(1995).
RN   [6]
RP   REVIEW ON VARIANTS.
RX   MEDLINE=9138660; PubMed=9073285;
RA   Andresen B.S., Olpin S., Poorthuis B.J.H.M., Scholte H.R.,
RA   Vianey-Saban C., Wanders R., Ijlst L., Morris A., Pourfarzam M.,
RA   Bartlett K., Baumgartner E.R., de Klerk J.B.C., Schroeder L.D.;
RA   Corydon T.J., Lund H., Winter V., Bross P., Bolund L., Gregersen N.;
RT   "Clear correlation of genotype with disease phenotype in very-long-
RT   chain acyl-CoA dehydrogenase deficiency.";
RL   Am. J. Hum. Genet. 64:479-494(1999).
RN   [7]
RP   VARIANTS VLCAD DEFICIENCY GLU-130 DEL; LYS-299 DEL; GLN-382 AND
RP   TRP-613.
RX   MEDLINE=96108870; PubMed=8554073;
RA   Souri M., Aoyama T., Orii K., Yamaguchi S., Hashimoto T.;
RT   "Mutation analysis of very-long-chain acyl-coenzyme A dehydrogenase
RT   (VLCAD) deficiency: identification and characterization of mutant
RT   VLCAD cDNAs from four patients.";
RL   Am. J. Hum. Genet. 58:97-106(1996).
RN   [8]
RP   VARIANT VLCAD DEFICIENCY HIS-450.
RX   MEDLINE=98206416; PubMed=9546340;
RA   Smelt A.H., Poorthuis B.J.H.M., Onkenhout W., Scholte H.R.,
RA   Andresen B.S., van Duinen S.G., Gregersen N., Wintzen A.R.;
RT   "Very long chain acyl-coenzyme A dehydrogenase deficiency with adult
RT   onset.";
RL   Ann. Neurol. 43:540-544(1998).
RN   [9]
RP   VARIANTS VLCAD DEFICIENCY.
RX   MEDLINE=9177129; PubMed=10077518;
RA   Mathur A., Sims H.F., Gopalakrishnan D., Gibson B., Rinaldo P.,
RA   Vockley J., Hug G., Strauss A.W.;
RT   "Molecular heterogeneity in very-long-chain acyl-CoA dehydrogenase
RT   deficiency causing pediatric cardiomyopathy and sudden death.";
```

```
RL   Circulation 99:1337-1343(1999).
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P49748-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P49748-2; Sequence=VSP_007734;
CC         Note=No experimental confirmation available;
CC   -!- DISEASE: Defects in ACADVL are the cause of very long chain acyl-
CC       CoA dehydrogenase deficiency (VLCAD deficiency) [MIM:201475].
CC       VLCAD deficiency is an autosomal recessive disease which leads to
CC       impaired long-chain fatty acid beta-oxidation. It is clinically
CC       heterogenous, with three major phenotypes: a severe childhood
CC       form, with early onset, high mortality, and high incidence of
CC       cardiomyopathy; a milder childhood form, with later onset, usually
CC       with hypoketotic hypoglycemia as the main presenting feature, low
CC       mortality, and rare cardiomyopathy; and an adult form, with
CC       isolated skeletal muscle involvement, rhabdomyolysis, and
CC       myoglobinuria, usually triggered by exercise or fasting.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; D43682; BAA07781.1; -.
DR   EMBL; L46590; AAA79002.1; -.
DR   EMBL; X86556; CAA60253.1; -.
DR   EMBL; D78298; BAA29057.1; -.
DR   EMBL; D78279; BAA29057.1; JOINED.
DR   EMBL; D78280; BAA29057.1; JOINED.
DR   EMBL; D78281; BAA29057.1; JOINED.
DR   EMBL; D78282; BAA29057.1; JOINED.
DR   EMBL; D78283; BAA29057.1; JOINED.
DR   EMBL; D78284; BAA29057.1; JOINED.
DR   EMBL; D78285; BAA29057.1; JOINED.
DR   EMBL; D78286; BAA29057.1; JOINED.
DR   EMBL; D78287; BAA29057.1; JOINED.
DR   EMBL; D78288; BAA29057.1; JOINED.
DR   EMBL; D78289; BAA29057.1; JOINED.
DR   EMBL; D78290; BAA29057.1; JOINED.
DR   EMBL; D78291; BAA29057.1; JOINED.
DR   EMBL; D78292; BAA29057.1; JOINED.
DR   EMBL; D78293; BAA29057.1; JOINED.
DR   EMBL; D78294; BAA29057.1; JOINED.
DR   EMBL; D78295; BAA29057.1; JOINED.
DR   EMBL; D78296; BAA29057.1; JOINED.
DR   EMBL; D78297; BAA29057.1; JOINED.
DR   EMBL; BC000399; AAH00399.1; -.
DR   EMBL; BC012912; AAH12912.1; -.
DR   EMBL; BC020218; AAH20218.1; -.
DR   PIR; S54183; S54183.
DR   HSSP; Q06319; 1BUC.
DR   Genew; HGNC:92; ACADVL.
DR   H-InvDB; HIX0013488; -.
DR   Reactome; P49748; -.
DR   MIM; 201475; -.
```

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DR    GO; GO:0005739; C:mitochondrion; TAS.
DR    GO; GO:0004466; F:long-chain-acyl-CoA dehydrogenase activity; TAS.
DR    GO; GO:0015980; P:energy derivation by oxidation of organic c. . .; TAS.
DR    GO; GO:0006635; P:fatty acid beta-oxidation; TAS.
DR    InterPro; IPR006089; Acyl-CoA dh.
DR    InterPro; IPR006090; Acyl-CoA_dh_C.
DR    InterPro; IPR006091; Acyl-CoA_dh_M.
DR    InterPro; IPR006092; Acyl-CoA_dh_N.
DR    InterPro; IPR009100; AcylCoA_dehyd_NM.
DR    InterPro; IPR009075; AcylCoADH_C_like.
DR    Pfam; PF00441; Acyl-CoA_dh; 1.
DR    Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR    Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR    PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR    PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW    Alternative splicing; Cardiomyopathy; Disease mutation; FAD;
KW    Fatty acid metabolism; Flavoprotein; Mitochondrion; Oxidoreductase;
KW    Polymorphism; Transit peptide.
FT    TRANSIT       1     40         Mitochondrion (By similarity).
FT    CHAIN        41    655         Acyl-CoA dehydrogenase, very-long-chain

Alignment Scores:
Pred. No.:
Score:                  6.3e-78       Length:          655
                        1321.00       Matches:         297
Percent Similarity:     61.52%        Conservative:    109
Best Local Similarity:  45.00%        Mismatches:      213
Query Match:            29.33%        Indels:           41
DB:                     1     655     Gaps:             13
```

This page contains dense nucleotide/protein sequence alignment data between a query (Qy) and database (Db) sequence (ACDV_HUMAN), with rows labeled "Qy" and "Db" showing base-pairing match lines.

```
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW   Oxidoreductase; Transit peptide.
FT   TRANSIT       1     40       Mitochondrion (By similarity).
FT   CHAIN        41    655       Acyl-CoA dehydrogenase, very-long-chain
FT                                specific.
FT   DOMAIN       41    482       Catalytic.
SQ   SEQUENCE    655 AA;  70443 MW;  DCC7A89BEFCB333 CRC64;

Alignment Scores:
Pred. No.:                              Length:               655
Score:               1319.00            Matches:              294
Percent Similarity:  62.15%             Conservative:         110
Best Local Similarity: 45.23%           Mismatches:           219
Query Match:         29.29%             Indels:                27
DB:                                     Gaps:                  11

US-09-945-326-1 (1-2452) x ACDV_MACFA (1-655)

Qy    30  GGGAGACTGAGGCTGAGGCTGGGGAACATCGGGCAGCAGATGAGGCGTCGGGGGCTCTT---  86
              ||||||  |||           ||  ||||||              ||||||
Db    11  GlyArgGlnLeuLeuArgPheGly-----GlyGlySerSerArgProThrAlaLeuLeu  28

Qy    87  ---------------CCTGCGCACCAGCGTCGCGGCTCGTCGCTGCCGGGGTCTGGT  128
                         ||||||           ||||||
Db    29  GlyGlnProTrpProGlyProAlaArgArg-ProTyrAlaGlyGlyAlaAlaGlnLeuAl  48

Qy   129  GGTCTCTACCGGCAACCGGCGGCTA------------CTGCGCACCAGCCCGCCTGTACGAGC  179
              :::     |||          ||| :::                        |||
Db    48  aLeuAspLysSerAspSerHisLeuSerAspAlaLeuAsnLysAlaLysProAlaLysAl  68

Qy   180  T-----------TTCGCAAAGAGCTTTCCTAGGCAAATCAAGAGAAGAAAGAAGTTT  227
             ||||||     ::||||  ||||||              :::|||
Db    68  aGluSerLysSerPheAlaValAlaMetPheLysGlyGlnLeuThrThrAspGlnValPh  88

Qy   228  CCCATTTCCAGAAGTT---AGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGACC  284
             ||||:||         ||||||     ::  ::         ||||||
Db    88  eProTyrProSerValLeuAsnGlnGlnThrGlnPheLeuLysGluLeuValGluPr  108

Qy   285  CCTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAATTGACCAGGAGGGAAAAT  344
             ||||           ||||||        ||||||        ||
Db   108  oValSerArgPheGlyGluValAsnAspProAlaLysAsnAspThrLeuGluMetVa  128

Qy   345  CCCAGATGAAACTTTGAGAAATTGAAGAGCCTAGGGTCTTTTGGGCTGCAAGTCCCAGA  404
             :::     ||||||||:::   |||||  |||||||:::|||
Db   128  IGluGluThrThrLeuGlnGlyLeuLysGluLeuGlyValAlaPheLeuLeuGlnValProSe  148

Qy   405  AGAATATGGTGGCCTGGCTTCTCCAACACCATGTACTCAAGACTAGGGAGAGATCATCAG  464
             ||||           |||:::|||           ||:||:||
Db   148  rGluLeuGlyValGlyLeuCysAsnThrGlnThrGlnTyrAlaArgLeuValGluIleGl  168

Qy   465  CATG---GATGGGTCCATCATGTGACCCTGGCAGCCGCACCAGGCTATTGGCCTCAAGGG  521
             ||||           ||||||:::        ||||||||:::|||
Db   168  yMetHisAspLeuValGlyIleThrLeuGlyAlaHisGlnSerIleGlyPheLysGl  188

Qy   522  GATCATCTTGGCTGGCACTGAGGAGCGAGAAGCCAAATACTTGCCTAAACTGCGCTCCGG  581
             ||||           ||:::||||||                    ||||||
Db   188  yIleLeuLeuPheGlyThrLysAlaGlnLysGluLysLysGluLysLysLeuAlaSerGl  208

Qy   582  GGAGCACATTGCAGCCTTCTGCCTCACGGAGCCAGCCAGTGGGAGCCAGCCTCAAT  641
             |||||           |||||||       ||||||||||:::|||
Db   208  yGluThrLeuAlaAlaPheCysGluThrGluProSerSerGlySerAspAlaAlaSerIl  228

Qy   642  CCGGAGCAGAGCCACACTAAGTGAAGACAAGAAGACTACATCCTCAATGGCTCCAAGGT  701
             ||||||  |||::||||||  :::|||   ||:::|||
Db   228  eArgThrSerAlaValProSerProCysGlyLysThrTyrThrLeuAsnGlySerLysSe  248

Qy   702  CTGGATTACTAATGGAGGACTGGCCAATATTTTACTGTGTTTGCAAAGACTGAGGTCGT  761
             ||||||           ||||||||:::||||||||||||
Db   248  uTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrProValTh  268

Qy   762  TGAT---TCTGATGGATCAGTGAAAGACAAATCACAGCATTCATAGTAGAAAGAGACTT  818
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Qy  1686  GTATGCGATGACGGACGGCCGTGCGTGTCGCGGGGGGCCAGCCAGCCGCTCCATCCGCCATTGGGCGTCCGCAA  1745
             ||||   |||                    |||||||||||||||:::
Db   575  uTyrAlaMetValValValLeuSerArgAlaSerArgArgSerLeuSerGluArgSerGlyHisProTh  595

Qy  1746  CCACGACCACGAGGTTCTCTTGGCCACACCTTCGCGTGAA-----------GCTTACTTGCA  1799
             ||||||   :::||||   ::||||||||||||:::
Db   595  rAlaGlnHisGluLysMetLeuCysAspThrTrpCysArgIleGluAlaAlaAlaArgIleAr  615

Qy  1800  GAATCTTCTTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAAACCTAGATGAGCAGAT  1859
             |||   :::|||           ||||:::
Db   615  gGluGlyMetAlaAlaLeuGlnSerAspProTrpGlnGlu---LeuTyrArgArgAsnPh  634

Qy  1860  TAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTG  1917
             ||| ::::|||::: :::||||||:::||||||
Db   634  eLysSerIleSerLysAlaLeuValGluArgGlyValGlyValGlyValValThrSerAsnProLeu  653

RESULT 11
ACDV_MACFA
ID   ACDV_MACFA     STANDARD;      PRT;   655 AA.
AC   Q8HXY7;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD) (QccE-11706).
GN   Name=ACADVL; Synonyms=VLCAD;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain cortex;
RA   Kusuda J., Osada N., Hida M., Sugano S., Hashimoto K.;
RT   "Isolation and characterization of cDNA for macaque neurological
RT   disease genes.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AB083302; BAC20581.1; -.
HSSP; Q05319; 1BUC.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADh_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
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Db        624 pProArgGlnHisGluLeuTyrArgAsnPheLysSerIleSerLysAlaLeuValGluAr 644
              |  | |||    |||
Qy       1890 GGGAGCCTATATCTGTGCCCACCCTCTG 1917
                       |||:|||||
Db        644 gGlyGlyValThrAsnAsnProLeu 653
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RESULT 12
Q9V8T1
ID   Q9V8T1      PRELIMINARY;      PRT;     655 AA.
AC   Q9V8T1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG7461-PA.
GN   ORFNames=CG7461;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila;
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen T.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
```

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Db        268 rAspProAlaThrGlyAlaValLysGluLysIleThrAlaPheValValGluArgGlyPh 288
              |||        |:: :    ||||:         |||||||  |||||||
Qy        819 TGGTGGAGTCACTAATGGGAAACCGGAGATAAATTAGGCATTCGGGCTCCAACACTTG 878
              ||||||||||:::|   |||||       ||:::: |||||||   ||||||
Db        288 eGlyGlyValThrHisGlyProProGluLysMetGlyIleLeuLysAlaSerAsnThrAl 308

Qy        879 TGAAGTCCATTTGAAAACACCAAGATACCTGTGAAAAACATCCTTGGAGAGGTCGGAGA 938
              |||||||         |||:: :    |||||:|     ||   ||  |||
Db        308 aGluValLeuPheAspGlyValArgValProSerGluAsnValLeuGlyValGlySe 328

Qy        939 TGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGCCGGTCAGCAGGCCGTCGT 998
              ||||||||||||        ||| :||   ||||| ||   |||||||
Db        328 rGlyPheLysValAlaMetHisIleLeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLe 348

Qy        999 GGCTGGGCGTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGACAAGGAAACA 1058
              :|:||       |::::| |::|||          ::|||  :   || |||||
Db        348 uAlaGlyThrMetArgGlyIleIleThrLysAlaValAspTyrAlaThrAsnArgIleGl 368

Qy       1059 GTTTAACAGAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAAATTTGCACTGATGGTCA 1118
              :::::           ||||||     |||||||       || |||    ::::
Db        368 nPheGlyGluLysIleHisAsnPheGlyLeuIleGlnGluLysGluLeuValAlaArgMetValMe 388

Qy       1119 GAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGAGGTGCTCGGACCAACCTGG 1178
              ||||:||   ::| |||||          :|| ||||| ||| |||  ::|||||||
Db        388 tLeuGlnTyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln---Gl 407

Qy       1179 CTTTCCGACTGCTCCATGGAGCAGCCATGGTGAAGGTGTTCAGCTCCCAGGCCGCCTG 1238
              |||        ||||:|||  |     |:|||  |||  ||||||| |||
Db        407 ySerThrAspPheGlnIleGluAlaIleSerIleSerLysIlePheGlySerGluAlaAlaTr 427

Qy       1239 GCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGCTGGGCTACACAAGGGACTATCC 1298
              |||       |  :|        ||       :|||   ||  ::
Db        427 pLysValThrAspGluCysIleGlnIleMetGlyMetGlyPheMetLysGluProGl 447

Qy       1299 GTACGACGCATACTGGTCGACACCCGCCATCCTCCTCATCTTCGAGGGAACCAATGAGAT 1358
              ||||:||:::    :||     | |||  ::||||||| ||||||
Db        447 yValGluArgValLeuArgArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIl 467

Qy       1359 TCTCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCCGCCATCCTGACTACCAG 1418
              ||||||| |||   ||        |||||  :| |::|
Db        467 eLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysLysGlyLysGluLeuSerGlyLe 487

Qy       1419 GATCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGTCATGGATACCGTTGGCCG 1472
              ||||||            :::::
Db        487 uGlySerAlaLeuLysLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLy 507

Qy       1473 GAGGCTTCGGGACTCCCTGGCCGCAACCTGGGCTGGACCTGGGCTGCAACCATGGAGT 1532
              :::|||||||      ||||||         |||||||         ||||||
Db        507 sGlnLeuArgArgArgAlaGlyLeuLeuGlyLeuSerLeuSer-------GlyIl 524

Qy       1533 TGTGCACCCCAGTCTTGCGACAGTGCCAACAAGTTTGAGGAGAACACCTACTGCTTCGG 1592
              ||||      ||     :|        |||  |     :|||   ||   ||||
Db        524 eValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAlaLeuGluGlnPheAl 544

Qy       1593 CCCGGACCGTCGGAGACACTGCTCTCCGTTGGCAAGAGCCATCATGAGGAGGAGCAGCTGGT 1652
              ||||:||||| :|         :|||||||  ||||| |||||| ||||||||
Db        544 aThrValValGluAlaLysGluLeuLysLysHisGlyIleLeuLysLysGlyIleValAsnGluGlnPheLeu 564

Qy       1653 ACTGAAGCGGTGGCCAACATCCTCATCAACCTGTATGGCATGACGGCCGTGTCTCCG 1712
              ||||||:|||||||          |::|   |  |        :|| |:||:|||
Db        564 uLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValValLeuSerAr 584

Qy       1713 GGCCAGGCCGCTCCATCCGCATTGGGCTCCGCAACGACCACGAGGTTCTCTTGGCCAA 1772
              |||||          ||         :|||  :  ||||  :|  ::
Db        584 gAlaSerArgSerLeuSerGluGluGlyHisHisThrAlaGlnHisGlyHisIleLysMetLeuCysAs 604

Qy       1773 CACCTTCTGCGTGGAAGCTTACTTGACTGGCATTGCAGAATCTTCAGCCTCTCAGCTGGACAAGTA 1832
              :|||:|||||||       ||::           :::    ||:: |
Db        604 pThrTrpCysIleGluAlaAlaAlaAlaArgIleArgGluGluGlyMetAlaAlaLeuGlnSerAs 624

Qy       1833 TGCTCCAGAAAAC---CTTAGAGCAGAATTAAGAAAAGTGTCCCAGCAGATCCTTGAGAA 1889
              :::::: |||         ||| ||: :::::|||||:::
```

```
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; AE003796; AAF57579.1; -.
DR   HSSP; Q06319; 1BUC.
DR   IntAct; Q9V8T1; -.
DR   FlyBase; FBgn0034432; CG7461.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE   655 AA;  71326 MW;  00916BD701E127CB CRC64;
```

Alignment Scores:

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Pred. No.:                2.96e-76       Length:       655
Score:                    1295.50        Matches:      280
Percent Similarity:       61.84%         Conservative: 104
Best Local Similarity:    45.09%         Mismatches:   212
Query Match:              28.76%         Indels:       25
DB:                                      Gaps:         9
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US-09-945-326-1 (1-2452) x Q9V8T1 (1-655)

Qy    106  GCTCGTGCCGCCGGGGTCTGGTGGTC--------------TCTACCGGCGAACCGG  147
                |||     |||||               :::   ||||||
Db     44  AlaSerLeuCysArgGlnIleAlaThrHisSerProLysLeuGlyAlaGluSerAsnArg  63

Qy    148  CGGCTACTGGCGCACCAGCCCCGCCCTGTACGACGCTTTCGCCAAAGAGCTTTTCCTAGGCAAA  207
                             :::  |||              :::||||     ||||
Db    148  SerLysGluLysAlaSerGluAsn---GluSerPheMetAlaAsnIlePheArgGlySer  82

Qy    208  ATCCAAGAAGAAAGAGAGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAAAATC  267
                :::|||||||||:||     |||:::     ||||:::
Db     83  LeuValSerSerGlnValLeuThrLeuAlaGluGlnLysGluLeu  102
```

Qy/Db alignment block (right column):

```
Qy   268  ---AATCAGTTCTTGGACCCCTGGAAAAATTCTTCACTGAGAGGTGGACTCCCGAAAA  324
                 :::   |||:||||||:||::::  ||||||
Db   103  ThrAsnSerLeuIleAspProPheGluArgPheSerAspValAsnAspAlaAlaArg  122

Qy   325  ATTGACCAGGAGGGAGAAATTCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTT  384
                |||                |||     :::     |||
Db   123  AsnAspAlaAsnSerLysIleAspAspThrThrSerThrAlaLeuTrpGluLeuGlyAla  142

Qy   385  TTTGGGCTGCAAGTCCCAGAGAAATATGGTGGCCGTTCTCCAACACCATGTACTCCA  444
                |||:::|||||||     :::||||
Db   143  PheGlyLeuGlnValProSerGluPheGlyLeuGlyLeuAsnAsnThrGlnThrGlyGly  162

Qy   445  AGACTAGGGGGAGATCATCAGCATG--GATGGGTCCATCACTGACCCTGGCAGCGCAC  501
                ||||                ||||:::  :::     |||:::
Db   163  ArgLeuCysAlaIleValGlyValAsnAspLeuGlyLeuGlyIleThrIleGlyAlaHis  182

Qy   502  CAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAATAC  561
                |||:::|||||||              ||||
Db   183  GlnSerIleGlyPheLysGlyIleIleLeuLeuTyrGlyThrProGluGlnLysGluLysTyr  202

Qy   562  TTGCCTAAACTGGCGTCCGGGAGCACATTGCAGTCCTTCTGCCTCACGGAGCCAGCCAGT  621
                |||:::||||||:::  :::     |||
Db   203  LeuProLysValAlaAlaGluGlnValTyrAlaAlaPheAlaAlaLeuThrGluProSerSer  222

Qy   622  GGGAGGCGATGAGCAGCCTCAATCCGGACGCAGAGCCACACTAAGTGAAGACAAGAAGCACTAC  681
                |||||||||              :::     |||
Db   223  GlySerAspAlaGlySerIleArgCysAsuGlyArgAlaValLysSerAlaAspGlyLysHisTyr  242

Qy   682  ATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGGCACTGCCAATATTTTTACTGTG  741
                :::|||||||             |||:::     |||||||
Db   243  ValLeuAsnGlyServLysIleTrpIleSerAsnGlyGlyIleAlaGluIleMetThrVal  262

Qy   742  TTTGCAAAGACTGAGGTCGTTGAT--TCTGATGGATCCAGTGAAAGACAAAATCACAGCA  798
                |||:::|||||||               ||||  |||
Db   263  PheAlaGlnThrGluValValAspProLysThrGlyGluLysLysAspLysValThrAla  282

Qy   799  TTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGC  858
                |||||||||||||              |||:::     |||
Db   283  PheIleValGluArgSerPheGlyGlyValThrAsnGlyLysProGluLysLysMetGly  302

Qy   859  ATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAACACACCAAGATACCTGTGGAAAAC  918
                |||:::     |||||||              |||
Db   303  IleLysAlaSerAsnThrAlaGluValTyrPheGluGluGluHisAspLysAsuProIleGluAsn  322

Qy   919  ATCCTTGGAGGTCGCGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCGCGG  978
                :::|||||||||||              |||:::
Db   323  ValLeuGlyLysGluGlyAspGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArg  342

Qy   979  TTCAGCATGGGCAGCGTCGTCGTGCTGGCTGGCTGCTCAAGAGATTGAATGACTGCTGAG  1038
                |||:::     :::     |||:::     ||||
Db   343  PheGlyMetGlyAlaThrLeuSerGlyThrMetLysLysGlyIleGluGlnIleAlaThrGlu  362

Qy   1039  TACGCCTGCACAAGGAAACAGTTAACAAGGAGGCTCAGTGAATTGATTCAGGAGGAG  1098
                :::|||              :::||||              |||
Db   363  HisAlaAsnAsnArgValGlnPheGlyGlnLysLeuLysAsnTyrGlySerIleGlnGlu  382

Qy   1099  AAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGAACTACCTCACAGCA  1158
                :::     |||||||     :::              ||||:::
Db   383  LysLeuLeuAlaGlnIleMetAsnIleLeuGlnTyrAlaThrGluSerMetAsnPheThrIleSer  402

Qy   1159  GGGATGCTGGACCAACCTGGCTTTCCGACTGCTCCATCGAGGCAGCAGCCATGGTGAAGGTG  1218
                :::|||                        |||||||
Db   403  GlnAsnMetAsp---AlaGlySerLysAspTyrHisLeuGluAlaAlaIleSerLysIle  421

Qy   1219  TTCAGCTCCGAGGGCCGCCACCAGTCGTGTGGAGATCCTCCGGGGCTTG  1278
                :::||||||||||              :::||||
Db   422  TyrAlaSerGluSerAlaTrpTyrValCysAspGluAlaIleGlnIleLeuLeuGlyMet  441

Qy   1279  GGCTACCAAGGGACTATCCTACGAGCCGCATACTGCGTGACACCCGACCATCCTCCTCATC  1338
                :::|||||||||||              ||||:::
Db   442  GlyTyrMetValAspAsnGlyLeuGluArgValLeuAsnGlyLeuArgIlePheArgIle  461
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DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
FT   NON_TER   1
SQ   SEQUENCE   639 AA;   70246 MW; 46790371A4D12CB5 CRC64;

Alignment Scores:

Pred. No.:   9.11e-76   Length: 639
Score: 1288.00   Matches: 282
Percent Similarity: 62.66%   Conservative: 109
Best Local Similarity: 45.19%   Mismatches: 187
Query Match: 28.60%   Indels: 46
DB: 2   Gaps: 11

US-09-945-326-1 (1-2452) x Q70868 (1-639)

Qy   145 CGGCGGCTACTGCGCACCAGCCG-------------------------------- 168
          |||||| ||| |:::||||
Db   28 ArgArgCysLeuSerAlaAlaProGlnAlaLysGlnAlaGluAlaGlnAlaThrPro   47

Qy   169 -----------------------CCTGTACGAGCTTCGCCAAAGAGCTTTTCCTAGGCAAAATC 210
                                 ||||||||||||||::||||
Db   48 SerGluAlaGluLysArgProAsnMetSerPheLeuThrAsnIlePheArgGlyGlnVal   67

Qy   211 AAGGAAGAAAGAAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA---ATC 267
          ::: ||||||||||||| ||:||||
Db   68 GlnProAlaGlnValPheProTyrProGluAlaLeuAspAlaGluGlnLysGluTyrIle   87

Qy   268 AATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGACTCCCGAAAAATT 327
          |||::| ||||||| |||
Db   88 AlaSerPheValAspProValThrLysPheGluValAlaAsnAspProValLysAsn 107

Qy   328 GACCAGGAAGGAGAAAATCCCAGATGAACATTTGAGAAATTGAGAGCGTAGGGCTTTTTT 387
          ||||| |||||| ||
Db   108 AspThrLysGluGlyGluAsnIleAspThrCysGluLeuArgTrpAspLeuGlyAlaPhe 127

Qy   388 GGGCTGCAAGTCCCAGAGAATATGTGGCGCTGGCTTCTCCAACACCATGTACTCCAAGA 447
          ||| ||||||||||||| :::|||||||
Db   128 SerLeuMetValProProAspTyrGlyGlyLeuAsnAsnThrGlnThrTyrSerArg 147

Qy   448 CTAGGGGAGATCATC---AGCAATGGATGGGTCCATCACTGTGACCCTGGCAGCCACCAG 504
          ::: :::|||||||||| ||| ||:
Db   148 MetCysAspIleGluGlyGlyLeuGlnAspLeuGlyLeuPheIleGlyAlaHisGln 167

Qy   505 GCTATTGGCCTCAAGGAGCATCTTGGCTGGCACTGAGCAGCAGAAAGCCAAATACTTG 564
          ||||||||||||||||| ::: |||
Db   168 SerIleGlyPheLysGlyIleLeuLeuTyrGlyAspGlnArgGlnLysGlyTyrLeu 187

Qy   565 CCTAAACTGGCTCGCGGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCAGTGGG 624
          ||||| :::|||||||
Db   188 ProMetValSerThrGlyLysValTyrAlaAlaPheAlaLeuThrGluProSerGly 207

Qy   625 AGCGATGAGCGCCTCAATCCGGAGCAGAGCCACTAAGTGAACAAGAACAAGAGCACTACATC 684
          ||| ||| ::||||||
Db   208 SerAspAlaGlySerIleArgCysArgAlaValLysSerAlaAspGlyLysHisTyrVal 227

Qy   685 CTCAATGGCTCCAAGTCTGGATTACTAATGAAGGACTGGCCAATATTTTTACTGTGTT 744
          ||||||||||||||||||:::|||
Db   228 LeuAsnGlySerLysTrpIleSerAsnGlyIleAlaAspIleAlaAspIleMetThrValPhe 247

Qy   745 GCAAAGACTGAGGTCGTTGAT---TCTGATGATCAGTGAAAGACAAAATCACAGCATTC 801
          |||::|||||||||| ||||
Db   248 AlaGlnThrGluValGluAspProLysThrGlnLysLysAspLeuLysAspValThrAlaPhe 267

Qy   802 ATAGTAGAAAAGAGACTTTGGTGAGTCACTAATTGGAAACCCGAAGATAAATTAGGCATT 861
          |||||| :::
Db   268 IleValGluArgGlyPheGlyValSerSerGlyProProGluAsnLysMetGlyIle 287

1339 TTCGAGGGAACCAATGAGAATTCTCCGATGTACATCGCCCTGACGGGTCTGCAGCATGCC 1398
      ||||||||||||||||||:::||||||||||:::|||
462   PheGluGlyThrAsnGluAsnSerProMetTyrIleAlaLeuThrGlyLeuGlnHisAla 481

1399 GGCCGCGATCCTGACTACCAGGATCCATGAGCTTAAACAG-----------GCC 1440
      ||||||||||| :::
482   Gly------------SerHisLeuLysGluLysGlnArgAlaPheLysAsnProSerAla 497

1441 AAAGTGAGCACAGTCATGGATACCGGTTGGCCGGAGGCTTCCGGGACTCCCTGGGCCGAACT 1500
      ||||||
498   AsnLeuGlyLeuIlePheLysGluLysGluAlaSerArgArg-----------AlaAlaSerThr 513

1501 GTGGACCTGGGGCTGACAGGCAACCATGAGTGTGCACCCAGTCTTGCGCACAGTGCC 1560
      |||:||||| ||| |||
514   ValGlyLeuLeuGlyLeuThrAspLeuSerGlyHisValValGlyHisGluLeuProTyrAla 533

1561 AACAAGTTTGAGGAGGAACACCTACTGCTTCGGCCGCCGAGACACTGCTGCTCCGC 1620
      |||||| |||||||:::|||||||||||||
534   LysLysThrAlaHisCysIleLeuAspPheGlyGlnSerValGluGluLeuLeuLeuArg 553

1621 TTTGGCAAGACCACCATGAGGACGGAGCAGCTGTACTGAAGCCGGTGGCCAACATCCTCATC 1680
      ::: ||||||| ||||||||||||||:::||||||
554   TyrAsnLysAsnIleValAsnGluGlnIleLeuLeuThrArgLeuAlaAsnAlaAlaIle 573

1681 AACCTGTATGGCATGACGCGCCGTGTCGTGCGGGGCCAGCCGCTCCATCCGCCATTCGGGCTC 1740
      :::||||| ||| ||||||:::||||||||
574   AspIleTyrArgAlaMetValValThrArgArgSerArgSerAlaValAlaAsnLeuAsnLeu 593

1741 CGCAACCACGACCACGAGTTCTCTTGGCCAACACCTTCTGCGTGGAAGTTACTTGCAG 1800
      ::: ||||||||||||||||
594   ProThrAlaGlnHisGluLeuAsnMetThrLysAlaLeuThrIleGlnAlaSerAspArg 613

1801 AATCTCTTCAGCCTCTCTCCAGCTGGACAAGATGTGCTCCAGAAAACCTAGATGAGCAGATT 1860
      :::||||||| ::|||
614   ValIleLeuAsnLeuGlnIleAlaAlaAlaThrSerSerHisSerHisSerArgSerLeuAsnGluLysLysIle 633

1861 AAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTGGAC 1920
      :::::::::|||||
634   SerThrIleAlaLysThrPheThrLeuGluAsnGlyGlyValThrThrThrGlyIleLeuAsp 653

1921 AGG 1923
      :::
654   Gln 654

RESULT 13
Q70868
ID   Q70868   PRELIMINARY;   PRT;   639 AA.
AC   Q70868;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP15352 (Fragment).
GN   Name=agCG50940; ORFNames=ENSANGG0000009991;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -!- CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
DR   EMBL; AAAB01008944; EAA10216.1; -.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.

```
Db   634 AsnProLeuAsp 637
         :::||||||||

RESULT 14
Q7Q870
ID   Q7Q870;                    PRELIMINARY;    PRT;   604 AA.
AC   Q7Q870;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP15349 (Fragment).
GN   Name=agCG50939; ORFNames=ENSANGG00000009986;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008944; EAA10215.1; -.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C-like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh_1;
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
FT   NON_TER       1      1
SQ   SEQUENCE   604 AA;  65510 MW;  F48852A94F3EF51A CRC64;

Alignment Scores:
Pred. No.:            1
Score:               7.97e-75
                     1273.50
Percent Similarity:  64.72%
Best Local Similarity: 64.30%
Query Match:         28.27%
DB:

                                         Length:       604
                                         Matches:      269
                                         Conservative: 107
                                         Mismatches:   170
                                         Indels:        35
                                         Gaps:          10

US-09-945-326-1 (1-2452) x Q7Q870 (1-604)

Qy  163 AGCCCGCCTGTACGA---GCTTTCGCCCAAAGAGCTTTTCCTAGGCAAAATCAAGAGAAA 219
         :::|||
Db   17 AlaProThrValAsnThrSerPheMetAlaAsnLeuPheArgGlyGluIleGluProLeu 36

Qy  220 GAAGTTTCCCATTTCCAGAA--GTTAGCCAAGAAGATGAACTTAATGAAATCAATCAGTTC 276
         :::||||||||
Db   37 GlnValPheProPheProAspSerLeuAsnProAspGlnLysMetIleGlySerLeu 56

Qy  277 TTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTCGACTCCGAAAATTGACACCAGGAA 336
         |||  |||
Db   57 IleAspProValThrLysPhePhe--AspGlyTyrAspProValLysAlaGluLysAsn 75

Qy  337 GGGAAAATCCCAGATGACGATGAAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTTGGGGCTGCAA 396
         |||||
Db   76 GlyGlyProAspGluAlaThrPheGlnSerMetTrpGluMetGlyMetGln 95

Qy  397 GTCCCAGAAGAATATGATGGTGGCCTGGCGTTCTCCAACACCATGTACTCAAGACTAGGGGAG 456
         |||||
Db   96 AlaProGluGluTyrGlyGlyLeuAlaLeuProAsnThrGlyTyrAlaArgMetGlyGlu 115


Qy  862 CGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGAAAAACATC 921
         :::|  ||||||   :::
Db  288 LysCysSerAsnThrAlaGluValTyrPheGluAspValLysIleProAlaGluAsnAsnVal 307

Qy  922 CTTGGAGAGGTCGGAGATGGGTTTAAGGTGCCATGAACACTCCTCAACAGCGGCGGCCGGTTC 981
         |||   ||   :::
Db  308 LeuGlyGluGlyAspGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArgArgPhe 327

Qy  982 AGCATGGGCAGCGTCGTGGCTGGCTCTCAAGAGATTGATTGAAATGACTGCTGAGTAC 1041
         |||  ::: :::
Db  328 GlyMetAlaAlaThrLeuSerGlyThrMetArgAlaCysIleGlnLysAlaAlaGluHis 347

Qy 1042 GCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAA 1101
         |||      :::::::::
Db  348 AlaThrAlaAsnArgValGlnPheGlyLysLysIleGluThrPheGlyLysValGlnGluLys 367

Qy 1102 TTTGCACTGATGGCTCAGAAGCTTACGTCATGGAGAGTGATGAACTACCTCACAGCAGGG 1161
         |||   ::: :::
Db  368 LeuAlaLeuMetAlaMetHisHisTyrValThrGlnSerMetAlaTyrMetIleSerGly 387

Qy 1162 ATGCTGGACCAACCTGGCTTTCCGACTGCTCCATGAGCCATGGTGAAGGTGTTC 1221
         :::||    :::||||||
Db  388 AsnMetAsp--ThrGlySerLeuAspTyrHisGluValGluAlaAlaIleSerLysLysValPhe 406

Qy 1222 AGTCCGAGGCCGCCTGGCAGTGTGTGAGTGGAGGCGCTGCAGATCCTCGGGGGCTGGGC 1281
         :::
Db  407 AlaSerGluSerAlaTrpTyrValCysAspGluGlnIleIleLeuLeuGlyMetGly 426

Qy 1282 TACACAAGGACTATCGTACGAGGCCATACTGGCTGCCGCCATCCTCCATCATTC 1341
         ::: :::||
Db  427 PheMetLysAspCysLeuGluArgValMetArgAspLeuArgIlePheArgIlePhe 446

Qy 1342 GAGGGAACCAATGAGATTCCGGATGTACATCCGCCTGACGGGTCTGCAGCATGCCGGC 1401
         ||    :::||||||
Db  447 GluGlyThrAsnAspIleProAspValHisProProAspGlySerGlnTyrAlaGly 466

Qy 1402 CGGATCCTGACTACCAGGATCCATGAGCTTAAACAGGCC------AAAGTGAGCACAGTC 1455
         :::  ::: :::
Db  467 ------SerHisLeuLysGluLeuGlnArgAlaPheLysAsnProAlaThrAsn 482

Qy 1456 ATGGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGGACTGCTGGACCTGGGGCTG 1515
         ::: :::  :::
Db  483 MetGlyLeuIlePheGluGluGlyGlyGlySerArgArgAlaIleArgSerIleGlyTyrGlyGly 502

Qy 1516 ACAGGCAACCACATGGAGTTGTGCACCCAGTTGCACCCAGTTGCCAACAAGTTTGAGGAG 1575
         |||   :::    :::
Db  503 ThrAspLeuSerAlaPheGluValAlaAlaAspProLeuLysLysValProLeuAlaLysGlnCysSerGlu 522

Qy 1576 AACACCTACTGCTTCGGCCGACCGGACACACCTGCTGCTCCGCCTTTGGCCAAGACCATC 1635
         |||||||||
Db  523 AsnThrTyrCysPheGlyArgProAspThrProAlaAlaArgProLeuAlaLysThrIle 542

Qy 1636 ATGGAGGAGCAGTCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATG 1695
         :::   :::   |||||||||
Db  543 ValAspGluGlnSerGlyThrGluAlaGlyGlyGlnHisProHisGlnProValTrpHisGlnMet 562

Qy 1696 ACGGCCGTGCTGTCGCGGCCAGCGCGCTCCATCGCCATTGGCTCCGCAACCACGACCAC 1755
         |||   :::   :::
Db  563 ThrAlaValLeuSerArgProAlaArgSerHisArgHisTrpLeuArgAsnHisAspThr 582

Qy 1756 AACACCTACTGCTTCGGCCGACCGTGGCAGAGCTTACTTGCAGAATCCTTCAGCCTC 1815
         |||||||   :::
Db  583 AsnThrTyrCysPheGlyArgProTrpGlnSerLeuLeuAlaGluSerPheSerLeu 602

Qy 1816 GAGGTTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCGGAAGCTCCAGCCTC 1869
         :::   :::|||||||
Db  603 GluValLeuGlyGlnHisLeuLeuArgGlyLysLeuLeuAlaGluAlaSerSer 616

Qy 1870 TCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC------ 1908
         :::
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Qy 1909 CACCCTCTGGAC 1920
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Qy   457  ATCATC--AGCATGGATGGGTCCATCACTGTGACCCTGGCGAGCGCACCAGGCTATTGGC  513
               ::::  :::   ::::: ||||||||||||||||||||||  ::::||||||||||
Db   116  LeuValGlyAlaAlaAlaAspLeuGlyLeuAlaValPheGlyAlaHisGlnSerIleGly  135

Qy   514  CTCAAGGGGATCATCTTGGCTGCACTGAGGAGCAGAAGCCAAATACTTGCCTAAACTG    573
          ||||||||:::::||| :::::::  ||||||||||||||||||  ::::::::::||||
Db   136  TrpLysGlyValLeuLeuTyrGlyThrGluGlnLysArgLysThrLeuProGlnVal    155

Qy   574  GGGTCCGGGGAGCAATTGCAGCCTTCTGCCTCACGGAGCCAGTGGGAGCGATGCA     633
          :::||| |||||||||||||  ::::::||||| ||||||||||||||||||||||
Db   156  ValThrGlyGlyThrIleAlaCysPheCysLeuThrGluProSerGlySerAspAla     175

Qy   634  GCCTCAATCCGGAGCAGCAGAGCCACACTAAGTGAAGACAAGAAGCACTACAATCCTCAATGGC  693
          ||||||||||||||||||  :::  :::: ||||||||||||||||||||||:::::::||||
Db   176  GlySerIleArgSerArgAlaAlaValLysSerAlaAlaAspGlySerHisTyrValLeuAsnGly  195

Qy   694  TCCAAGGTCTCGATTACTAATGGAGGACTGGCCAATATTTTACTCGTGTTTGCAAAGACT  753
          ||||||||||||  ::::::::::: ||||||||||:::|||||||||||||||||||||
Db   196  SerLysIleTrpIleSerGlyGlyLeuAlaAspIlePheThrValPheAlaGlnThr  215

Qy   754  GAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAA  810
          ||| ||||||    ||| |||||||||||||||  ::::||||||||||||||||||||
Db   216  GluValThrAspProLysThrGlyGlnLysAspLysAspLysValThrAlaPheIleValGlu  235

Qy   811  AGAGACTTTGGTGGAGTCACTAATGGGAAAACCGAAGATAAATTAGGCATTCGGGGGCTCC  870
          ||||||||||||||||:::::::||||||||||||||||||||||||||||||||||||
Db   236  ArgGlyPheGlyGlyValThrSerGlyValThrSerGlyProGluAspLysMetGlyIleLeuLysCysSer  255

Qy   871  AACACTTGTGAAGTCATTTGAAAACACCAAGATACCTGTGGAAAACATCCTGGAGAG  930
          ||||||| |||||||   ::::::::::||||||||||  :::::::::|||||||
Db   256  AsnThrAlaGluValTyrPheAspAspValLysIleProAlaGluAsnValLeuGlyGly  275

Qy   931  GTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCGGGTTCAGCATGGGC  990
          ||  :::||||||  ||||||||||||:::||||||||||||||||||||||||||||
Db   276  GluGlyAsnGlyPheLysValAlaMetAsnIleLeuAsnGlyArgGlyPheMetSer  295

Qy   991  AGGGTGCTGCTGGCGCTCCAAGAGATTCGATTGAAATGAAATGACTGTCGAGTACGCCTGCACA  1050
          :::||||||  ::::::::||||||||||||  ::::||||||||||||||||||
Db   296  GlyThrLeuLeuAlaGlyThrMetAlaHisCysIleArgLysIleArgLysAlaAlaAlaGluHisAlaThrThr  315

Qy   1051 AGGAAACAGTTTAACAAGAGGCTCAGTGAGTGAGAAATTGATTCAGGAGAAAATTTGCACTG  1110
          ||| |||||  :::::::: ||||||||||||||||||| :::::::||||||||||||
Db   316  ArgValGlnPheAsnLysArgLeuSerGluSerIleGluGlnValGlnLysLeuAlaArg  335

Qy   1111 ATGGCTCAGAAGGCTTACGTCATGAGAGTATGACCTACCTCACAGACAGGGATGCTGAC  1170
          ||||| :::||||||||||  :::||| ::::::||||||||:::||||||||||||||
Db   336  MetAlaMetHisGlnTyrValSerGlnSerMetGlyTyrMetIleSerGlyAsnMetAsp  355

Qy   1171 CAACCTGGCTTTCCCGACTGCGCTCCATCGAGCAGCCATCGTTGAAGGTGTTCAGCTCCCAG  1230
          :::|||||| |||   :::||||||||||||||||  ::::||||||||||||||||
Db   356  --AlaGlyHisThrAspTyrHisLeuGluLeuAlaIleAlaIleSerLysSerSerGlu  374

Qy   1231 GCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGCTTGGGCTACACACAAGG  1290
          ||||||||||||||||:::::::||||||||||||||||||||:::::||||||
Db   375  AlaAlaTrpTyrValCysAspGluAlaLeuGlnIleLeuIleLeuGlyGlyAsnGlyPheMetLys  394

Qy   1291 GACTATCCGTACGAGCCGCATACTGCGTGACACCCCGCATCCTCCTCCTCGAGGGAACC  1350
          :::|||| ||||||||||||||:::||||||||||||||||||||||||||||||||
Db   395  SerSerGlyLeuGluLysGluProCysAspIleAlaArgIleTyrArgIlePheGluGluGlyAla  414

Qy   1351 AATGAGAGATTCTCCGGATGTACATCGCCCCCGACGGGTCTGCAGCATGCGGCCGCCATCCTG  1410
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Db   415  AsnAspIleLeuArgPheLeuArgLeuPheValThrGlnThrLeuThrGlnTyrIleGlnTyrAlaGly--------  431

Qy   1411 ACTACCAGGATCCATGAGCTTAAACAG---------GCCAAAGTGAGCACA  1452
          ||||||| |||  :::||||||||||          :::   :::
Db   432  ---SerHisLeuLysGluLeuGlnArgAlaPheLysAsnProThrAlaAsnLeuGlyLeu  450

Qy   1453 GTCATGGATACCGTTGGGCCGAGGCTTCGGGACTGTGGACCTGGGG  1512
          ::: |||||||||||  ::::||||||||||||||||||||||||
Db   451  IlePheGluLysGlySerArgArgAlaValArgSerIleGly---------TyrGly  466
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Qy   1513 CTGACAGGCAACCATGGAGTTGTGCACCCCAGTGTCTTGCGACAGTGCCAACAAGTTTGAG  1572
               :||         :::  ||||||||||||||||||||||||||  :::||||||||||
Db   467  GlyThrAspLeuSerThrPheValAspProLeuValAspLysGluSerAlaAlaLeuCysAla  486

Qy   1573 GAGAACACCTACTGCTTCGGCCGGACCGTGGAGACACTGCTGCTCCGCTTGGCCAGAGACC  1632
               :::::  :::   ||| :::  :::||||||||||||||||||||||||||||||||
Db   487  AspSerIleAspArgPheSerLysThrIleGluAlaLeuLeuLeuLeuLysHisGlyLysGly  506

Qy   1633 ATCATGGAGGAGCAGCTGGTACTGAAGCGGTGGTGGCCAACATCCTCAACCTGTATGGC  1692
          :::::::||||||||||  ::::::||||||:::||||||||||||||||||||||||
Db   507  IleValAspGlnGlnPheLeuLeuIleLeuArgLeuAlaAspSerAlaIleAspIleTyrGly  526

Qy   1693 ATGACGGCCGTGCTGTCGCGGGCCCAGCCGCGCTCCATTGGGCTCCGCAACCACGAC  1752
          ||||||:::::::::||||||  :::::||||||||||||||||||||||||:::   :::
Db   527  MetSerCysValLeuSerArgAlaSerArgAlaValArgGluAsnAlaSerAlaLeuAsnProSerArgAlaGlu  546

Qy   1753 CACGAGGTTCTTCTTGGCCAACACCTTCTGCCTGGAAGCT----------  1791
          ||||||::::|||:::::||||  ::::||||||||||||
Db   547  HisGluLeuMetAlaLysAlaLysGluAlaAsnAspArgValArgIleAsn  566

Qy   1792 ----------------------------TACTTGCAGAATCTTCTTCAGCCTCTCAGCTGGAC  1827
                                       :::::||||||||||||||||||||||||||
Db   567  IleArgArgValAsnAsnGlyValPheValLysAsnTyrAspThrMetSerAlaIleAlaAla  586

Qy   1828 AAG  1830
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Db   587  Lys  587
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RESULT 15
Q19057
ID   Q19057;       PRELIMINARY;       PRT;       613 AA.
AC   Q19057;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein E04F6.5.
GN   Name=E04F6.5; ORFNames=E04F6.5;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   WormBase Consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Pauley A.;
RT   "The sequence of C. elegans cosmid E04F6.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
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RG   WormBase Consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; U28943; AAA68357.1; -.
DR   PIR; T15905; T15905.
     HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh_1;
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Hypothetical protein; Oxidoreductase.
SQ   SEQUENCE   613 AA;   66171 MW;   C1F2883ECE34551B CRC64;
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Alignment Scores:

Pred. No.:	1.09e-70	Length:	613
Score:	1210.50	Matches:	272
Percent Similarity:	61.16%	Conservative:	109
Best Local Similarity:	43.66%	Mismatches:	205
Query Match:	26.88%	Indels:	37
DB:		Gaps:	14

US-09-945-326-1 (1-2452) x Q19057 (1-613)

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Qy   85 TTCCTGCGCCACCGGCTCGGGCTCGTGCCGCGGGGTCGTGGTCTTCTACCCGCGAAC 144
         |||::||||   ||  ::||||||| :::
Db   16 PheIleArgLeuSerHisSerAlaAlaAlaAlaAlaLys---------AspAlaLysPro 31

Qy  145 CGGCGGCTACTGCGCCACCAGCCCGCTGTACGAGCTTCGC---------AspAlaLysPro 204
         :::::||||||   |||    |||
Db   32 LysAlaValAlaAlaAlaAspSerPro------SerPheValMetAsnLeuPheArgGly 49

Qy  205 AAAATCAAGAAGAAGAAAGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA 264
         ::||||||  |||  :: |||||
Db   50 LysAlaValThrAspGlnValPheProTyrProLeuAsnMetThrAspGluGlnLysGlu 69

Qy  265 --ATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGA 321
          :: ||||||  ||||||||
Db   70 ThrLeuGlyMetValMetSerProLeuGluLysMetLeuValGluValGluAsnAspValVal 89

Qy  322 AAAATTGACCAGGAAGGAGAAAATCCAGATGAAAACTTGGAGAAATTGAAGAGCCTAGGG 381
         ||||| ||||||  |||:::|||:::
Db   90 LysAsnAspGluThrSerAspIleProArgAlaValLeuAspGlnPheAlaGluLeuGly 109

Qy  382 CTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTTCCCAACACCATGTAC 441
         ||||||||    ||||||:::
Db  110 ThrPheGlyValLeuValProGluGluProProLeuGlySerGlyAsnAsnSerGlnMet 129

Qy  442 TCAAGACTAGGGGGGGATCATC---AGCATGATGGTCCATCACTGTGACCCTGCAGCG 498
         :::||||||||:::|||::: |||
Db  130 AlaArgValAlaGluIleValAlaTyrAspLeuGlyPheLeuGlyValMetGlyAla 149

Qy  499 CACCAGGCTATTGGCCTCAAGGGATCATCTTGGCTGCACTGAGGACAGAAAGCCAAA 558
         |||||||||||:::||| ||:::
Db  150 HisGlnSerIleGlyTyrLysGlyIleLeuLeuGluGlyLeuGlyThrAspAlaGlnLysLys 169

Qy  559 TACTTGCCTAAACTGCGCGTCCGGGAGCACATTGCAGCCTTCGCCTTCACGGAGCCAGCC 618
         ||||||||||| |:: ||||||
Db  170 TyrLeuProAspLeuAlaThrGlyArgLysPheAlaAlaPheAlaLeuThrGluProThr 189

Qy  619 AGTGGAGGCGATGCAGCCTCAATCCGGAGCCACCACCAGTGAAGACAAGAAGGAC 678
         ::::||||||||||:::|||||:::
Db  190 ThrGlySerAspAlaSerValArgThrArgAlaGluLeuSerAspGlyGlyLysHis 209

Qy  679 TACATCCTCAATGGCTCCAAGGTCCTGGATTACTAATGGAGGACTGGCCAATATTTTTACT 738
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Db  210 TyrValLeuAsnGlyGlyGlyLysIleTrpIleSerAsnGlyGlyPheAlaAspValPheThr 229
Qy  739 GTGTTGCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGGAAGACAAAATCACAGCA 798
Db  230 ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysAspLysSerMetSerAla 249
Qy  799 TTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAAACCCGAGATAAATTAGGC 858
Db  250 PheIleValGluArgAlaPheGlyGlyValThrSerGlyProGlnLysLysMetGly 269
Qy  859 ATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAAACCAAGATACCTGTGGAAAAC 918
Db  270 IleLysGlySerAsnThrThrGluValHisPheAspAsnLeuLysLysProValGluAsn 289
Qy  919 ATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCTCAACAGCGGCCGG 978
Db  290 LeuLeuGlyLysGluGlyLysGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArg 309
Qy  979 TTCAGCATGGGCAGCGTCGTGGCTGGCTGCCTCAAGAGATTGATTGAAATGACTGCTGAG 1038
Db  310 PheGlyIleProAlaAlaCysThrValHisGlnLysCysIleGlnLysThrValAsp 329
Qy 1039 TACGCCCTGCACAAGGAAGAACAGTTAACAAGAGAGCTCAGTGAATTTGAATTGATTGAG 1098
Db  330 HisIleThrThrArgValGlnPheGlyLysLeuGlnPheGlyLysAsnIleGluGlnGlu 349
Qy 1099 AAATTTGCACTGATGCCTCAGAAGCTTAGGTCCATGGAGAGTATGACCTACCTCACAGCA 1158
Db  350 LysLeuValGluMetIleSerLysLeuTyrAlaThrGluSerIleValThrTyrMetLeuSer 369
Qy 1159 GGGATGCTGGACCAACCTGGCTTCCATGAGCCAGCCAGTGGTGAAGGTG 1218
Db  370 SerAsnMetAspArg---GlyIleLysGluTyrGlnLeuGluAlaAlaIleGlyLysLysVal 388
Qy 1219 TTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGGGCTGCAGATCCTCCGGGGCTTG 1278
Db  389 LeuAlaSerGluAsnAlaTrpLeuValCysAspAspAlaIleGlnValHisGlyGlyMet 408
Qy 1279 GGCTACCACCAAGGGACTATCCGTACGAGCGCCGCATACTGCGTGACACCCGACCTCCTCATC 1338
Db  409 GlyPheMetArgGluThrGlyLeuAspLeuGluArgValLeuArgAspLeuProPheArgIle 428
Qy 1339 TTCGAGGGAACCAATGAGATTCTCCGGATGTACATCCCCGATGACGGGTCTGCAGCATGCC 1398
Db  429 PheGluGlyAlaAsnAspValLeuArgLeuArgPheIleAlaLeuValThrGlyAlaGlnHisAla 448
Qy 1399 GGCCGCATCGTCGACTACCAGGATCCATGAGAGCTTAAACAGCCAAAGTGAGCACAGTCATG 1458
Db  449 GlyLys------HisLeuAlaGluGlnAla-----SerGlyValGly 460
Qy 1459 GATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGCCGAACTGTGGACCTGGGCCTGACA 1518
Db  461 GlyLeuLeuGlyLeuLeuValSerArgValThrGly------GlyAsnThr 475
Qy 1519 GGC---AACCATGGA---GTTGTGCACCCCAGTCTTGCGCAGTGCCAACAGTTTGAG 1572
Db  476 GlySerAsnPheGlyLeuGlnValValAlaSerLeuGlnAsnSerAlaLysValLeuAsp 495
Qy 1573 GAGAACACCTACTGCTTCGGCCGGACCGTGGAGACACTGCTCCTCCCGTTTGCCAAGACC 1632
Db  496 GlnGlnIleAlaLeuPheGlyValGlnThrValGlnThrAspAlaGlnIleLysLysGly 515
Qy 1633 ATCATGGAGGACGCAGCTGTACTGAGCGGCGGTGGCCAACATCCTCATCAACCTGTATGGC 1692
Db  516 IleIleIleAspArgGlnTyrGluMetHisArgValAlaAlaAlaAspAlaAlaIleIleTyrSer 535
Qy 1693 ATGACGGCCCGTGCTGTCGGCGACCTCCATCCGCCATTGGGCTCCCAACCACCAGCAC 1752
Db  536 SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLysAsnLysSerSerAlaAlaAsp 555
Qy 1753 CACGAGGTTCTTCTGCCAACACCTTCTGCGGGAAGCTTACTGCAGAATCTCTTCAGC 1812
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Db    556 PheGluArgLysValAla---ThrTyrTyrValAspLysAlaMetLys--------Ser 571

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              ::::::       |||    |||              :::::   |||  :::

Db    572 SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAsnAlaSerLysValAlaThr 591

Qy   1873 CAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC------------------CAC 1911
              :::  |||   |||          ::::|||     ::::|||         |||

Db    592 IleGluSerLeuAlaLysGlu------ValCysGlyAsnGlyGlyLeuThrLeuGlnHis 609

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Db    610 ProValGlu 612
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Search completed: May 2, 2005, 15:32:15
Job time : 455.764 secs

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            GenCore version 5.1.6

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OM nucleic - protein search, using frame_plus_n2p model


Run on:    May  2, 2005, 13:09:41 ; Search time 239.621 Seconds
                             (without alignments)
                   6013.950 Million cell updates/sec

Title:       US-09-945-326-3
Perfect score: 3423
Sequence:    1 atgagcggctgcgggctct........acccctggacaggacatgc 1863

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
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Searched:    2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:    4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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  -Q=/cgn2_1/USPTO_spool_p/US09945326/runat_02052005_135410_22344/app_query.fasta_1.4686
  -DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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  -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
  -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MXNLEN=0 -MAXLEN=2000000000
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  -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
  -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  A_Geneseq_16Dec04:*
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         2: geneseqp19990s:*
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         4: geneseqp20018:*
         5: geneseqp20028:*
         6: geneseqp20003as:*
         7: geneseqp20003bs:*
         8: geneseqp20048:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
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2	3153	92.1	621	4	AAB94839	Aab94839 Human pro
3	3153	92.1	621	5	AAE21680	Aae21680 Human acy
4	3153	92.1	621	7	ADJ69253	Adj69253 Human hea
5	3153	92.1	621	8	ADJ70247	Adj70247 Human hea
6	3153	92.1	621	8	ADM87327	Adm87327 Human pro
7	3153	92.1	628	4	AAU23008	Aau23008 Novel hum
8	3129	91.4	628	8	ADM87776	Adm87776 Human EST
9	2864	83.7	565	3	AAB41800	Aab41800 Human ORF
10	2526	73.8	498	4	AAB94077	Aab94077 Human pro
11	1537	44.9	306	4	AAU23012	Aau23012 Novel hum
12	1360	39.7	655	5	ABB06992	Abb06992 Mouse ver
13	1356.5	39.6	653	5	ABB06991	Abb06991 Rat very
14	1356.5	39.6	655	7	ADE56093	Ade56093 Rat Prote
15	1345	39.3	655	5	ABB06993	Abb06993 Bovine ve
16	1308	38.2	655	5	ABB06988	Abb06988 Human MD2
17	1308	38.2	655	8	ADJ68728	Adj68728 Human hea
18	1308	38.2	655	7	ABM81815	Abm81815 Tumour-as
19	1299	37.9	655	7	ADJ68514	Adj68514 Human hea
20	1295.5	37.8	655	4	ABB63264	Abb63264 Drosophil
21	1284.5	37.5	618	7	ADC14242	Adc14242 Human enz
22	1210.5	35.4	613	8	ADN22791	Adn22791 Bacterial
23	1122	32.8	527	7	ADC14245	Adc14245 Human enz
24	980	28.6	202	8	AAU23009	Aau23009 Novel hum
25	954	27.9	188	7	ADJ70246	Adj70246 Human hea
26	954	27.9	188	8	ADJ69636	Adj69636 Human hea
27	844.5	24.7	594	8	ADS27671	Ads27671 Bacterial
28	821	24.0	594	8	ADS28396	Ads28396 Bacterial
29	818	23.9	169	6	ABP76260	Abp76260 Human GEN
30	816	23.8	581	8	ADS30391	Ads30391 Bacterial
31	815.5	23.8	360	7	ADC14211	Adc14211 Human enz
32	815.5	23.8	594	8	ADS44855	Ads44855 Bacterial
33	799	23.3	585	8	ADN27112	Adn27112 Bacterial
34	795.5	23.2	583	8	ADN27118	Adn27118 Bacterial
35	765	22.3	583	8	ADS21350	Ads21350 Bacterial
36	704	20.6	373	8	ADS27581	Ads27581 Bacterial
37	699	20.4	382	8	ADS27762	Ads27762 Bacterial
38	691.5	20.2	390	7	ABO77312	Abo77312 Pseudomon
39	690	20.2	379	8	ADS28427	Ads28427 Bacterial
40	686.5	20.1	377	8	ADN27173	Adn27173 Bacterial
41	682	19.9	378	8	ADS44766	Ads44766 Bacterial
42	678	19.8	381	8	ADS27885	Ads27885 Bacterial
43	675.5	19.7	379	8	ADS27580	Ads27580 Bacterial
44	666	19.5	389	6	ADA35093	Ada35093 Acinetoba
45	658	19.2	380	8	ADS28426	Ads28426 Bacterial

ALIGNMENTS

```
RESULT 1
AAB73691
ID   AAB73691 standard; protein; 621 AA.
XX
AC   AAB73691;
XX
DT   11-SEP-2001  (first entry)
XX
DE   Human oxidoreductase protein ORP-24.
XX
KW   Human oxidoreductase protein; ORP; cell proliferative disorder;
KW   arteriosclerosis; cirrhosis; psoriasis; cancer; endocrine disorder;
KW   diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhoea;
KW   osteoporosis; metabolic disorder; obesity; phenylketonuria;
KW   hypercholesterolaemia; reproductive disorder; infertility;
KW   ovulatory defect; menstrual cycle defect; endometriosis;
KW   polycystic ovary disease; spermatogenesis disruption; impotence;
KW   neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW   Huntington's disease; Parkinson's disease; Creutzfeldt-Jakob disease;
KW   meningitis; cerebral palsy; muscular dystrophy; mood disorder; anxiety;
KW   schizophrenic disorder; infection; autoimmune disorder;
KW   inflammatory disorder; acquired immunodeficiency syndrome; AIDS; asthma;
KW   allergy; Crohn's disease; atopic dermatitis; gout; multiple sclerosis;
KW   rheumatoid arthritis; ulcerative colitis; drug screening;
KW   toxicity screening; transgenic animal; SNP detection; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO20014448-A2.
XX
PD   21-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-US033158.
XX
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PR   16-DEC-1999;  99US-0172367P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Lal P, Tang YT, Hillman JL, Baughn MR, Azimzai Y, Lu DAM;
XX
DR   WPI; 2001-390245/41.
DR   N-PSDB; AAH24246.
XX
PT   Novel human oxidoreductase protein (ORP) useful for diagnosing, treating
PT   and preventing cell proliferative, neurological, viral, reproductive and
PT   autoimmune/inflammatory disorders associated with abnormal expression of
PT   ORP.
XX
PS   Claim 1; Page 117-119; 136pp; English.
XX
CC   Sequences AAB73668-AAB73694 represent 27 novel human oxidoreductase
CC   proteins, designated ORP-1 to ORP-27 respectively, and sequences AAH24223
CC   -AAH24249 represent cDNAs encoding ORP-1 to ORP-27. Human ORP proteins
CC   and nucleic acids are useful for diagnosing, treating or preventing cell
CC   proliferative disorders (e.g. arteriosclerosis, cirrhosis, psoriasis,
CC   cancers); endocrine disorders (e.g., type I or II diabetes mellitus,
CC   diabetes insipidus, dwarfism, hirsutism, amenorrhoea, osteoporosis);
CC   metabolic disorders (e.g., obesity, phenylketonuria);
CC   hypercholesterolaemia); reproductive disorders (e.g., infertility,
CC   ovulatory and menstrual cycle defects, endometriosis, polycystic ovary
CC   disease, disruption of spermatogenesis, impotence); neurological
CC   disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
CC   disease, Parkinson's disease, meningitis, Creutzfeldt-Jakob disease,
CC   cerebral palsy, muscular dystrophy, mood, anxiety and schizophrenic
CC   disorders); viral, bacterial, fungal and parasitic infections; and
CC   autoimmune/inflammatory disorders such as acquired immunodeficiency
CC   syndrome (AIDS), allergies, asthma, Crohn's disease, atopic dermatitis,
CC   gout, multiple sclerosis, rheumatoid arthritis or ulcerative colitis.
CC   Human ORP proteins and nucleotides can be used to identify compounds
CC   which modulate their activity or expression. ORP nucleic acid sequences
CC   may also be used for assessing the toxicity of a test compound, to detect
CC   upstream sequences such as promoters and regulatory elements, and to
CC   create knock out or knock in animals or transgenic animals to model human
CC   disease. Oligonucleotide primers derived from ORP gene sequences may be
CC   used to detect single nucleotide polymorphisms (SNPs) and for mapping the
CC   naturally occurring genomic sequences. Antibodies specific for ORP
CC   proteins may be used in the diagnosis of disorders associated with
CC   aberrant ORP expression, in assays to monitor patients being treated with
CC   ORP or modulators thereof, and for assessing toxicity of potential drugs
XX
SQ   Sequence 621 AA;
```

Alignment Scores:

```
Pred. No.:
Score:                  1.33e-287        Length:        621
Percent Similarity:     100.00%          Matches:       621
Best Local Similarity:  100.00%          Conservative:  0
Query Match:            92.11%           Mismatches:    0
DB:                                      Indels:        0
                                         Gaps:          4
```

US-09-945-326-3 (1-1863) x AAB73691 (1-621)

```
Qy  241 GAGGTGGACTCCCGAAAAATTGACCAGGAGGAGGAAATCCCAGATGAAACTTTGGAGAAA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerArgLysIleAspGlnGluGluGluIleProAspGluThrLeuGluLys 100

Qy  301 TTGAAGAGCTTTTGGGCTGCAAGTCCCAAGAAGATATGTGGCCTGGGCTTC 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuLysSerLeuLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe 120

Qy  361 TCCAACCATGTACTCAAGACTAGGGGAGATCATCACGATGGTCCATCACTGTG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy  421 ACCCTGGCAGCGCACCAGGTATTGGCCTCAAGGGGATCATCTTGGCTGCACTGAGGAG 480
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Db  141 ThrLeuAlaAlaHisGlnAlaIleAlaLeuGlyIleIleLeuAlaGlyThrGluGlu 160

Qy  481 CAGAAGCCAAATACTTGCCTAAACTGGCTCCGGGGAGCACATGGCAGCCTTCTGCCTC 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180

Qy  541 ACGGAGCCAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGCAGCCACACTAAGTGAA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy  601 GACAAGAAGCACTACATCCTCAATGGCTGGATTACTAATGGAGGACTGGCC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 AspLysLysHisTyrIleLeuAsnGlySerIleValTrpIleThrAsnGlyGlyLeuAla 220

Qy  661 AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGAC 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240

Qy  721 AAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGGAGTCACTAATGGGAAACCCGAA 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LysIleThrAlaPheIleValGluArgAspLeuValGluSerLeuMetGlyLysProGlu 260

Qy  781 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheLysAsnThrLysIle 280

Qy  841 CCTGTGGAAAACATCCTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTC 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 ProValGluAsnIleLeuGluGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy  901 AACAGCGGCCGGTTCAGCATGGGCAGCGTGTCGGGCGTTGCTCAAGAGATTGATTGAA 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyValAlaGlnGluLeuLeuGlu 320

Qy  961 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTGGA 1020
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Db  321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340

Qy 1021 TTGATTCAGGAGAAATTGGCACTGATGGCTCAGAGAGCTTACGTCATGGAGGAGATGACC 1080
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Db  341 LeuIleGlnGluLysLeuAlaLeuMetAlaGlnArgAlaTyrValMetGluSerMetThr 360

Qy 1081 TACCTCACAGCAGGATGCTGGACCAACCTGGCTTCCCGACTGCTCATCGAGCGAGCAGCC 1140
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Db  361 TyrLeuThrAlaGlyMetLeuAspThrGlnProGlyPheProAspCysSerIleGluAlaAla 380

Qy 1141 ATGGTGAAGGTGTTGTCAGCTCCGAGCGCCGCTGGCAGTGTGTGAGGGCGCTGCAGATC 1200
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Db  381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy 1201 CTCGGGGGCTGGGCTACACAAGGACTATCCGTACGAGCGCATCTGCTGACACCCGC 1260
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Db  401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy 1261 ATCCTCCTCCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrArgGly 440

Qy    1 ATGAGCGGCTGGGGCTTCTTCTGCCACCACGGCTGCGGCTGCGCTGCGCCGGCGGGGTCTG 60
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Db    1 MetSerGlyCysPheLeuPheLeuArgThrThrAlaAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy   61 GTGGTCTCTACCGGCAACCGGCTACTGCGCACCAGCCGCCGCTGAGAGCTTTCGCC 120
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Db   21 ValValSerThrAlaAsnArgLeuLeuArgLeuLeuArgThrSerAsnArgAlaPheAla 40

Qy  121 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAGAAAGAAAGTTTCCATTTCCAGAAGTTAGC 180
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Db   41 LysGluLeuPheLeuGlyLysIleLysLysArgLysLysValPhePheProPheProValSer 60

Qy  181 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCTGAAAAATTCTTCACTGAA 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProGluLysPhePheThrGlu 80
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US-09-945-326-3 (1-1863) x AAB94839 (1-621)

```
Qy      1 ATGAGCGGCTGCGGGGCTTCTTCCTGGCACCACGGCTGCGGCTCGGCGGGGTCTG  60
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Db      1 MetSerGlyCysGlyGlyPheLeuArgThrThrAlaAlaArgAlaCysArgGlyLeu  20

Qy     61 GTGGTCTCACCGGAACCGGCGCGTACTGCGGCACCAGCCCGCTGTACGAGCTTTCGCC  120
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Db     21 ValValSerThrAlaAsnArgArgLeuArgThrSerProProValArgAlaPheAla  40

Qy    121 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAGAAGAGTTTTCCCATTTCCAGAAGTTAGC  180
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Db     41 LysGluLeuPheLeuGlyLysIleLysLysLysLysSerPhePheProGluValSer  60

Qy    181 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA  240
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Db     61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu  80

Qy    241 GAGGTGGACTCCGAAAATTGACCAGGAAGGAAATCCCAGATGAAACTTTGGAGAAA  300
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Db     81 GluValAspSerGluIleAspGlnGluGlyIleProLysIleLysProGluThrLeuGluLys  100

Qy    301 TTGAAGAGCCTAGGGCGTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGGCCTGGGCTTC  360
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Db    101 LeuLysSerLeuGlyPheLeuGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe  120

Qy    361 TCCAACCATGTACTCAAGACTAGGGGAGCATCATCAGCATGGATGGTCCATCACTGTG  420
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Db    121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal  140

Qy    421 ACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG  480
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Db    141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu  160
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Qy   1321 CTGCAGCATGCCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
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Db   441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluHisLeuLysGlnAlaLysVal 460

Qy   1381 AGCACAGTCATGGATACCGTTGGCCGGAGCGTTCGGACCTTCCGGACTCCCTGGGCCGAACTGTGAC 1440
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Db   461 SerThrValMetAspThrValGlyArgArgAspArgThrPheArgThrProTrpAlaGluLeuTrpAsp 480

Qy   1441 CTGGGGCTGACGCAACCATGAGTGTGCACCCAGTCTTGCGACAGTGCCAACAAG 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrGlnProHisGluCysAlaProAlaHisProSerLeuAlaAspSerAlaAsnLys 500

Qy   1501 TTTGGAGGAAACAACTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1560
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Db   501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520

Qy   1561 AAGACCCATGAGGAGCAGCTGGTACTGAAGCGGGTGCCAACATCCTCATCAACCTG 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrHisGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540

Qy   1621 TATGGCATGACGGCCGTGCTGTCCGGGGCCAGCCGCCGTCCATCCGCATTGGCTCCGCAAC 1680
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Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgArgSerIleArgIleGlyLeuArgArgAsn 560

Qy   1681 CACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGAAGCTTACTTCAGAATCTC 1740
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Db   561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGlnAlaTyrLeuGlnAsnLeu 580

Qy   1741 TTCAGCCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600

Qy   1801 GTGTCCCAGCAGATCCTTGAGAAGGGAGCCTATATCTGTGCCACCCTCTGGACAGGACA 1860
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Db   601 ValSerGlnGlnIleLeuGluLysGlyAlaTyrIleCysAlaThrLeuTrpThrGlyThr 620

Qy   1861 TGC 1863
          |||
Db   621 Cys 621

RESULT 2
AAB94839
ID AAB94839 standard; protein; 621 AA.
XX
AC AAB94839;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:16010.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX

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Qy 1561 AAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGTGGCCAACATCCTCATCAACCTG 1620
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Db  521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540

Qy 1621 TATGGCATGACGGCCGTGCTGCGCGGGCCCAGCGCCGCTCCATCCGCATTGGCTCCCAAC 1680
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Db  541 TyrGlyMetThrAlaValLeuArgSerArgAlaSerArgIleGlyLeuArgAsn 560

Qy 1681 CACGACCAGGAGTTCTTCTGGCCAACACCTTCGCGTGGAAGCTACTTCCGAGAATCTC 1740
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Db  561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy 1741 TTCAGCCTCTCAGCTGGACAAGTAGTGCTCCAGAAAACCTAGACGACAGATTAAGAAA 1800
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Db  581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGlnIleLysLysLys 600

Qy 1801 GTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCTCTGGACACGGACA 1860
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Db  601 ValSerGlnGlnIleLeuGluLeuGluLysAlaArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy 1861 TGC 1863
        |||
Db  621 Cys 621
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RESULT 3
AAE21680
ID   AAE21680 standard; protein; 621 AA.
XX
AC   AAE21680;
XX
DT   16-JUL-2002 (first entry)
XX
DE   Human acyl dehydrogenase DHDR-7 (62112 protein).
XX
KW   Human; dehydrogenase-7; DHDR-7; 62112 protein; CNS disorder; epilepsy;
KW   Alzheimer's disease; AS; Pick's disease; differentiation disorder;
KW   Huntington's disease; autonomic function disorder; hyperthyroidism;
KW   depression; schizophrenia; panic migraine; cardiac related disorder;
KW   anxiety; obesity; arteriosclerosis; restenosis; Parkinson's disease;
KW   angina; hypertension; cardiomyopathy; arrhythmia; muscle weaknes;
KW   arterial inflammation; cell proliferation disorder; growth disorder;
KW   diabetes mellitus; hypertension; migration disorder; gene therapy;
KW   fertility disorder; autoimmune disorder; metabolic disorder; ataxia;
KW   cancer; hepatic disease; acyl-CoA dehydrogenase; beta-oxidation; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Domain   1..36
FT   /note= "Dehydrogenase domain"
FT   Domain   23..123
FT   /note= "Dehydrogenase precursor domain"
FT   Domain   37..426
FT   /note= "Acyl-coA very long chain dehydrogenase domain"
FT   Domain   70..432
FT   /note= "Dehydrogenase-related long acyl-coA chain
FT   oxidoreductase domain"
FT   Domain   74..448
FT   /note= "Short chain related acyl-coA dehydrogenase
FT   specific domain"
FT   Domain   85..438
FT   /note= "Acyl CoA dehydrogenase domain"
FT   Domain   85..177
FT   /note= "Acyl CoA dehydrogenase middle domain"
FT   Domain   147..431
FT   /note= "ACD-3 acyl-coA dehydrogenase domain"
FT   Domain   172..549
FT   /note= "Oxidoreductase acyl-coA dehydrogenase family
FT   domain"
FT   Domain   179..286
FT   /note= "Acyl CoA dehydrogenase C-terminal domain"
FT   Region   179..191
FT   /note= "Acyl CoA dehydrogenase signature 1"

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Qy  481 CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCACATTGAGCCTTCTGCCTC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleGluAlaAlaPheCysLeu 180

Qy  541 ACGGAGCCAGCCAGTGGAGCCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy  601 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC 660
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Db  201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy  661 AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATCAGTGAAAGAC 720
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Db  221 AsnIleLeuThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAspAsp 240

Qy  721 AAAATCACAGCATTCATAGTAGAAAAAGACTTGGTGGAGTCACTAATGGGAAACCCGAA 780
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Db  241 LysIleThrAlaPheIleValGluValGluArgAspAspPheGlyGlyValValThrArgAsnGlyLysProGlu 260

Qy  781 GATAAATTAGGCATTCGGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA 840
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Db  261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy  841 CCTGTGGAAAAACATCCTTGGAGAGTCGGATGGGTTAAGGTGGCCATGAACATCCTC 900
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Db  281 ProValGluLysIleLeuGlyLeuGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy  901 AACAGCGGCGCCGGTTCAGCATGGCAGCGTCGTGGCCGGTGCTCAAGAGATTGATTGAA 960
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Db  301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320

Qy  961 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAGAGAGGCTCAGTGAATTTGGA 1020
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Db  321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgGluSerGluPheGly 340

Qy 1021 TTGATTCAGGAGAAATTGCACTGATGGCCTCAGAAGGCCTACGTCATGGAGAGTATGACC 1080
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Db  341 LeuIleGlnGluLysLeuHisAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360

Qy 1081 TACCTCCACAGCAGGGGATGCTGGACCAACCTGGCTTTCCCAACTGCTCCATGCAGGCAGCC 1140
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Db  361 TyrLeuThrAlaGlyMetLeuAspGlnGlnProGlyPhePheAspProAspCysSerIleGluAlaAla 380

Qy 1141 ATGGTGAAGGTGTTCAGCTCGAGGCCGCCTCCGCAGTGTGTGAGTGAGGCGCTGCAGATC 1200
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Db  381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy 1201 CTCGGGGGCTTGGCTCACACAAGGGACTATCCGTACGACGCCATACTGCGTGACCACCCGC 1260
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Db  401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy 1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCCGCCTGACGGGT 1320
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Db  421 IleLeuLeuIlePheGluGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440

Qy 1321 CTGCAGCATGCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
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Db  441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy 1381 AGCACAGTCATGGGATACCGTTGGCCGGAGGCTTCGGGACTTCCGGGCCGAACTGTGGAC 1440
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Db  461 SerThrValMetAspThrArgTrpProGluAlaSerGlyThrSerGlyLeuArgArgAspThrValAsp 480

Qy 1441 CTGGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAG 1500
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Db  481 LeuGlyLeuThrGlyAsnHisGlyValValHisGlyValProSerLeuGlyAlaAspSerArgAlaAsnLys 500

Qy 1501 TTTGAGGAGAACAACTACTGCTTCGGGCCCGGACCGTGGAGACACTGCTCCGCTTTGGC 1560
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Db  501 PheGluGluAsnAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly 520
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FT		/note="Acyl-coA oxidase dehydrogenase oxidoreductase
FT		flavoprotein domain"
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FT	Domain	432..580
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FT	Domain	438..621
FT		/note="very long chain dehydrogenase domain"
FT	Region	460..476
FT		/note="Sugar transport protein signature"
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PN	WO200218582-A2.
XX
PD	07-MAR-2002.
XX
PF	31-AUG-2001; 2001WO-US027186.
XX
PR	31-AUG-2000; 2000US-0229831P.
XX
PA	(MILL-) MILLENNIUM PHARM INC.
XX
PI	Meyers R, Hunter JJ;
XX
DR	WPI; 2002-329775/36.
DR	N-PSDB: AAD34006.
XX
PT	New human dehydrogenase polypeptide for diagnosing and treating
PT	dehydrogenase-7 associated diseases and disorders e.g. Alzheimer's
PT	disease, and to identify modulators of therapeutic use.
XX
PS	Claim 13; Fig 1; 124pp; English.
XX
CC	The invention relates to human dehydrogenase (DHDR)-7 polypeptides
CC	referred to as 62112 and nucleic acid molecules encoding such
CC	polypeptides. DHDR-7 is an acyl-CoA dehydrogenase, a mitochondrial
CC	flavoprotein which catalyses the first step of fatty acid beta-
CC	oxidation. Sequences of the invention and their antibodies are useful for
CC	treating a disorder, disease or condition which is caused by
CC	misregulation (e.g. downregulation or upregulation) of DHDR activity.
CC	Examples of disorders include central nervous system (CNS) disorders e.g.
CC	Alzheimer's disease (AS), Pick's disease, Parkinson's, Huntington's
CC	disease, Gilles de la Tourette's syndrome, multiple sclerosis, epilepsy,
CC	amyotrophic lateral sclerosis and Creutzfeldt-Jakob disease; autonomic
CC	function disorders e.g. hypertension, depression, schizophrenia, panic
CC	migraine, anxiety, obsessive-compulsive disorder and obesity; cardiac
CC	related disorder e.g. arteriosclerosis, ischaemia reperfusion injury,
CC	restenosis, arterial inflammation, angina, hypertension, cardiomyopathy
CC	and arrhythmia; disorders of musculus skeletal system paralysis, muscle
CC	weakness e.g. ataxia; cell proliferation, growth, differentiation or
CC	migration disorders e.g. cancer, diabetes mellitus, hypothyroidism or
CC	hyperthyroidism; reproductive or fertility disorders; autoimmune or or
CC	immune deficiency disorders; hepatic disease or dysfunction and metabolic
CC	disorders. They are used for screening assays, predictive medicine e.g.
CC	diagnostic assays, prognostic assays, monitoring clinical trails, and
CC	pharmacogenetics. Polypeptides of the invention are used to identify
CC	modulators that modulate their activity. Polynucleotides of the invention
CC	are used in gene therapy. The present sequence is human DHDR-7
XX
SQ	Sequence 621 AA;

Alignment Scores:

Pred. No.:	1.33e-287	Length:	621
Score:	3153.00	Matches:	621
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	92.11%	Indels:	0
DB:	5	Gaps:	0

US-09-945-326-3 (1-1863) x AAB21680 (1-621)

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Qy      1 ATGAGCGGCTGCGGGCTTCTCCTGCGACCACGGCTGGGCTGTGCCTGCCGCGGGTCTG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaAlaArgAlaCysArgGlyLeu  20

Qy     61 GTGGTCTCTACCGGCAACCGGCGGCTACTGGCACCAGCCCGCCGCCCTGTACGAGCTTTCGCC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 ValValSerThrGlyAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla  40

Qy    121 AAAGAGCTTTCCTAGGCAAATCAAGAAGAAAGAAGTTTCCCATTCCAGAAGTTAGC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer  60

Qy    181 CAAGATGAACTAATGAAATCAATCAGTTCTTGGGACCGTGGAAAAATTCTTCACTGAA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu  80

Qy    241 GAGGTGGACTCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAAA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProLysGluThrLeuGluLys  100

Qy    301 TTGAAGAGCCTAGGGCTTTTGGCTGCAAGTCCCAAGAAGAATATGTGGCCTGGGCTTC  360
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Db    101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGlnGluTyrGlyGlyLeuGlyPhe  120

Qy    361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGATGGGTCCATCACTGTG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal  140

Qy    421 ACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG  480
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Db    141 ThrLeuAlaAlaHisGlnAlaIleAlaLeuGlyLeuIleLeuAlaGlyThrGluGlu  160

Qy    481 CAGAAAGCCAAATACTTGCCTAAACTGGCTCCGGGAGCACCATTGCAGCCTTCTGCCTC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyLeuHisIleAlaAlaPheCysLeu  180

Qy    541 ACGGAGCCAGCCAGTGGAGCCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu  200

Qy    601 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGACTGGCC  660
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Db    201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyAspTrpAla  220

Qy    661 AATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCGATGATGATCAGTGAAAGAC  720
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Db    221 AsnIlePheThrValPheAlaLysThrGluValAspSerAspGlySerValLysAsp  240

Qy    721 AAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGCGAGTCACTAATGGGAAACCCGAA  780
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Db    241 LysIleThrAlaPheIleValGluArgAspLeuValGlyValThrAsnGlyLysProGlu  260

Qy    781 GATAAATTAGGCATTGGGGGTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle  280

Qy    841 CCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGTTTAAGGTGGCCCATGAACATCCTC  900
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Db    281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu  300

Qy    901 AACAGCGCCGGTTCAGCATGGGCAGCGCTCGTGTGGCTGCTCAAGAGATTGATTGAA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AsnSerGlyArgpPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuGlu  320

Qy    961 ATGAGCTGCTGAGTACCCTGCACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTTGGA  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 MetThrAlaGluTyrAlaCysThrArgArgLysGlnPheAsnLysArgLeuSerGluPheGly  340

Qy   1021 TTGATTCAGGAGAAATTTGCACTGATGCCTCAGAAGGCTTACGTCATGGAGAGTATGACC  1080
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Db    341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr  360
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Qy   1081  TACCTCACAGCAGGGATGCTGACCAACCTGCTTCCGACTGCTCCATCGAGGCAGCC  1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla  380

Qy   1141  ATGGTGAAGGTGTTCAGCTCCGAGGGCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381  MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle  400

Qy   1201  CTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACAGCGCCATACGCGTGACACCCGC  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401  LeuGlyGlyLeuGlyTyrTyrArgAspTyrProTyrGluArgIleLeuArgAspThrArg  420

Qy   1261  ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGCATCGCCCTGACGGGT  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly  440

Qy   1321  CTGCAGCAGTGCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG  1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441  LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal  460

Qy   1381  AGCACAGTCATGGATACCGTTGGCCGAGGCTTCGGGGACTCCCTGGGACCGAACGTGGAC  1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461  SerThrValMetAspThrValGlyArgGlyLeuArgAspSerLeuGlyArgThrValAsp  480

Qy   1441  CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG  1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  LeuGlyLeuThrGlyAsnHisGlyValHisProSerLeuAlaAspSerAlaAsnLys  500

Qy   1501  TTTGAGGAGAACACCTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGCTTGGC  1560
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Db    501  PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly  520

Qy   1561  AAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTGCCAACATCCTCATCAACCTG  1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521  LysThrIleMetGluGluGlnLeuValLeuValLysArgValAlaAsnIleLeuIleAsnLeu  540

Qy   1621  TATGGCATGACGGCCGTGCTCGGGGGCCAGCCGCTCCATCCGGATTGGGCTCCGCAAC  1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn  560

Qy   1681  CACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC  1740
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Db    561  HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu  580

Qy   1741  TTCAGGCCTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581  PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys  600

Qy   1801  GTGTCCCAGACGATCCTTGGAGAAGCGAGCCTATATCTGTGCCCACCCTCTGGACAGGACA  1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ValSerGlnThrIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr  620

Qy   1861  TGC  1863
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Db    621  Cys  621
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Alignment Scores:

Pred. No.:		Length:	621
Score:	1.33e-287	Matches:	621
Percent Similarity:	3153.00	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	92.11%	Gaps:	0
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US-09-945-326-3 (1-1863) x ADJ69253 (1-621)

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Db     1  MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu  20

Qy    61  GTGGTCTCACCGGCGAACCGGCGGCTACTGCGACCAGCCGCCGCCTACGAGCTTTCGCC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21  ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla  40

Qy   121  AAAGAGCTTTTCCTAGGCAAAATCAAGAGAGAAAGAAGTTTCCATTTCCAGAAGTTAGC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41  LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer  60

Qy   181  CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGAAAAATTCTTCACTGAA  240
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Db    61  GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluPhePheLysPheGluThrGlu  80
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Qy    241  GAGGTGGACTCCCGAAAAAATTGACCAGGAGGAAGGGAAAATCCCAGATGAAACTTTGAGAAA   300
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Db     81  GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys   100

Qy    301  TTGAAGAGCCTAGGGCTTTTGGGCTGCCAAGTCCCAGAAGAAGAATATGGTGGCCTGGGCTTC   360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101  LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluGluTyrGlyGlyLeuGlyPhe   120

Qy    361  TCCAACCATGTACTCCAAGACTAGGGAGATCATCGACGATGGGTCCATCATCACTGTG   420
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Db    121  SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal   140

Qy    421  ACCCTGGCCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGCCTGCACTGAGGAG   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141  ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuLeuGlyThrGluGlu   160

Qy    481  CAGAAGCCAAATACTTGCCTAAACTGGCCTCCGGGGAGCACATTGCAGCCTTCTGCCTC   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu   180

Qy    541  ACGGAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAGTGAA   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ThrGluProAlaSerGlySerAspSerAlaAlaSerIleArgSerArgAlaThrLeuSerGlu   200

Qy    601  GACAAGAAGCACTACATCCTCCAAGGTCTGATTACTAATGGAGGACTGGCC   660
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201  AspLysLysHisTyrIleLeuGlnGlySerLysValTrpIleThrAsnGlyGlyLeuAla   220

Qy    661  AATATTTTACTGTGTTGCAAAGACTGAGTCGTTGATTCTGATCAGTGAAAGAC   720
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Db    221  AsnIlePheThrValPheAlaLysThrGluSerLeuIleLeuIleSerGluArgValLysAsp   240

Qy    721  AAAATCACAGCATTCATAGTAGAAAAGAGACTTGGTGGAGTCACTAATGGAAACCCGAA   780
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Db    241  LysIleThrAlaPheIleValGluLysArgLeuGlyGlyValThrAsnGlyLysProGlu   260

Qy    781  GATAAATTAGGCAATCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA   840
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Db    261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle   280

Qy    841  CCTGTGGAAAAACATCCTTGAGAGAGTCGGAGATGGGTTTAAGGTGCCATGAACATCCTC   900
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Db    281  ProValGluAsnIleLeuGluGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu   300

Qy    901  AACAGCGGCGGTTCAGCATGGGCAGCGTCGTGGCTGCTCCAAGAGATTGATTGAA   960
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Db    301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysLysArgLeuGlu   320

Qy    961  ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTAACAAGAGGGCTCAGTGAATTTGGA   1020
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Db    321  MetThrAlaGluTyrAlaCysThrArgLysGlnLeuAsnLysArgLeuSerGluPheGly   340

Qy   1021  TTGATTCAGAGAAATTTGCACTGATGGCTCAGAAGGCTCATGGAGAGTATGACC   1080
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Db    341  LeuIleGlnArgAsnLeuHisLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr   360

Qy   1081  TACCCACAGCAGGATGCTGGACCAACCCTGGCTTTCCCAGACTGCTCCATCGAGGCAGCC   1140
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Db    361  TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProGlyCysSerIleGluAlaAla   380

Qy   1141  ATGGTGAAGGTGTTCAGCTCAGGGAGTCTGAGTGTGTGAGTGAGGCGCTGCAGATC   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381  MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIleIle   400

Qy   1201  CTCGGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGC   1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401  LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg   420

Qy   1261  ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTGTACTACGCCCTGACGGGT   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  IleLeuLeuIleLeuPheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly   440

Qy   1321  CTGCAGCCAATGCCGGCCCGCATCCTGACTACCAGGATCCATCCAGCTTAAACAGGCCAAAGTG   1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    441  LeuGlnHisAlaGlyLysArgIleIleLeuThrThrArgIleHisGluHisGlnAlaLysVal   460

Qy   1381  AGCACAGTCATGGATACCGTTGGCCGGAGGCTTCGGCAGTCCTGGGCACTCCTGGACTGTGAC   1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461  SerThrValMetAspThrValGlyArgArgLeuArgGlnSerTrpAlaLeuLeuAspCysAsp   480

Qy   1441  CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAG   1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys   500

Qy   1501  TTTGAGGAGACACCTACTGCTTCGGCCGGACCGTGAGACACTGCTGCCGCCTTTGGC   1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501  PheGluGluAsnThrThrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly   520

Qy   1561  AAGACCATCATGGAGGAGCAGCTGGTACTGGAAGCGGTGGCCAACATCCTCATCCAACCTG   1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521  LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu   540

Qy   1621  TATGGCATGACGGCCCGTCGTGCGCGGCCGTCCATCCGATTGGGCTTCCGCAAC   1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgIleArgIleGlyLeuArgAsn   560

Qy   1681  CACGACCAGGAGGTTCTTCTTGCCAACACCTTCTGTGGAGCTTACTTGGCAGAATCTC   1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561  HisAspHisGluValLeuLeuAlaAsnThrPheCysGlyAlaTyrLeuGlnAsnLeu   580

Qy   1741  TTCAGCCTCTCAGCTGGACAAGATGCTCCAGAAAACCTAGATGAGCAGATTAACAGAAA   1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581  PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys   600

Qy   1801  GTGTCCCAGCAGATCCTTGAGAAGCCGAGCCTATATCGTGTGCCCACCCTCTGACACGGACA   1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ValSerGlnGlnIleLeuGluLysProSerLeuTyrIleCysAlaHisProLeuAspArgThr   620

Qy   1861  TGC   1863
           |||
Db    621  Cys   621
```

RESULT 5
ADJ70247
ID   ADJ70247   standard; protein; 621 AA.
XX
AC   ADJ70247;
XX
DT   06-MAY-2004 (first entry)
DE   Human heat mitochondrial protein as a therapeutic target SeqID2053.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200308768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 2053; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 621 AA;

Alignment Scores:
Pred. No.:   Length: 621
Score: 1.33e-287   Matches: 621
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 92.11%   Indels: 0
DB: 7   Gaps: 0

US-09-945-326-3 (1-1863) x ADJ70247 (1-621)

Qy   1 ATGAGCGGCTGCGGCTCTTCCTGGCCACCACGGCTCGGCGGCTGCCGGGTCTG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetSerGlyCysGlyLeuPheLeuAlaThrThrAlaAlaAlaArgArgLeuLeuGlyLeu   20

Qy   61 GTGGTCTCTACCGGCGAACCGGCGGCTACTGCGCCACCAGCCGCCTGTACGAGCTTTCGCC   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla   40

Qy 121 AAAGAGCTTTTCCTAGGCAAATCAAGAAGAAAGAGTTTTCCCATTTCCAGAAGTTAGC   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysLysGluValPhePheProProGluValSer 60

Qy 181 CAAGATGAACTTAATGAAATCAAATCAGTTCTTGGGACCCGTGAAAAATTCTTCACTGAA   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGluIleLysSerArgLeuLeuGlyProValGluLysPhePheThrGlu 80

Qy 241 GAGGTGGACTCCCGAAAAATTGACCAGGAAGGGAGAAATCCAGATGAAACTTTGGAGAAA   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerArgLysIleAspGlnGluGlyArgAsnProAspGluThrLeuGluLys   100

Qy 301 TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAAGAGAAATATGGTGCCTGGGCTTC   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProArgGluIleTrpGlyLeuGlyPhe   120

Qy 361 TCCAACACCATGTACTACCTAGGACTAGGGAGATCATCAGCATGATGGGTCCATCACTGTG   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SerAsnThrMetTyrSerArgLeuGlyLeuGlyIleIleSerMetAspGlySerIleThrVal 140

Qy 421 ACCCTGGCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGGCTGCACTGAGGAG   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLysLeuLysGlyIleIleLeuAlaAlaLeuArgArg 160

Qy 481 CAGAAAGCCAAATACTTGCCTAAACTGGCCTCCGGGAGCCACATTTGCAGCCTTCGCCTC   540
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 521 LysThrIleMetGluGluThrGlyGlnLeuValLeuLeuLysArgValAlaAsnIleLeuAsnLeu 540

Qy 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGlyGluHisIleAlaAlaPheCysLeu 180
Db 541 ACGGAGCCAGCCAGTGGGAGCGGAGGATGATGACCGACCAGAGCCCAGAGCCAGCCACTAAGTGAA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgArgAlaThrLeuSerGlu 200

Db 601 GACAAGAAGCACTACATCCTCAAGGTCTGGATTACTAATGGAGGACTCGCC   660
         ||||||||||||||||||||||||||||||||||||||||||
Qy 201 AspLysLysHisTyrIleLeuLysGlySerLysValTrpIleThrAsnGlyGlyLeuAla   220

Qy 661 AATATTTTACTGTGTTGAAAGACTGAGTCGTTGATTCTGATGGATCAGTGAAAGAC   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAspAsp 240

Qy 721 AAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGGAGTCACTAATGGGAAACCCGAA   780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu   260

Qy 781 GATAAATTAGGCATTCGGGGCTCCACACTTGTGAAGTCCATTTGAAAACACCAAGATA   840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle   280

Qy 841 CCTGTGGAAAACATCCTTGAGAGGTTCGGAGATGGTTAAGGTGCCATGAACATCCTC   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu   300

Qy 901 AACAGCGCCGGTCAGCATGGCAGCGTGCTGCGGCGTCTGGGCTCCAAGAGATTGATTGAA   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysSerArgLeuIleGlu 320

Qy 961 ATGAGCTGCTGAGTACCCCTGCACAAGGAAACAGTTAACACAGAGGCTCAGTGAATTTGGA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 MetThrAlaGluTyrAlaCysThrArgLysThrArgLysLysPheAsnLysSerGluPheGly 340

Qy 1021 TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACC   1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr   360

Qy 1081 TACCTTCCACAGCAGGATGCTGGACCAACCTGGCTTCCCGACTGCGTCCATGGAGCGCAGCC 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerHisGluAlaAla   380

Qy 1141 ATGGTGAAGTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGGTGGAGGGCTGCCAGATC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluValAlaLeuGlnIle 400

Qy 1201 CTCGGGGGCTTGGGCTACACAAGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGC   1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg   420

Qy 1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTTCCGGATGTACATCGCCCTGACGGGT 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly   440

Qy 1321 CTGCAGCATGCCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 LeuGlnHisAlaGlyArgHisProAspTyrGlnAspProHisGluLeuGluLysLysLeuAla 460

Qy 1381 AGCACAGTCATGGATACCGTTGGCCGAGGCTTCCGGACTTCCCTGGCCAACTGTGGAC   1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 461 SerThrValMetAspThrValGlyArgGlyPheArgLeuArgAspPheSerLeuGlyArgArg 480

Qy 1441 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGTGCCACAGTGCCAACAAG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuValProSerAlaAsnLys   500

Qy 1501 TTTGAGGAGAACACCTACTGCTTCGGCCCGAGACACTGCGTCTCCGGCTTTGGC   1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 PheGluGluAsnThrTyrCysPheGlyProArgThrValGluThrLeuArgLeuArgPheGly 520

Qy 1561 AAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTG   1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||

```
Qy  1621  TATGGCATGACGGGCCGTGTGTCGCGGGGCCAGCCGCTCCATCCGGCCTCCGGCAAC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560

Qy  1681  CACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561  HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy  1741  TTCAGCCCTCTCAGCTGACAACGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||
Db   581  PheSerLeuSerGlnLeuSerTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600

Qy  1801  GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTGGACAGGACA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy  1861  TGC 1863
          |||
Db   621  Cys 621


RESULT 6
ADM87327
ID   ADM87327 standard; protein; 621 AA.
XX
AC   ADM87327;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human protein SEQ ID NO:420.
XX
KW   respiratory; cytostatic; antiarthritic; antiinflammatory;
KW   gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW   antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW   chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW   inflammatory condition; arthritis; inflammatory bowel disease;
KW   Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW   graft versus host disease; human.
XX
OS   Homo sapiens.
XX
PN   WO2004009834-A2.
XX
PD   29-JAN-2004.
XX
PF   19-JUL-2002; 2002WO-US022858.
XX
PR   21-JUL-2001; 2001US-0306971P.
PR   28-MAR-2002; 2002US-00112944.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI   Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
DR   WPI; 2004-143291/14.
DR   N-PSDB; ADM87083.
XX
PT   New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT   cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT   Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT   versus host disease.
XX
PS   Claim 20; SEQ ID NO 420; 591pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I): (a)
CC   comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC   which encodes a polypeptide with biological activity, where the
CC   polynucleotide hybridises to (I) under stringent hybridisation conditions
CC   or has greater than 99% sequence identity with (I). (I) has respiratory,
CC   cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
CC   antibacterial, immunosuppressive, antidiabetic and antirheumatic
CC   activities, and can be used for
CC   generating polynucleotides encoding chimeric or fusion proteins and
CC   heterologous protein sequences. The polynucleotides can be used to
CC   express recombinant protein for analysis, characterisation or therapeutic
CC   use; as markers for tissues in which the corresponding protein is
CC   preferentially expressed; as molecular weight markers on gels; as
CC   chromosome markers or tags to identify chromosomes or to map related gene
CC   positions; to compare with endogenous DNA sequences in patients to
CC   identify potential genetic disorders; as probes to hybridise and discover
CC   genes, related DNA sequences; as a source of information to derive PCR
CC   primers for genetic fingerprinting; as a probe to subtract-out known
CC   sequences in the process of discovering other novel polynucleotides; for
CC   selecting and making oligomers for attachment to a gene chip or other
CC   support, including for examination of expression patterns; to raise anti-
CC   protein antibodies using DNA immunisation techniques; and as an antigen
CC   to raise anti-DNA antibodies or elicit another immune response. The
CC   polynucleotides and polypeptides can also be used as nutritional sources
CC   or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC   source, as a nitrogen source or as a source of carbohydrates. The
CC   polynucleotides and polypeptides can also be used treat cancer. The
CC   compositions are useful for promoting better or faster closure of non-
CC   healing wounds, for the generation and regeneration of tissues, for gut
CC   protection or regeneration and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues, and conditions resulting from
CC   systemic cytokine damage. The compositions can also be used to treat
CC   inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC   Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC   or graft versus host disease. The present sequence represents a novel
CC   human polypeptide sequence from the present invention. N.B. The sequences
CC   for this patent were obtained from the USPTO web site from an equivalent
CC   US patent US2004004824 9A1.
XX
SQ   Sequence 621 AA;


Alignment Scores:
Pred. No.:                              Length:           621
Score:              1.33e-287           Matches:          621
                    3153.00             Conservative:       0
Percent Similarity: 100.00%             Mismatches:         0
Best Local Similarity: 100.00%          Indels:             0
Query Match:        92.11%              Gaps:               8
DB:                                                         8

US-09-945-326-3 (1-1863) x ADM87327 (1-621)

Qy    1  ATGAGGCGGCTGCGGGCTCTTCCTGGGCACCACGGCTGCGGCGTGCCTGCCTGGCGGGTCTG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu   20

Qy   61  GTGGTCTCTACCGGCGAACCGGCGGCTACTCGGCACCAGCCCGCCGCTCTGCGAGAGCTTTCGCC  120
         |||||||||||||||||||||||||||||||||||||||||||||
Db   21  ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla   40

Qy  121  AAAGAGCTTTTCCTAGGCAAAATCAAGAGACAAAGAGAGTTTCCCATTCCAGAAGTTAGC  180
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   41  LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer   60

Qy  181  CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA  240
         ||||||||||||||||||||||||||||||||||||||||||||
Db   61  GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu   80

Qy  241  GAGGTGGACTCCGAAAATTGACCAGGAGGAGAAAATCCCAGATGAAACTTTGGAGAAA  300
         ||||||||||||||||||||||||||||||||||||||||||
Db   81  GluValAspSerArgArgLeuAspGlnGluGluLysIleProAspGluThrLeuGluLys  100

Qy  301  TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCAGAAGAAATATGGTGGCCTGGGCTTC  360
         |||||||||||||||||||||||||||||||||||||||||||
Db  101  LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe  120

Qy  361  TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGTCCATCACTGTG  420
         |||||||||||||||||||||||||||||||||||||||||||
Db  121  SerAsnThrMetTyrSerArgLeuGlyIleIleSerMetAspGlySerIleThrVal  140

Qy  421  ACCCTGCAGCGCACCAGGCTATTGCGCCTCAAGGGGATCATCTTGCCTGGCACTGAGGAG  480
         ||||||||||||||||||||||||||||||||||||||||||||
```

Db   141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160

Qy   481 CAGAAAGCCAAATACTTGCCTAAACTGGCCTCCGGGGAGCACAATTGCAGCCTTCTGCCTC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisAsnIleAlaAlaPheCysLeu 180

Qy   541 ACGGAGCCAGTGGAGCGATGGAGACTTCCGGAGCAGAGCCACACTAAGTGAA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy   601 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGATTACTAATGGAGGACTGGCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy   661 AATATTTTACTGTGTTGCAAAGACTGAGTCGTTGATTCTGATGATCAGTGAAAGAC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePheThrValPheAlaLysThrGluValLeuAspSerAspGlySerValLysAsp 240

Qy   721 AAAATCACAGCATTCATAGTAGAAAAGAACTTGGTGGAGTCACTAATGGAAACCCGAA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAlaPheIleValGluLysGluLeuValGluSerLeuMetGluThrArgThr 260

Qy   781 GATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   841 CCTGTGGAAAACATCCTTGAGAGTGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTC 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ProValGluAsnIleLeuGluSerValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy   901 AACAGCCGCCGGTTCAGCATGGGCAGCCTGTCGTGGCTGGCCGTCTCAAGAGATTGATTGAA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyValLeuLeuLysArgLeuIleGlu 320

Qy   961 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTAACAAGGAGGCTCAGTGAATTTGGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrAlaGluTyrAlaCysThrArgLysGlnLeuThrArgArgLeuSerGluPheGly 340

Qy   1021 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAGAGGCTTACGTCATGAGAGTATGACC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysLeuHisAlaLeuMetAlaGlnArgGlyLeuAlaTyrArgValMetGluSerMetThr 360

Qy   1081 TACCTCACAGCAGCGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGCCAGCC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrAlaAlaAspAlaGlyMetLeuAspGlnProGlyPheProGlyCysSerIleGluAlaAla 380

Qy   1141 ATGGTGAAGGTGTTCAGCTTCCGAGGCCCGGCCGTGAGTGCGCTGCAGATC 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy   1201 CTCGGGGGCTTGGGCTACAACAAGGGACTATCCGTACGAGCGGCCATACTGCGTGACACCCGC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy   1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440

Qy   1321 CTGCAGCATGCCGGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy   1381 AGCACAGTCATGGATACCGTTGGCCGGAGGCTTCGGACTCCCTGGGCCGAACTGTGGAC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrValGlyArgArgLeuArgThrProTrpAlaGluLeuTrpThrValAsp 480

Qy   1441 CTGGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG 1500
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Db   481 LeuGlyLeuThrGlyAsnHisGluLeuValHisValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy   1501 TTTGAGGAGAAACCTACTGCTTCGGCCGGACCGTGAGAGACTGCTCCGCGTTTGGC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGluLysAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly 520

Qy   1561 AAGACCATCATGAGGAGGAGCAGTCTGGTACTGGAAGCGGGTGGCCAACATCCTCATCAACCTG 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrIleMetGluGluGluGlnSerLeuValLeuGluAlaGlyGlyGlnAsnIleLeuIleAsnLeu 540

Qy   1621 TATGGCATGACGGCCGTGCTGTCGCGGGCCAGCCGCCTCCATCCGCATTGGGCTCCGCAAC 1680
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Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgAlaSerIleArgIleGlyLeuArgAsn 560

Qy   1681 CACGACCAGAGGTTCTCTTGGCCAACACCTTCGCTGCTGGAAGCTTACTTGCAGAATCTC 1740
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Db   561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy   1741 TTCAGCCTCTTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLysLys 600

Qy   1801 GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCGTGCCCACCCTGGACAGGACA 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy   1861 TGC 1863
           |||
Db   621 Cys 621

RESULT 7
AAU23008
ID   AAU23008   standard; protein; 628 AA.
XX
AC   AAU23008;
XX
DT   17-DEC-2001 (first entry)
DE   Novel human enzyme polypeptide #94.
XX
KW   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW   nephrotropic; anticoagulant.
XX
OS   Homo sapiens.
XX
PN   WO200155301-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001239.
XX
PR   31-JAN-2000; 2000US-01790065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
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PR   11-JUL-2000; 2000US-0217496P.
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PR   14-AUG-2000; 2000US-0225214P.
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PR   22-AUG-2000;  2000US-0226868P.
PR   22-AUG-2000;  2000US-0227182P.
PR   23-AUG-2000;  2000US-0227009P.
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PR   01-SEP-2000;  2000US-0229287P.
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PR   01-DEC-2000;  2000US-0250160P.
PR   01-DEC-2000;  2000US-0250391P.
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PR   08-DEC-2000;  2000US-0251869P.
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PR   08-DEC-2000;  2000US-0251990P.
PR   11-DEC-2000;  2000US-0254097P.
PR   05-JAN-2001;  2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465566/50.
DR   N-PSDB; AAS40878.
XX
PT   Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT   treating neural, immune system, muscular, reproductive, pulmonary,
PT   cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS   Claim 11; SEQ ID NO 1004; 1180pp; English.
XX
CC   The present invention relates to the isolation of novel human enzyme
CC   polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC   encoding them. The enzyme polypeptides of the invention may comprise the
CC   functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC   isomerases or ligases. The sequences of the invention are useful in the
CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease) metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. Influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC   the novel human enzyme polypeptide genes of the invention. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
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SQ   Sequence 628 AA;

Alignment Scores:
Pred. No.:   1.34e-287
Score: 3153.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 92.11%
DB:

Length: 628
Matches: 621
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 4

US-09-945-326-3 (1-1863) x AAU23008 (1-628)

Qy   1 ATGAGCGGCTCGGGGCTTCCTCGCCACCACGGCTGCGGGCTCGTGCCTGCGGGGGTCTG   60
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Db   1 ATGAGCGGCTCGGGGCTTCCTCGCCACCACGGCTGCGGGCTCGTGCCTGCGGGGGTCTG   60

Db   8 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu   27

Qy   61 GTGGTCTCACCGCAACCGCGGCTACTGCCACCAGCCCCGCCTGTACGAGCTTTCGCC 120
Db   28 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla   47

Qy   121 AAAGAGCTTTTCCTAGGCAAAATCAAGAGAAAGAGTTTCCCATTTCCAGAAGTTAGC 180
Db   48 LysGluLeuPheLeuGlyLysIleLysLysLysSerPheProPheProGluValSer   67

Qy   181 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 240
Db   68 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu   87

Qy   241 GAGGTTGGACTCCCGAAAAAATGACCAGGAAGGAGAAATCCCAGATGAAACTTTGGAGAAA 300
Db   88 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 107

Qy   301 TTGAAGAGCCTAGGGCTTTTGGGCTCGCAAGTCCCAGAGAATATGGTGGCCTGGCTTC 360
Db   108 LeuLysSerLeuGlyLeuLeuGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe 127

Qy   361 TCCAACACCATGACTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCACTGTG 420
Db   128 SerAsnThrMetThrTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 147

Qy   421 ACCCTGCAGCGCACCAGGCTATTGGCCTCAAGGGATCATCTTGGCTGGACTGAGGAG 480
Db   148 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLeuGlyIleIleLeuGluLeuAlaGlyThrGluGlu 167

Qy   481 CAGAAAGCCAAATACTGGCCTAAACTGGCCGTCCGGGGAGCCATTGCAGCCTTCTGCCTC 540
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Qy   541 ACGGAGCCAGTGGAGCGATGGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
Db   188 ThrGluProAlaSerGlySerAspAlaAlaSerIleLeuArgSerArgAlaThrLeuSerGlu 207

Qy   601 GACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC 660
Db   208 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 227

Qy   661 AATATTTTTACTGTGTTGCAAGACTGAGGTCGTTGATVGTVGATGGATCAGTGAAAGAC 720
Db   228 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspLysSerValLysAsp 247

Qy   721 AAAATCACAGCCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAA 780
Db   248 LysIleThrAlaPheHisSerArgLysArgLeuTrpLeuGluValProLeuAspArgThr 267

Qy   781 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTTCATTTTGAAAACACCAAGATA 840
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Qy   841 CCTGTGGAAAACATCCTTGGAGAGTTCGGAGACTGGCCATGAACATCCTC 900
Db   288 ProValGluAsnIleLeuGlyGluValGlyAspGlyTyrPheLysAlaMetAsnIleLeu 307

Qy   901 AACACAGCGGCCGGTTCAGCATGGGACGCGTCGTGGCTGGCTGCTCAAGAGATTGATTGAA 960

Db   308 AsnSerGlyArgPheSerMetGlySerValAlaValAlaGlyLeuLeuLysArgLeuIleGlu 327

Qy   961 ATGACTGCTGAGTACGCCTGCACAAGAGAAACAGTTAACAGAGGCTCAGTGAATTGGA 1020
Db   328 MetThrAlaGluTyrAlaCysThrArgLysThrValAsnLysArgLeuSerGluPheGly 347

Qy   1021 TTGATTCAGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACC 1080
Db   348 LeuIleGlnLysGluLysAsnGlyLysProAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 367

Qy   1081 TACCTCACAGGAGGATGGCTGGACCAACCTGGCTTCCCGACTGCTCCATGAGGCAGCC 1140
Db   368 TyrLeuThrAlaGlyMetLeuAspTrpGlnProGlyPheProAspCysSerMetGluAlaAla 387

Qy   1141 ATGGTGAAGGTGTTCAGCTCCGAGGCTCCGAGTGTGTGAGTGAGGGCCTGCAGATC 1200
Db   388 MetValLysValPheSerSerGluAlaSerGluValSerGluAlaLeuGlnIle 407

Qy   1201 CTCGGGGGCCTTGGGTACACAAGGGACTATCCGTACGAGAGCCGGATATCTGCGTGACACCCGC 1260
Db   408 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 427

Qy   1261 ATCCTCCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
Db   428 IleLeuIleLeuPheGluGlyGlyThrAsnGluIleLeuLeuArgMetTyrIleAlaLeuThrGly 447

Qy   1321 CTGCAGCATGCCGCGGCATCCTGACTACCAGGATCCATGAGCTTAAAACACGGCCAAAGTG 1380
Db   448 LeuGlnHisAlaAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysLysGlnAlaLysVal 467

Qy   1381 AGCACAGTCATGGATACCGTTGGCCCGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGAC 1440
Db   468 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 487

Qy   1441 CTGGGGCTGCACGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCACAAG 1500
Db   488 LeuGlyLeuThrGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp SerAlaAsnLys 507

Qy   1501 TTTGAGGAAGAACACTACTGCTTCGGCCGAACCGTGGAGACACTGCTTCGCGTTTGGC 1560
Db   508 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 527

Qy   1561 AAGACCATCATGGAGGAGCAGCTGGTACTGGAGCGGGTGGCCAACATCCTCATCAACCTG 1620
Db   528 LysThrIleMetGluGluGlnLeuValLeuGluArgValAlaAsnIleLeuIleAsnLeu 547

Qy   1621 TATGGCATGAGCGGCCGTGCTGCGCGGGCCAGCCGCTCCATCCGCATTGGGCTCCGCAAC 1680
Db   548 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 567

Qy   1681 CACGACCACGAGGGTTCTTCTGCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTCCAGAATCTC 1740
Db   568 HisAspHisGluGluLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 587

Qy   1741 TTCAGCCTCTCCAGCTGGACAAGATGCTCCAGAAAACCTAGATGAGCAGCAGATTAAGAAA 1800
Db   588 PheSerLeuSerGlnLeuAspLysLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 607

Qy   1801 GTGTCCCAGCAGATCCTTGAGAGGGAGCCTATATCTGTGCCACCCTCTGACAGGACA 1860
Db   608 ValSerGlnGlnIleLeuGluGlyGluLysAlaHisProLeuAspAsnArgThr 627

Qy   1861 TGC 1863
           |||
Db   628 Cys 628

RESULT 8
ADM87776
ID   ADM87776 standard; protein; 628 AA.
XX
AC   ADM87776;
XX

DT   03-JUN-2004   (first entry)
XX
DE   Human EST derived amino acid sequence SEQ ID NO:869.
XX
KW   respiratory; cytostatic; antiarthritic; antiinflammatory;
KW   gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW   antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW   chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW   inflammatory condition; arthritis; inflammatory bowel disease;
KW   Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW   graft versus host disease; human; expressed sequence tag; EST.
XX
OS   Homo sapiens.
XX
PN   WO200409834-A2.
XX
PD   29-JAN-2004.
XX
PF   19-JUL-2002; 2002WO-US022858.
XX
PR   21-JUL-2001; 2001US-0306971P.
PR   28-MAR-2002; 2002US-00112944.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI   Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
DR   WPI; 2004-143291/14.
DR   N-PSDB; ADM87558.
XX
PT   New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT   cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT   Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT   versus host disease.
XX
PS   Example 2; SEQ ID NO 869; 591pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I): (a)
CC   comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC   which encodes a polypeptide with biological activity, where the
CC   polynucleotide hybridises to (I) under stringent hybridisation conditions
CC   or has greater than 99% sequence identity with (I). (I) has respiratory,
CC   cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
CC   antibacterial, immunosuppressive, antidiabetic and antirheumatic
CC   activities, and can be used in gene therapy. (I) can be used for
CC   generating polynucleotides encoding chimeric or fusion proteins and
CC   heterologous protein sequences. The polynucleotides can be used to
CC   express recombinant protein for analysis, characterisation or therapeutic
CC   use; as markers for tissues in which the corresponding protein is
CC   preferentially expressed; as molecular weight markers on gels; as
CC   chromosome markers or tags to identify chromosomes or to map related gene
CC   positions; to compare with endogenous DNA sequences in patients to
CC   identify potential genetic disorders; as probes to hybridise and discover
CC   genes, related DNA sequences; as a source of information to derive PCR
CC   primers for genetic fingerprinting; as a probe to subtract-out known
CC   sequences in the process of discovering other novel polynucleotides; for
CC   selecting and making oligomers for attachment to a gene chip or other
CC   support, including for examination of expression patterns; to raise anti-
CC   protein antibodies using DNA immunisation techniques; and as an antigen
CC   to raise anti-DNA antibodies or elicit another immune response. The
CC   polynucleotides and polypeptides can also be used as nutritional sources
CC   or supplements, e.g. a protein or amino acid supplement, as a carbon
CC   source, as a nitrogen source or as a source of carbohydrates. The
CC   polynucleotides and polypeptides can also be used to treat cancer. The
CC   compositions are useful for promoting better or faster closure of non-
CC   healing wounds, for the generation and regeneration of tissues, for gut
CC   protection or regeneration and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues, and conditions resulting from
CC   systemic cytokine damage. The compositions can also be used to treat
CC   inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC   Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC   or graft versus host disease. The present sequence represents an

CC   expressed sequence tag (EST) derived amino acid sequence from the present
CC   invention. N.B. The sequences for this patent were obtained from the
CC   USPTO web site from an equivalent US patent US20040048249A1.
XX
SQ   Sequence 628 AA;

Alignment Scores:
Pred. No.:   Length: 628
Score: 2.46e-285   Matches: 616
Score: 3129.00   Conservative: 2
Percent Similarity: 99.52%   Mismatches: 3
Best Local Similarity: 99.19%   Indels: 0
Query Match: 91.41%   Gaps: 0
DB:

US-09-945-326-3 (1-1863) x ADM87776 (1-628)

```
Qy     1 ATGAGCGGCTGCGGCTCTTCCTGCGCCACCACGGTCGGCGGCTGCTGCCTGCCGCGGGGTCTG  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     8 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu   27

Qy    61 GTGGTCTTCACCGGAACCGGCGGCTACTGCGCCACCAGCCCCTGTACGAGCTTTCGCC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla  47

Qy   121 AAAGAGCTTTCCTAGGCAAAATCAAGAAGAAAGAGAGTTTTCCCATTTCCAGAAGTTAGC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    48 LysGluLeuPheLeuGlyLysIleLysIleLysLysLysGluValPheProPheProGluValSer  67

Qy   181 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGACACCGGTGGAAAAATTCTTCACTGAA  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68 GlnAspGluLeuAsnGluIleAsnGlnPheLeuLeuAspThrGlyGlyLysIleLeuPheThrGlu  87

Qy   241 GAGGTGGACTCCGCAAAAATTGACCAGGAACGGGAAAATCCCAGTAGAAACTTTGGAGAA  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 GluValAspSerArgLysIleAspGlnGluArgGluAsnProSerArgAsnPheGlyGlu  107

Qy   301 TTGAAGAGCCTAGGCTTTTGGGCTGCAAGTCCAGAAGAATATGGTGGCCTGGGCTTC  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGlyTyrGlyGlyLeuGlyPhe  127

Qy   361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGGTCCATCACTGTG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal  147

Qy   421 ACCCTGCAGCGACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 ThrLeuAlaAlaHisGlnAlaAlaIleGlyLeuLysGlyIleIleLeuLeuAlaGlyThrGluGlu  167

Qy   481 CAGAAAGCCAAATACTTGCCTAAACTGGCTGGCCGTCCGGGGACACATTGCAGGCCTTCTGCCTC  540
           |||||||||||||||||||||||||||||||||||||||||||| ::::||||||||||||||||
Db   168 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyArgGlyLeuAlaLeuAlaAlaPheCysLeu  187

Qy   541 ACGGAGCCAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA  600
           ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db   188 ThrGluProAlaAsnGlySerAspAlaAla***IleArgSerArgAlaThrLeuSerGlu  207

Qy   601 GACAAGAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGGAGGACTGCGCC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla  227

Qy   661 AATATTTTACTGTGTTTGCAAAGACTGAGTGCGTCGTTGATTCTGATGGATCAGTGAAAGAC  720
           ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db   228 AsnIlePheThrCysValPheAlaLysThrGluValValAlaAspSerAspGlySerValLysAsp  247

Qy   721 AAAATCACAGCATTCATAGTAGAAAAGAGACTTTGGTGGAGTCACTAATGGGAAAACCCGAA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 LysIleThrAlaPheIleValGluArgGlyArgAspPheGlyValThrAsnGlyLysProGlu  267

Qy   781 GATAAATTAGGACATTCGGGCTCCACACTTGTGAAGTCCATTTGAAAACACCAAGATA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 AspLysLeuGlyHisSerGlySerAsnThrCysGluValHisPheGluAsnThrLysIle  287

Qy   841 CCTGTGGAAAACATCCTTGGAGAGTTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTC  900
```

ID	AAB41800 standard; protein; 565 AA.
AC	AAB41800;
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	Human ORFX ORF1564 polypeptide sequence SEQ ID NO:3128.
XX	
KW	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW	vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW	cholesterol ester storage; systemic lupus erythematosus; infection;
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW	thrombosis; contraceptive.
XX	
OS	Homo sapiens.
XX	
PN	WO200058473-A2.
XX	
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000WO-US008621.
XX	
PR	31-MAR-1999;　99US-0127607P.
PR	02-APR-1999;　99US-0127636P.
PR	05-APR-1999;　99US-0127728P.
PR	30-MAR-2000; 2000US-00540763.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
XX	
DR	WPI; 2000-602362/57.
DR	N-PSDB; AAC76009.
XX	
PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders,
PT	neurodegenerative disorders and cardiovascular disease.
XX	
PS	Claim 11; Page 2345-2346; 5507pp; English.
XX	
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC	which represent the human ORF open reading frames 1 to 3161. The ORFX
CC	sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC	antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC	anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC	cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC	dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC	antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC	sequences can be used for determining the presence of or predisposition
CC	to, or preventing or treating pathological conditions associated with an
CC	ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC	proteins in gene therapy vectors. The proteins and nucleic acids may be
CC	used to treat cancers, proliferative disorders, neurodegenerative
CC	disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC	diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC	storage, systemic lupus erythematosus, severe combined immunodeficiency
CC	(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC	disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC	cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC	enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX	
SQ	Sequence 565 AA;

Alignment Scores:

```
Db   288 ProValGluAsnIleLeuGlyGluValGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu 307
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   901 AACAGCGGCCGGTTCAGCATGGGCAGCCTGCTCGTGGCTGGCCTGCTCAAGAGATTGATTGAA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   308 AsnSerGlyArgPheSerMetGlySerValAlaAlaGlyLeuLeuLysLysArgLeuIleGlu 327

Qy   961 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAAGAGAGGCTCAGTGAATTTGGA 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgGlySerGluPheGly 347

Qy  1021 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAGGGCTTACGTCATGGAGAGTATGACC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   348 LeuIleGlnGluLysLeuHisMetAlaGlnArgAlaTyrValMetGluSerMetThr 367

Qy  1081 TACCTCCACGACAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 TyrLeuThrAlaGlyMetLeuAspProGlyPheProAspCysSerIleGluAlaAla 387

Qy  1141 ATGGTGAAGGTGTTCAGCTCCGAGGGCCGCCTGGCAGTGTGTGAGTGAGGGCGCTGCAGATC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIleIle 407

Qy  1201 CTCGGGGGCTTGGGTACACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   408 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 427

Qy  1261 ATCCTCCTCATCTTCGAGGGAACCAAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428 IleLeuLeuIlePheGluGluThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 447

Qy  1321 CTGCAGCATGCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 467

Qy  1381 AGCACAGTCATGGATACCGTTGGCGGAGGCTTCGGAGCTCCCTGGGCCGGAACTGTGGAC 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   468 SerThrValMetAspThrValGlyGlyGlyPheGlyAlaProTrpAlaGlyThrValAsp 487

Qy  1441 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAG 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuArgThrValProAsnLys 507

Qy  1501 TTTGAGGAGAACACCTACTGCTTCGGCGACCGTGGAGACACTGCTCCGCTTTGGC 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   508 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly 527

Qy  1561 AAGACCATGAGGAGGAGCTGTACTGAAGCGGGTGCCAACATCCTCATCAACCTG 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   528 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 547

Qy  1621 TATGGCATGACGGCCGTGTCTCCGCGGCCCAGCCGCTCCATCGGCATTGGGCTCCGCAAC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   548 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerRIleArgIleGlyLeuArgAsn 567

Qy  1681 CACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   568 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 587

Qy  1741 TTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   588 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 607

Qy  1801 GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCCTGGACAGGACA 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 627

Qy  1861 TGC 1863
         |||
Db   628 Cys 628
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RESULT 9
AAB41800

Pred. No.:
Score: 2.29e-260
Percent Similarity: 100.00%
Best Local Similarity: 83.67%
DB:

Length: 565
Matches: 2864.00
Conservative: 100.00%
Mismatches: 0
Indels: 3
Gaps: 0

Length: 564
Matches: 0
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-945-326-3 (1-1863) x AAB41800 (1-565)

```
Qy    172 GAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGACCCGTTGGAAAAATTC  231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GluValSerGlnAspGluLeuAsnGluIleAsnGlnPheLeuAspProLeuGluLysPhe  21

Qy    232 TTCACTGAAGAGGTGACTCCCGAAAAATTGACCAGGAAGGAAATCCAGATGAAACT  291
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 PheThrGluGluValAspSerArgLysIleAspPheGluGlyLysIleProGluThr  41

Qy    292 TTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAGATATGTGGC  351
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     42 LeuGluLysLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluIleTyrGlyGly  61

Qy    352 CTGGGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCC  411
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 LeuGlyPheSerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySer  81

Qy    412 ATCACTGTGACCCTGCAGCGCCACCAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGC  471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 IleThrValThrLeuAlaAlaHisAlaIleGlyLeuLysGlyIleIleLeuAlaGly  101

Qy    472 ACTGAGGAGCAGAAGCCAAATACTTGCCTAAACTGGCTCGGGAGCACATTGCAGCC  531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    102 ThrGluGluGlnLysLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAla  121

Qy    532 TTCTGCCTCACGGAGCCAGCCAGTGGATGATGGGCCGGATGGGAGCAGCAGAGCCACA  591
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 PheCysLeuThrGluProAlaSerGlyAspAspAlaSerArgIleArgSerArgAlaThr  141

Qy    592 CTAAGTGAAGACAAGAAGCACTACATCCTCAAGGTCTGGATTACTAATGGA  651
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 LeuSerGluAspLysLysHisTyrIleLeuLysValTrpIleThrAsnGly  161

Qy    652 GGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGGTCGTTGATTCTGATGATCA  711
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    162 GlyLeuAlaAsnIlePheThrValPheAlaLysThrGluGlyValValAspSerAspAspHis  181

Qy    712 GTGAAAGACAAAATCACAGCATTCATAGTGAAAGAGACTTTGGTGCAGTCACTAATGGG  771
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 ValLysAspLysIleThrAlaPheIleValLysGluThrLeuValGlnSerLeuMetGly  201

Qy    772 AAACCCGAAGATAAATTAGGCATTCGGGGTCCACACTTGTGAAGTCCATTTGAAAAC  831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 LysProGluAspLysLeuGlyIleArgGlySerHisThrCysGluValHisPheGluAsn  221

Qy    832 ACCAAGATACCTGTGGAAAACATCCCTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATG  891
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    222 ThrLysIleProValGluAsnIleProGlyGluValGlyAspGlyLeuArgTrpProMet  241

Qy    892 AACATCCTACAACAGCCGCCGGTTCAGCATGGGCAGCGTCGTGGCTCGGCTGCTCAAGAGA  951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 AsnIleLeuLeuAsnGlyArgPheSerMetGlyPheSerValValAlaGlyLeuLeuLeuArg  261

Qy    952 TTGATTGAAATGACTGCTGAGTACCGCCTGCACACAAGGAAACAGTTTAACAAGAGGCTCAGT 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 LeuIleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnGlnArgLeuSer  281

Qy   1012 GAATTTGGATTGATTGAGAGAAATTGCACTGCTGATGGCTCAGAAGGCTTACGTCATGTGGAG 1071
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    282 GluPheGlyLeuIleGlnLysLeuGluAlaAlaLeuMetAlaGlnLysAlaTyrValMetGlu  301

Qy   1072 AGTATGACCTACCTCACAGCAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATC 1131
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 SerMetThrTyrLeuThrAlaGlyMetLeuAspArgGlnProGlyProAspCysSerIle  321
```

```
Qy   1132 GAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAGCCGCCCTGCAGTGTGTGAGTGAGGCG 1191
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAla  341

Qy   1192 CTGCAGATCCTGGGGGCTTGGCTACACAAGGGACTATCCTACGAGCGCCATACTGCGT 1251
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    342 LeuGlnIleLeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArg  361

Qy   1252 GACACCCGCCATCCTCCATCTTCGAGGGAACCAATAGAGATTCCGATGTACATCGCC 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 AspThrArgIleLeuLeuIlePheGluGlyGlyThrAsnGluIleLeuGlyMetTyrIleAla  381

Qy   1312 CTGACGGGTCTGCAGCATGCCGGCCCGCCATCCTGACTACCAGGATCATGAGCTTAAACAG 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 LeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisArgLeuLysGln  401

Qy   1372 GCCAAATGAGCACAGTCATGATAACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGA 1431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    402 AlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArg  421

Qy   1432 ACTGTGACCTGGGGCTGACAGGCAACAGGCAACCCAGTCTTGCGGACAGT 1491
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 ThrValAspLeuGlyLeuThrGlyAsnHisGlyValHisProSerLeuAlaAspSer  441

Qy   1492 GCCAACAAGTTGAGGAGAACACCTACTGCTTCGGCCGGACCCTGGAGACACTGCTGCTC 1551
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 AlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeu  461

Qy   1552 CGCTTTGGCCAAGACCATCATGGAGGAGCCCGTGCTACTGAAGGCGGTGGCCAACATCCTC 1611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    462 ArgPheGlyLysTyrHisHisGlyGlyAlaArgAlaThrGluGlyGlyValLeuLeuThrArgGly  481

Qy   1612 ATCAACCTGTATGGCATGACGCCCGTGCTGCGCGGCCCAGCCGTCATCCGCATTGGG 1671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 IleAsnLeuTyrGlyMetThrAlaValLeuArgAlaSerArgAlaSerIleArgIleGly  501

Qy   1672 CTCCCGCAACCACGACCAGAGTTCTTCTTGCGTGGAAGCTTACTTG 1731
              |||||||||||||||||||||||||||||||||||||||||||||
Db    502 LeuArgAsnHisAspHisGluValLeuLeuLeuAlaAsnThrPheCysValGluAlaTyrLeu  521

Qy   1732 CAGAATCTTCTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAG 1791
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln  541

Qy   1792 ATTAAGAAGTGTCCAGACATCCTTGAAGAGCGAGCCTATATCTGTCCACCCTCTG 1851
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 IleLysLysValSerGlnGlnIleIleLeuGluGluArgAlaTyrIleCysAlaHisProLeu  561

Qy   1852 GACAGGACATGC 1863
              ||||||||||||
Db    562 AspArgThrCys  565
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PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000;   2000JP-00118776.
PR   02-MAY-2000;   2000JP-00183767.
PR   09-JUN-2000;   2000JP-00241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT   length cDNAs defined in the specification, and for the detection and/or
PT   diagnosis of the abnormality of the proteins encoded by the full-length
PT   cDNAs.
XX
PS   Claim 8; SEQ ID NO 14271; 2537pp + Sequence Listing; English.
XX
CC   The present invention describes primer sets for synthesising 5602 full-
CC   length cDNAs defined in the specification. Where a primer set comprises:
CC   (a) an oligo-dT primer and an oligonucleotide complementary to the
CC   complementary strand of a polynucleotide which comprises one of the 5602
CC   nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in the
CC   specification. The primer sets can be used in antisense therapy and in
CC   gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC   represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC   oligonucleotides, all of which are used in the exemplification of the
CC   present invention
XX
SQ   Sequence 498 AA;

Alignment Scores:
Pred. No.:   1.62e-228   Length: 498
Score: 2526.00   Matches: 498
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 73.79%   Indels: 0
DB: 4   Gaps: 0

US-09-945-326-3 (1-1863) x AAB94077 (1-498)

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Qy    370  ATGTACTCAAGACTAGGGAGATCATCAGCATGATGGTTCCATCACTGTGACCCTGGCA  429
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Db      1  MetTyrSerArgLeuGlyIleIleSerMetAspGlySerIleThrValThrLeuAla   20

Qy    430  GCGCACCAGGCTATTGGCTCCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCC  489
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21  AlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGluGlnLysAla  40

Qy    490  AAATACTTGCCTAAACTGGGCTCCGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCA   549
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41  LysTyrLeuProLysLeuGlySerGlySerThrLeuGlnProSerAlaAlaPheCysSerGlyGluPro  60

Qy    550  GCCAGTGGGAGCGGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAG  609
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Db     61  AlaSerGlySerAspAlaAlaSerIleArgSerArgArgAlaThrLeuSerGluGluThrArgLeuAla  80

Qy    610  CACTACATCCTCAATGGCCTCCAAGGTCTCGATTACTAATAATGGAGGACTGGCCAATATTTTT  669
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81  HisTyrIleLeuAsnGlySerLysValSerValTrpIleThrAsnGlyGlyLeuAlaAsnIlePhe  100

Qy    670  ACTGTGTTGCAAAGACTGAGTCGTTGATTCTGATGGATCAGTGAAAGACAAAATCACA   729
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101  ThrValPheAlaLysThrGluValValAspSerAspSerValLysAspLysIleThr    120

Qy    730  GCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAAACCCGAAGATAAATTA  789
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Db    121  AlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGluAspLysLeu  140

Qy    790  GGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAA   849
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Db    141  GlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIleProValGlu  160

Qy    850  AACATCCTTGAGAGTCGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGC     909
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Db    161  AsnIleLeuGluLeuGlyValGlyValGlyAspGlyPheLysValAlaMetAsnIleLeuAsnSerGly  180

Qy    910  CGGTTCAGCATGGCCATGGGCGTCGTGGCTGGCCTGCTCAAGAGATTGATTGAAATGACTGCT  969
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Db    181  ArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGluMetThrAla  200

Qy    970  GAGTACGCCTGCACAAGGAAACAGTTAACAGAGCTCAGTGAATTGGATTGATTCAG     1029
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Db    201  GluTyrAlaCysThrArgLysGlnLeuThrGluLeuSerGluLeuAspLeuIleGln     220

Qy   1030  GAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGATGACCTACCTCACA   1089
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Db    221  GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrTyrLeuThr  240

Qy   1090  GCAGGGGATGCTGGACCAACCTGGCTTCCCAGCTGCCACTGCTCCATCGAGGCCAGCCATGGTGAAG  1149
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Db    241  AlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAlaMetValLys  260

Qy   1150  GTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGGCGCTGAGATCCTCGGGGGC   1209
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Db    261  ValPheSerSerGluAlaAlaTrpGlnAlaTrpGlnCysValSerGluGlnIleLeuGlyGly  280

Qy   1210  TTGGGCTACACCAAGGACTATCCGTACGAGGCCATCTGGTGACCACCCGCATCCTCCTC   1269
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Db    281  LeuGlyTyrThrLysAspTyrProTyrGluArgIleLeuLeuArgAspThrArgIleLeuLeu  300

Qy   1270  ATCTTCGAGGGAACCAATGAAGATTCTCCGGATGTACATCGCCCTGCCCGGTGTCTGCAGCAT  1329
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Db    301  IlePheGluGlyThrAsnGluIleLeuLeuArgMetTyrIleAlaLeuThrGlyLeuGlnHis  320

Qy   1330  GCCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTC   1389
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Db    321  AlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysValSerThrVal  340

Qy   1390  ATGGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGACCTGTGGACCTGGGGCTG     1449
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Db    341  MetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAspLeuGlyLeu  360

Qy   1450  ACAGGCAACCATGGAGTTGTGCACCCCAGTGTTGCGGACAGTGCCAACAAGTTTGAGGAG   1509
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Db    361  ThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu  380

Qy   1510  AACACCTACTGCTTCGGCGGGACCGTGGAGACACTGGTCGTCCGCTTTGGCAAGACCATC   1569
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Db    381  AsnThrTyrCysPheGlyArgThrValGluThrLeuValValArgPheGlyLysThrIle  400

Qy   1570  ATGGAGGAGCAGCAGTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACTGTATGGCATG  1629
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Db    401  MetGluGluGlnGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeuTyrGlyMet  420

Qy   1630  ACGGCGTGCTGTGTGCGGGCCAGCCGCTCCATCCGCATTGGCTCCGCAACCACCAC     1689
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Qy   1690  GAGGTTCTCTTGGCCAACAACCTTCTGCGTGGAAGCTTACTTGCGGAAGAATCTTCTCCAGCCTC  1749
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Qy     1810 CAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTGGACAGGACATGC 1863
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Db      481 GlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThrCys 498

RESULT 11
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ID   AAU23012 standard; protein; 306 AA.
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AC   AAU23012;
XX
DT   18-DEC-2001  (first entry)
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DE   Novel human enzyme polypeptide #98.
XX
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KW   ligase; hyperproliferative disorder; immunodeficiency disorder;
KW   autoimmune disorder; neurological disorder; metabolic disorder;
KW   inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW   blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW   nephrotropic; anticoagulant.
XX
OS   Homo sapiens.
XX
PN   WO200155301-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001239.
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us-09-945-326-3.rag

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PR   05-JAN-2001;   2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465566/50.
DR   N-PSDB; AAS40882.
XX
PT   Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT   treating neural, immune system, muscular, reproductive, pulmonary,
PT   cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS   Claim 11; SEQ ID NO 1008; 1180pp; English.
XX
CC   The present invention relates to the isolation of novel human enzyme
CC   polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC   encoding them. The enzyme polypeptides of the invention may comprise the
CC   functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC   isomerases or ligases. The sequences of the invention are useful in the
CC   diagnosis, treatment, prevention and/or prognosis of a wide range of
CC   disorders including hyperproliferative disorders (e.g. cancer),
CC   immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC   arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC   disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC   cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC   (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC   infectious disorders (e.g. influenza). The polynucleotides of the
CC   invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC   the novel human enzyme polypeptides of the invention. Note:The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 306 AA;

Alignment Scores:
Pred. No.:                     12
Score:                         1537.00
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Best Local Similarity:         99.34%          Conservative:     2
Query Match:                   44.90%          Mismatches:       0
DB:                            4               Indels:           0
                                               Gaps:             0

US-09-945-326-3 (1-1863) x AAU23012 (1-306)

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Db      3 Leu***GluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSer 22

Qy   1012 GAATTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAG 1071
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Qy   1372 GCCAAAGTGAGCACAGTCATGGATACCGTTGGCCGGACCGCTTCGGGACTCCCTGGGCCGA 1431
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Qy   1492 GCCAACAAGTTGAGGAGAACACCTACTGCTTCGGCCGGACACCGTGGAGACACTGCTGCTC 1551
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln 282

Qy   1792 ATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGGCAGCCTATATCTGTGCCCACCCTCTG 1851
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 IleLysLysValSerGlnGlnIleLeuGluLysAlaAlaTyrIleCysAlaHisProLeu 302

Qy   1852 GACAGAGACATGC 1863
          |||||||||||||
Db    303 AspArgAspThrCys 306
```

```
RESULT 12
AB806992
ID   AB806992 standard; protein; 655 AA.
XX
AC   AB806992;
XX
DT   20-JUN-2002  (first entry)
XX
DE   Mouse very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID:10.
XX
KW   Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
KW   insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
KW   antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW   glucose transport; hyperglycaemic disorder.
```

```
XX
OS   Mus sp.
XX
PN   WO20021642B-A1.
XX
PD   28-FEB-2002.
XX
PF   20-AUG-2001; 2001WO-JP007117.
XX
PR   21-AUG-2000; 2000JP-00254263.
PR   07-SEP-2000; 2000JP-00276633.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Tojo H, Katayama N, Kakimoto S;
XX
DR   WPI; 2002-269344/31.
XX
PT   Protein binding to insulin-responsive aminopeptidase and glucose
PT   transporter 4, useful for prevention and treatment of diseases associated
PT   with blood sugar level disturbance.
XX
PS   Disclosure; Page 92-95; 103pp; Japanese.
XX
CC   The present invention describes human MD25 (very long chain acyl-CoA
CC   dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
CC   (IRAP)) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
CC   activity. IRAP and GLUT4 are involved in the intracellular regulation of
CC   glucose metabolism and glucose transport across the cell membrane.
CC   Expression of MD25 (whose ligands are these proteins) is also involved in
CC   this regulatory process. MD25 can be used in the prevention, treatment
CC   and diagnosis of diseases involving disturbances of glucose metabolism,
CC   such as diabetes and other hyperglycaemic disorders. The present sequence
CC   represents mouse VLCAD which is given in the exemplification of the
CC   present invention
XX
SQ   Sequence 655 AA;

Alignment Scores:
Pred. No.:                          Length:         655
Score:              1.96e-118       Matches:        1360.00
Percent Similarity: 66.05%          Conservative:   287
Best Local Similarity: 48.24%       Mismatches:     184
Query Match:        39.73%          Indels:         106
DB:                 5               Gaps:           9

US-09-945-326-3 (1-1863) x ABB06992 (1-655)
```

```
Qy      103 CCTGTACGAGCT--------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAG 150
                ||||||           ::|||   ||:|:::|:
Db       66 ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysPheGlnLeuThrIle 85

Qy      151 AAAGAAGTTTTCCCATTCCAGAAGTT---AGCCAAGATGAACTAATGAAATCAATCAG 207
               ::||||||||||||:::       ||| ::|:||||||| :: :|
Db       86 AspGlnValPheProTyrProSerValLeuSerGluGluGlnAlaGlnPheLeuLysGlu 105

Qy      208 TTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAG 267
               |||||:||||       ||   ::|:|||   |||       ||
Db      106 LeuValGlyProValAlaArgPheGluGlnValAlaAsnAspProAlaLysAspAla 125

Qy      268 GAAGGGAAAATCCCAGATGAACTTTGGAGAAATTGAAGAGGCCCTAGGGCTG 327
               :||:  |||::|||||||||::  |||| ||||||
Db      126 LeuGluLysValGluAspProThrLeuGlnLeuGlyLeuGlyLysLeuLysGlyLeuLeu 145

Qy      328 CAAGTCCCAGAAGAGATATGGTGGCCTGGGCTTCTCCAACAACATGTACTCAAGACTAGGG 387
               ||||| | |::|||           |||   |||::|   |||||   |||
Db      146 GlnValProSerGluLeuGlyLeuGlyLeuSerGluAsnThrGlnTyrAlaArgLeuAla 165

Qy      388 GAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGCAGCGCCACCAGGCTATT 444
               ||||||||:|||||   :::||||||||||||||||
Db      166 GluIleValHisProGluLeuSerArgSerGlyValAlaThrLeuAlaHisGlnSerIle 185

Qy      445 GGGCCTCAAGGGGATCATCTTGCTGCACTGAGGACGCAGAAAGCCAAATACTTGCCTAA 504
               |||
Qy.
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```
Db       186 GlyPheLysGlyIleLeuLeuTyrGlyThrGlyAlaGlnArgGluTyrLeuProArg 205
                  ||| |||||||||:::|||           ||||:::       ||||||||||:::
Qy       505 CTGGCCTCCGGGAGCACATTGCAGCCTTCTGCCCACGGAGCCAGTGGAGGCCGCAT 564

Db       206 ValAlaSerGlyValGlnAlaLeuAlaPheCysLeuThrGluProSerGlySerAsp 225
                  :::|||||||||||||       :::||||||||       ||  ||||||:|||:::
Qy       565 GCAGCCTCAATCCGGAGCAGAGCCCACTAAGTGAGACAGAAGCACTACATCCTCAAT 624

Db       226 ValAlaSerIleArgSerAlaIleProSerProCysGlyLysTyrTyrThrLeuAsn 245
                  |||   |||||||||       ||||||||||   ||||   |||||:||||:||
Qy       625 GGCTCCAAGGTCTGGATTACTAATGAGGAGGACTGGCCAATATTTTACTGTGTTGCAAAG 684

Db       246 GlySerLysIleTrpIleSerAsnGluGluAspTrpLeuAlaAspIlePheThrValPheAlaLys 265
                  |||::::|||||   ||||||||:::|||||||||:::|||||||:||||||||:::
Qy       685 ACTGAGGTCGTTGAT---TCTGATGATCAGTGAAAGACAAAATCACAGCATTCATAGTA 741

Db       266 ThrProIleLysAspAlaAlaThrArgIleAlaValLysGluLysLysIleThrAlaPheValVal 285
                  :::   :::|||||||||||:::|||||||||||||:::||||||||  :::|||:::
Qy       742 GAAAGAGACTTTGGTGGAGTCACTAATGGGCACTAAGTGGAACCCGAAGATAAATTAGGCATTCGGGGC 801

Db       286 GluArgSerPheGlyValThrHisGlyLeuProGluLysMetGlyIleLeuLysAla 305
                  |||:||||||:::||||||||||||   ::|||||||||||||||   |||:::
Qy       802 TCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGA 861

Db       306 SerAsnThrSerGluValTyrPheAspGlyValProSerGluAsnValLeuGly 325
                  ||||||:::    |||:::||||||||:||||||||||||:::||||||||:::
Qy       862 GAGGTCGGAGATGGGTTTAAGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATG 921

Db       326 GluValGlyAspGlyPheLysValAlaValAlaAsnIleLeuAsnAsnGlyArgPheGlyMet 345
                  ||||||||:::   :|||||||||||||||:::|::|||||:||||||||||:::
Qy       922 GGCAGCGTGGCTGGCCTCAAGAGATGTGATGAAATGATCAGATTTGTGAAGTACGCCTGC 981

Db       346 AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysAlaAlaAspHisAlaThr 365
                  :::    :::|||   |||||||||||||||:||||||||||||||||||:::
Qy       982 ACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTGGATTGATTCAGGAGAAATTTGCA 1041

Db       366 AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGluGlnLysLeuAla 385
                  |||   :::    :::|||   ::|||||||||||||||||||||:::
Qy      1042 CTGATGGCTCAGAAGGCTTAGTCATGGAGAGTATGACCTACCTCACAGCAGGGATGCTG 1101

Db       386 ArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsnMet 405
                  |||||||||||||||||:::  ::|||||||||||||:||||||||||:::
Qy      1102 GACCAACCTGGCTTTCCGACTGTCCATGAGGCACCATCGAGCCATGTGGTTCAGCTCC 1161

Db       406 AspGln--GlyPheLysAspPheGlnIleLeuGluAlaIleSerLysIlePheCysSer 424
                  |||||   ::||||||:||||||||||||:|||||||:::
Qy      1162 GAGGCCGCGCTCGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGCTTGGGCTACACA 1221

Db       425 GluAlaAlaTrpLysValAlaAlaAspGluCysIleGlnIleIleGlyGlyMetGlyMet 444
                  |||||||||:::|||||   |||||||:::||||||||||||||:::
Qy      1222 AGGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGCATCCTCCTCATCTTCGAGGGA 1281

Db       445 LysGluLeuProGlyValLeuArgValLeuArgAspIlePheArgIlePheGluGly 464
                  :::  ::||||||||||||||||||:::||||||||:||||||:::
Qy      1282 ACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCCCGGCCGCATC 1341

Db       465 AlaAsnAspIleLeuArgLeuPheValAlaLeuGlnLysCysMetAspLysLysGlyGlu 484
                  |||||||||:|||||||||:||||||||:::        |||||||||:::
Qy      1342 CTGACTACCACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCAGTCATGGAT 1395

Db       485 LeuThrGlyLeuGlyAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly 504
                  :::       |||||||||||:::  :::||||||
Qy      1396 ACCGTTGGCGCCGGAGCTTGGCGGAGCTCCGGACTCCGGCCGAACTGTGACCTGGGGCTTG 1455

Db       505 GluAlaGlyLysGlnLeuArgArgArgThrGlyIleGlySerGlyLeuSerLeuSer--- 523
                  |||||||||:|||||||||||||:::       |||||||||:||||||||:::
Qy      1456 AACCATGGAGTTGTGACCCCAGTCTTGCGGACAGTGCCAACAAGTTGAGGAGAACACC 1515

Db       524 -----GlyIleValHisProGluLeuSerArgSerGlyValAlaLeuAlaValGlnAlaLeu 541
                  |||   :::|||||||||||||||:::
Qy      1516 TACTGCTTCGGCGGCCGGACCGTGGAGGACACTGCTCCGCTTTGGCAAGACCATCATGGAG 1575
```

```
Alignment Scores:
Pred. No.:              4.18e-118        Length:        653
Score:                  1356.50          Matches:       295
Percent Similarity:     63.36%           Conservative:  108
Best Local Similarity:  46.38%           Mismatches:    192
Query Match:            39.63%           Indels:        41
                                         DB:            12

US-09-945-326-3 (1-1863) x ABB06991 (1-653)

Qy     25 CGCACCACGGCTGCGCGTCGTGCCTGCCGGGGTCGTGTGTCTTCTACCGGCAACCGGCGG         84
          ||||||     |||::||||       |||||::::                  :::
Db     32 ----------ArgProThrSerAlaGlnArg--------LeuTyrAlaSerGluAlaThrGlnAla         47

Qy     85 CTACTGCGC------------------------------ACCAGCCGCCTGTACGA        111
          :::|||                                 |||    |||
Db     48 ----ValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAlaArg         67

Qy    112 GCT------------TTCGGCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGAAGTT        159
          :::            |||::|||         :::|||                     |||
Db     68 AlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnVal         87

Qy    160 TTCCCATTTCCAGAAGTTAGCCAAGATGAACTAATGAA----------ATCAAT        204
          |||||||                                         :::
Db     88 PheProTyrProSerVal-----------LeuAsnGluGlyGlnThrGlnPheLeuLys        103

Qy    205 CAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGAC        264
          |||||      :::|||||||     |||     |||       :::|||
Db    104 GluLeuValGlyProValAlaArgPhePheGluGluValAlaSerAspProAlaLysAsnAsp        123

Qy    265 CAGGAAGGGAGAAATCCAGATGAACTTGGAGAAATTGAAGAGCCTAGGGCTTTTTGGG        324
          ||||      |||       |||       |||     |||
Db    124 SerLeuGluLysValGluGluAspThrLeuGlnGlyLeuGluLysGlyAlaPheGly        143

Qy    325 CTGCAAGTCCCAGAAGAATATGGTGGCCTGGCTTCTCCACCACCATGTACTCAAGACTA        384
          :::|||                   |||             |||||||
Db    325 LeuGlnValProSerGluLeuGlyLeuGlyLeuSerAsnThrGlnThrTyrAlaArgLeu        163

Qy    385 GGGGAGATCATCAGCATG---GATGGTGTCCATCACTGTGACCCTGGCAGCGCCACCAGGCT        441
          ||||::||         |||     :::|||                     :::|||
Db    164 AlaGluIleValGlyMetHisSerAspLeuGlyValSerValThrLeuGlyAlaHisGlnSer        183

Qy    442 ATTGGCCTCAAGGGATCATCTTGGCTGGCCAAAGCCAAATACTTGCCT        501
          ||||       :::|||       |||||||       |||
Db    184 IleGlyPheLysGlyIleIleLeuLeuTyrGlyThrAlaGlnLeuLysGlyLeuTyrLeuPro        203

Qy    502 AAACTGGCGTCCGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCAGTGGAGC        561
          :::::||||||       :::|||
Db    204 ArgValAlaSerGlyGlnAlaLeuAlaLeuAlaPheCysLeuThrGluProSerGlySer        223

Qy    562 GATGCAGCCTCAATCCGGAGCAGAGCCACCTAAGTGAACAAGAGCCCAGCCACTACCATCCTC        621
          ||||       |||::|||                |||::|||
Db    224 AspValAlaSerIleArgSerArgSerAlaValProSerCysGlyGlyTyrTyrThrLeu        243

Qy    622 AATGGCCTCCAAGGTCTGGATTACTAATGAGGACTGGCCAATATTTTACTGTGTTTGCA        681
          ||||::||                |||             ||||||
Db    244 AsnGlySerLysTrpIleSerAsnGlyValLeuAlaAspIlePheThrValPheAla        263

Qy    682 AAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATA        738
          |||:::||    |||::|||
Db    264 LysThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPheVal        283

Qy    739 GTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAAGAATAAAATTAGGCATTCGG        798
          |||||||                |||:::|||             |||
Db    284 ValGluArgSerPheGlyGlyValThrHisGlyAsnProLysAsnLysMetGlyIleIleLys        303

Qy    799 GGCTCCAACACTTGTGAAGTCCATTTTGAAAAACACCAAGATACCTGTGGAAAACATCCTT        858
          |||       :::|||                |||       :::|||
Db    304 AlaSerAsnThrSerGluValTyrPheGluLysValProAlaGlyValLysValAsnValLeu        323

Qy    859 GGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGCCGGTTCAGC        918
          |||||||||||||||       ||||::||||||
```

```
Db    542 AspGlnPheAlaThrValValGluAlaLysAlaLysLeuValLysHisLysLysGlyIleValAsn        561

Qy   1576 GAGCAGCTGCTGACTGCAAGCGGGTGGCCAACATCCTCATCAACCTGTATGCATGACGGCC       1635
          ||||||     :::|||||||::|||
Db    562 GluGlnPheLeuLeuGlnPheLeuGlnArgLeuAlaLeuAspGlyAlaIleAlaAspLeuTyrAlaMetValVal       581

Qy   1636 GTGCTGTCGCGGGGCCAGCCGCCTCCATCCGCATTGGGCTCCGCAACCACGACCACGAGGTT       1695
          |||||||||||||||       ||||:::|||
Db    582 ValLeuSerArgArgSerArgSerArgLeuSerGluGluSerGluThrAlaGlnHisGluLys       601

Qy   1696 CTCTTGGCCAACAACCTTCTGCGTGGAAGCT--------TACTTGCAGAATCTTCCAGC       1746
          |||::||::|||||||||||||||                :::|||
Db    602 MetLeuCysAlaSerTrpCysIleGluGluAlaThrArgIleArgGluAsnMetAlaSer       621

Qy   1747 CTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCC       1806
          |||       ||||:::|||             :::|||
Db    622 LeuGlnSerSerProGlnHis------------GlnGluLeuPheArgAsnPheArgSerIleSer       639

Qy   1807 CAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCTCTG       1851
          :::     :::::|||                :::|||
Db    640 LysAlaMetValGluAsnGlyLeuValThrGlyAsnProLeu       654
```

RESULT 13
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ABB06991
ID   ABB06991 standard; protein; 653 AA.
XX
AC   ABB06991;
XX
DT   20-JUN-2002 (first entry)
XX
DE   Rat very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID NO:9.
XX
KW   Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
KW   insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
KW   antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW   glucose transport; hyperglycaemic disorder.
XX
OS   Rattus sp.
XX
PN   WO200216428-A1.
XX
PD   28-FEB-2002.
XX
PF   20-AUG-2001; 2001WO-JP007117.
XX
PR   21-AUG-2000; 2000JP-00254263.
PR   07-SEP-2000; 2000JP-00276633.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Tojo H, Katayama N, Kakimoto S;
XX
PR   WPI; 2002-269344/31.
XX
PT   Protein binding to insulin-responsive aminopeptidase and glucose
PT   transporter 4, useful for prevention and treatment of diseases associated
PT   with blood sugar level disturbance.
XX
PS   Disclosure; Page 90-92; 103pp; Japanese.
XX
CC   The present invention describes human MD25 (very long chain acyl-CoA
CC   dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
CC   (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
CC   activity. IRAP and GLUT4 are involved in the intracellular regulation of
CC   glucose metabolism and glucose transport across the cell membrane.
CC   Expression of MD25 (whose ligands are these proteins) is also involved in
CC   this regulatory process. MD25 can be used in the prevention, treatment
CC   and diagnosis of diseases involving disturbances of glucose metabolism,
CC   such as diabetes and other hyperglycaemic disorders. The present sequence
CC   represents rat VLCAD which is given in the exemplification of the present
CC   invention
XX
SQ   Sequence 653 AA;
```

```
Db    324 GlyGluValGlyAspGlyPheLysValAlaAlaAsnIleLeuAsnAsnGlyArgPheGly 343

Qy    919 ATGGGCAGCGTCGTGGCTGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCC 978
          |||    ::::|||||||||||     ::|||    |||||||        :::::|||
Db    344 MetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleAlaLysAlaValAspHisAla 363

Qy    979 TGCAAGGAAACACAGTTAACAAGAGGCTCAGTGAATTGGATTGATTCAGGAGAAATTT 1038
          ||||||     :::::::|||||  |||||||   :::|||||||||||||||||
Db    364 ThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGluGluLysLeu 383

Qy   1039 GCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGGATG 1098
          ||||     |||||  |||||||   ||||  |||  :::   |||
Db    384 AlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsn 403

Qy   1099 CTGGACCAACCTGGCTTCCCGACTGTCTCCATCGAGGCAGCCATGTGAAGGTGTTCAGC 1158
          :::|||  |||||  |||||  ||| ||||||||||||:::  |||||  ||||||
Db    404 MetAspGln--GlyPheLysAspPheGlnIleGluAlaAlaIleAlaIleSerLysIlePheGly 422

Qy   1159 TCCGAGGCCCCTGGCAGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGCTTGGGCTAC 1218
          ||||||||:::        |||    :::|||:::||:::|||||||:::||
Db    423 SerGluAlaAlaTrpLysValThrArgGluCysIleGlnIleMetGlyMetGlyPhe 442

Qy   1219 ACAAGGGACTATCCGTACGAGCCGCATACTGCGTGACACCCGCATCCTCCTCATCTTCGAG 1278
          :::::::    |||||  |||||  |||||  |||   ||||||   |||
Db    443 MetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGlu 462

Qy   1279 GGAACCAATGAGATTCTCCGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGTCATG 1338
          ||||||:::||::||::::|||||::::|||||::|    ||||:::
Db    463 GlyThrAsnGluIleLeuArgIleHisGluLeuLysGlnGlyCysMetAspLysAspLysLys 482

Qy   1339 ATCCTGACTACCAGGATCCATCATGAGCTTAAACAG------GCCAAAGTGAGCACAGTCATG 1392
          |||||     ::: ||||||                :::::|||||
Db    483 GluLeuThrGlyLeuGlyLeuAsnAlaLeuLysAsnProLeuGlyLeuAsnValGlyLeuIle 502

Qy   1393 GATACCGTTGGCCCGAGGCTTCGGGACTCCCTGGGCCAACATGTGACCTGGGCTGACA 1452
          :::::::||||||    |||||||||||||||||||||:::
Db    503 GlyGluAlaSerLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer 522

Qy   1453 GGCAACCATGGAGTGTGCACCCCAGTCTTGCGACAGTCGCCGACAGTTTGAGGAGAAC 1512
          ||||||:::||:::||:::        :::
Db    523 --------GlyIleValHisProGluLeuSerArgSerGlyArgGluLeuAlaValGlnAla 539

Qy   1513 ACCTACTGCTTCGGCCCGACCGTGGAGACACTGCTGCTCCGCTTTGGCCAAGACCATCATG 1572
          |||||||     ||||||     |||:::||   |||||
Db    540 LeuGluGlnPheAlaThrValGluAlaLysGluMetLysHisLysLysGlyIleVal 559

Qy   1573 GAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGATGCATGACG 1632
          ||||  |||     :::::::|||||||||        :::||||||||
Db    560 AsnGluGlnPheLeuLeuGlnAsnArgLeuAlaAspGlyAlaIleLeuAspLeuTyrAlaMetVal 579

Qy   1633 GCCGGTGCGTGCGGGGCCAGCCGCGCCTCATCCGCCATTGGGCCTCCCAACCACCACCAGAG 1692
          |||||:::||:::|||||||||||||       |||
Db    580 ValValLeuSerArgAlaSerArgLeuSerArgSerGluGlyTyrProThrAlaGlnHisGlu 599

Qy   1693 GTTCTCTTGGCCAACACCTTCTGCGTGGAAGCT------TACTTGCAGAATCTCTTC 1743
          ::::::      ||||||||||||||  :::||||||
Db    600 LysMetLeuCysAspSerTrpCysIleGluAlaAlaAlaThrArgIleArgArgGluGluAsnMetAla 619

Qy   1744 AGCCTCTTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTG 1803
          |||||     ::: ||||||||              :::
Db    620 SerLeuGlnIleSerAsnProGln------GlnGlnGluLeuPheArgAsnPheArgSerIle 637

Qy   1804 TCCCAGCAGATCCTTGAGAGAGCGGAGAGCCTATATCGTGCCCACCCTCTG 1851
          ||||:::  |||||||||||||||:::||  ::::::||||||||||||||
Db    638 SerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu 653
```

```
RESULT 14
ADE56093
ID   ADE56093    standard; protein; 655 AA.
XX
AC   ADE56093;
XX
DT   29-JAN-2004  (first entry)
```

The right-side feature block:

```
Db   DE   Rat Protein P45953, SEQ ID NO 1934.
     XX
     KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
     KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
     XX
     OS   Rattus norvegicus.
     XX
     PN   WO200301647S-A2.
     XX
     PD   27-FEB-2003.
     XX
     PF   14-AUG-2002; 2002WO-US025765.
     XX
     PR   14-AUG-2001; 2001US-0312147P.
     PR   01-NOV-2001; 2001US-0346382P.
     PR   26-NOV-2001; 2001US-0333347P.
     XX
     PA   (GEHO ) GEN HOSPITAL CORP.
     PA   (FARB ) BAYER AG.
     XX
     PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
     XX
     DR   WPI; 2003-268312/26.
     DR   GENBANK; P45953.
     XX
     PT   New composition comprising two or more isolated polypeptides, useful for
     PT   preparing a medicament for treating pain in an animal.
     XX
     PS   Claim 1; Page; 1017pp; English.
     XX
     CC   The invention discloses a composition comprising two or more isolated rat
     CC   or human polynucleotides or a polynucleotide which represents a fragment,
     CC   derivative or allelic variation of the nucleic acid sequence. Also
     CC   claimed are a vector comprising the novel polynucleotide, a host cell
     CC   comprising the vector, a method for identifying a nucleotide sequence
     CC   which is differentially regulated in an animal subjected to pain and a
     CC   kit to perform the method, an array, a method for identifying an agent
     CC   that increases or decreases the expression of the polynucleotide sequence
     CC   that is differentially expressed in neuronal tissue of a first animal
     CC   subjected to pain, a method for identifying a compound which regulates
     CC   the expression of a polynucleotide sequence which is differentially
     CC   expressed in an animal subjected to pain, a method for identifying a
     CC   compound that regulates the activity of one or more of the
     CC   polynucleotides, a method for producing a pharmaceutical composition, a
     CC   method for identifying a compound or small molecule that regulates the
     CC   activity in an animal of one or more of the polypeptides given in the
     CC   specification, a method for identifying a compound useful in treating
     CC   pain and a pharmaceutical composition comprising the one or more
     CC   polypeptides or their antibodies. The polynucleotide or the compound that
     CC   modulates its activity is useful for preparing a medicament for treating
     CC   pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
     CC   injury (CCI) and spared nerve injury (Chung), in an animal (e.g. gene
     CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
     CC   the specification) which is differentially expressed during pain. Note:
     CC   The sequence data for this patent did not form part of the printed
     CC   specification, but was obtained in electronic form directly from WIPO at
     CC   ftp.wipo.int/pub/published_pct_sequences.
     XX
     SQ   Sequence 655 AA;
```

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Alignment Scores:
Pred. No.:                                Length:              655
Score:            4.19e-118               Matches:             295
                  1356.50                 Conservative:        108
Percent Similarity:   63.36%              Mismatches:          192
Best Local Similarity:  46.38%            Indels:               41
Query Match:          39.63%              Gaps:                 12
DB:                    7
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US-09-945-326-3 (1-1863) x ADE56093 (1-655)

Qy    25 CGCACCACGGCTGCGCGCTCGTCGCTGCCGCGGGGTCTCGTGGTCTCTACCGCGAACCGCGG 84
         |||   ||||:::|||   ||:::||:||   |||       |||  |||    |||  :::
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```
Db    32 ArgProThrSerAlaGlnArg---------LeuTyrAlaSerGluAlaThrGlnAla    47
                                                                           Qy  1099 CTGGACCAACCTGGCTTCCCGACTGCTCCATGAGCGAGCCAGCCATGTGAAGGTGTTCAGC  1158
Qy    85 CTACTGCGC---------------------ACCAGCCCGCCTGTACGA              111        :::|||||   |||||   |||                  |||||||||||:::  |||||||
         :::||||                          |||||||||||:::               Db   404 MetAspGln---GlyPheLysAspPheGlnIleGluGluAlaAlaIleSerLysIlePheGly   422
Db    48 ValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAlaArg    67

Qy   112 GCT---------------TTCGCCAAAGAGCTTTCTAGGCAAAATCAAGAGAAGAGAAGTT  159        Qy  1159 TCCGAGGCCGCTGGCAGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGCTTGGGCTAC  1218
         |||            ::|||  ||||||||:||||||||||||||::|||           ||         |||||||||||||||||   ||   |||   |||||   |||   :::  |||||:||
Db    68 AlaGluSerLysSerPheAlaValGlyMetPheLysGlyIleGlnLeuThrArgAspGlnVal   87        Db   423 SerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleGlyMetGlyMetGlyPhe   442

Qy   160 TTCCCATTTCAGAAGTTAGCCAAGATGAACTTAATGAA--------ATCAAT  204        Qy  1219 ACAAGGGACTATCCGTACGACGGCCATACTGCGTGACACCCGCATCCTCCTCCTCGAG  1278
         |||||||||||||||||||||||||||||||||||||        :::                  ::::||   |||||   |||   |||::  ||||||||::|||||   ||||||||
Db    88 PheProTyrProSerVal---------LeuAsnGluGlyGlnThrGlnPheLeuLys  103        Db   443 MetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGlu   462

Qy   205 CAGTTCTTGGACCCGTGGGAAAAATTCTTCACTGAGGAGGTGGACTCCCCGAAAAATTGAC  264        Qy  1279 GGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCCGC  1338
         :::|||||||||||||||| :::|||||||||||||||||:||||||||||||| ||| |||              ||||||||:::|||   |||   ||||   |||||||:::|||||   |||||||||
Db   104 GluLeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaLysAspAsnAsp  123        Db   463 GlyThrAsnAspIleLeuArgLeuTyrIleAlaLeuThrGlyLeuGlnLysAlaGlyArgAla   482

Qy   265 CAGGAAGGAGAAATCCCAGATGAAACTTGGAGAAATTGAAGAGCCTAGGGCTTTTTGGG  324        Qy  1339 ATCCTGACTACCAGACCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGTCATG  1392
         |||::|||   |||||||   ||||||||||||||:::||||||||||||||||||                  :::||||||| ||| :::  ||||||   ||  |||||||  |||
Db   124 SerLeuGluLysValGluGluGluLeuAspThrLeuLeuLysLeuGluGluGlyAlaPheGly  143        Db   483 GluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyLeuLeuIle  502

Qy   325 CTGCAAGTCCCAGAAGATATGGTGGCCTGGCTTCTCCAACACCATGTACTCAAGACTA  384        Qy  1393 GATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGACCTGGGCTGACA  1452
         ||||||||||||||||   |||   |||||||||||||||||||||||||||||||||                |||||||||   :::  |||   |||||||   |||||||||||||||||| :::
Db   144 LeuGlnValProSerGluLeuGlyLeuGlyLeuGlyLeuLeuSerAsnThrGlnThrTyrAlaArgLeu  163        Db   503 GlyGluAlaSerLysGluLeuArgArgArgSerGlyIleGlySerGlyLeuSerLeuSer   522

Qy   385 GGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGCAGCCGCCACCAGGCT  441        Qy  1453 GGCAACCATGAGTTGTGCACCCAGTCTTGCGACAGTGCCAACAAGTTTGAGGAGAAC  1512
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Db   164 AlaGluIleValGlyMetHisAspLeuValSerValThrLeuGlyAlaHisGlnSer  183        Db   523 ---------GlyIleValHisProGluLeuSerArgArgSerGlyGluGluLeuAlaValGlnAla   539

Qy   442 ATTGGCCTCAAGGGGATCATCTGGCTGGACTGAGGAGCCAGAAATACTTGCCT  501        Qy  1513 ACCTACTGCTTCGGCCGGACGTGGAGACACTGCTCCGTTGGCAAGACCATCATG  1572
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Db   184 IleGlyPheLysGlyIleIleLeuLeuTyrTyrLysAlaGlnIleLysTyrLeuPro  203        Db   540 LeuGluGlnPheAlaThrValAlaGluLysLeuMetLysLeuHisGlyIleIleVal   559

Qy   502 AAACTGGCGTCCGGGGACACATTGCCTTCTCGCTCACGGGAGCCAGCCAGTGGGAGC  561        Qy  1573 GAGGAGCAGCGTCGTACTGGACGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACG  1632
         |||||||:::|||||||||||   ||||||||   |||||||||||||||||||||                ||||||||||||   ||   |||   |||   ||||||||||   |||||||||
Db   204 ArgValAlaSerGlyGlnAlaLeuAlaLeuAlaPheCysLeuThrGluProSerGlySer  223        Db   560 AsnGluGlnPheLeuLeuLeuGlnArgLeuLeuAlaAspGlyAlaIleAspLeuTyrAlaMetVal   579

Qy   562 GATGCAGCCTCAATCCGGAGCAGAGCAGCCACTGAAGACAAGAAGACTACATCCTC  621        Qy  1633 GCCGTGCTGTCGCGGGCCAGCGCTCCATCCGCCCGTCCCAACCACGACCAGCAG  1692
         |||   |||||||||||||||||||   |||||||   :::  |||||||||||                |||||||||||||||||||||   |||||||||||   ||||||||||
Db   224 AspValAlaSerIleArgSerSerAlaValProSerGlyLysTyrTyrThrLeu  243        Db   580 ValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrArgGlnHisGlu   599

Qy   622 AATGGCTCCAAGGTCTGGATTACTATGAGGACTGGCCAATATTTTTACTGTGTTTGCA  681        Qy  1693 GTTCTTCTGGCCAACACCTTCGCGTCGGAAGCT-----TACTTCCAGAATCTCTTC  1743
         |||||||||||||||||||   ||||   |||||||||   |||||||||||||||                ::|||   |||   |||   ||||   :::|||||||||
Db   244 AsnGlySerLysIleTrpIleSerArgAsnGlyGlyLeuAlaAspIlePheThrVal  263        Db   600 LysMetLeuCysAspSerTrpCysIleGluAlaThrArgIleGluArgGluAsnMetAla   619

Qy   682 AAGACTGAGGTCGTTGAT--TCTGATGAATCAGTGAAAGAATCACCAGCATTCATA  738        Qy  1744 AGCCTCCTCCAGTCTGGACAAGTATGCTCCCAGAAAACCTAGATGAGCAGATTAAGAAAGTG  1803
         ||||||||||   :::     |||||||   |||||||||||||||||||||||||                ||:||   |||||||                 |||
Db   264 LysThrProIleLysAspAlaThrGlyLeuAlaValAlaValLysIleIleThrAlaPheVal  283        Db   620 SerLeuGlnSerAsnProGln-----GlnGlnGluPheArgAsnPheArgSerIle  637

Qy   739 GTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCCG  798        Qy  1804 TCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTG  1851
         |||   :::|||||||||||   ::|||||||||:::   |||||||||                :::   :::|||||   |||||   ||||||
Db   284 ValGluArgSerPheGlyGlyValThrArgHisGlyMetGlyIleIleLys  303        Db   638 SerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu  653

Qy   799 GGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGAAAACATCCTT  858
         |||||||||||||||||   :::|||||||||||||||||:::|||||||||||
Db   304 AlaSerAsnThrSerGlnValTyrPheGluAspGlyValPheAspGlyValProAlaGlnValLeu  323

Qy   859 GGAGAGGTCCGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGCCGGTTCAGC  918
         ||||||||:::||| :::|||||||||||||||||||||||||||||||||||
Db   324 GlyGluValGlyAspGlyLeuPheLysValAlaValAlaAsnIleLeuAsnSerAlaGlyPheGly  343

Qy   919 ATGGGCCAGCCGTCGTCGCTGGGCGTCGCTGCTCAAGCAGATTGATTGAAAATGACTGCTAGTACGCC  978
         |||   :::|||||||||||||||||   :::|||||||||
Db   344 MetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleAlaLysAlaValAspHisAlaAla  363

Qy   979 TGCACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTTGATTCAGGAGAAATTT  1038
         |||||||||||||||||||||||||||||||||||||
Db   364 ThrAsnArgThrGlnPheGlyAspLysIleHisAsnProGlyValIleGluGluLysLeu  383

Qy  1039 GCACTGATGCGCTCAGAAGGCTTACGTCAGGAGTATGAGAGTMetAlaTyrMetLeuSerAlaAsn  1098
         ||||   :::   |||||||||||:::   ::: ||
Db   384 AlaArgMetAlaIleLeuAspLeuLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsn  403
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RESULT 15
ABB06993
ID   ABB06993 standard; protein; 655 AA.
XX
AC   ABB06993;
XX
DT   20-JUN-2002 (first entry)
XX
DE   Bovine very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID:11.
XX
KW   Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
KW   insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
KW   antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW   glucose transport; hyperglycaemic disorder.
XX
OS   Bos taurus.
XX
PN   WO200216428-A1.
XX
PD   28-FEB-2002.
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XX		
PF	20-AUG-2001; 2001WO-JP007117.	
XX		
PR	21-AUG-2000; 2000JP-00254263.	
PR	07-SEP-2000; 2000JP-00276633.	
XX		
PA	(TAKE) TAKEDA CHEM IND LTD.	
XX		
PI	Tojo H, Katayama N, Kakimoto S;	
XX		
DR	WPI; 2002-269344/31.	
XX		
PT	Protein binding to insulin-responsive aminopeptidase and glucose	
PT	transporter 4, useful for prevention and treatment of diseases associated	
PT	with blood sugar level disturbance.	
XX		
PS	Disclosure; Page 95-97; 103pp; Japanese.	
XX		
CC	The present invention describes human MD25 (very long chain acyl-CoA	
CC	dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase	
CC	(IRAP)) and to glucose transporter 4 (GLUT4)). MD25 has antidiabetic	
CC	activity. IRAP and GLUT4 are involved in the intracellular regulation of	
CC	glucose metabolism and glucose transport across the cell membrane.	
CC	Expression of MD25 (whose ligands are these proteins) is also involved in	
CC	this regulatory process. MD25 can be used in the prevention, treatment	
CC	and diagnosis of diseases involving disturbances of glucose metabolism,	
CC	such as diabetes and other hyperglycaemic disorders. The present sequence	
CC	represents bovine VLCAD which is given in the exemplification of the	
CC	present invention	
XX		
SQ	Sequence 655 AA;	

Alignment Scores:

Pred. NO.:	5.09e-117	Length:	655	
Score:	1345.00	Matches:	285	
Percent Similarity:	65.51%	Conservative:	110	
Best Local Similarity:	47.26%	Mismatches:	194	
Query Match:	39.29%	Indels:	14	
DB:	5	Gaps:	9	

US-09-945-326-3 (1-1863) x ABB06993 (1-655)

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Qy   ACGGAGCCAGCCAGTGGAGGGATGCAGCCCAATCCGGAGCAGAGCCACACTAAGTGAA    600
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Db   ThrGluProSerGlySerAspAlaSerIleArgSerAlaValProSerPro          236

Qy   GACAAGAGCACTACATCCTCCAAGGTCTGGATTACTAATGGAGGACTGGCC          660
     ||| :|||| ||||||:||||||||||||||||||||| ||||:|||||||||
Db   CysGlyLysTyrTyrThrLeuAsnGlySerLysSerIleTrpIleSerAsnGlyGlyLeuAla  256

Qy   AATATTTTACTGTGTTGCAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAA      717
     ::||||| ||||||||||||||||||||||||||||   ||||||:||::||||||
Db   AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys   276

Qy   GACAAAATCACAGCATTCATATGAGAAAGACTTGGTGGAGTCACTAATGGAAACCC      777
     :::||||||||| ||||||||||||:|||| |||||||||||||||||||||||||
Db   GluLysIleThrAlaPheValGluArgSerPheGlyValThrHisGlyValProPro   296

Qy   GAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAGTCCATTTGAAAACACCAAG      837
     |||| ||:||::||:|||||||||||||||| ||||||||||:||||| ::::::
Db   GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg  316

Qy   ATACCTGGAAAACATCCTTGGAGAGGTCCGAGATGGGTTTAAGGTGGCCATGAACATC      897
     || ||||||||||||||||:::|||||||||||||||| |||||||||:||||||||
Db   ValProLeuGluAsnValLeuGlyGluValGlyGlyPheLysValAlaMetHisHe    336

Qy   CTCAACAGCGGCCGGTTCAGCATGGGCAGGCCGTCGTGGCTCGCCTGCTCAAGAGATTGATT  957
     |||| |||| ||| |||| :||| ||||:||||||||||::::||||:::|
Db   LeuAsnAsnGlyArgPheGlyMetAlaAlaLeuAlaLeuAlaGlyThrMetLysGlyIleIle  356

Qy   GAAATGACTGCTGAGTACGCCCTGCACAAGGAAACAGTTAACAAGAGGCTCAGTGAATTT   1017
     :::::||| ||||||||||||||||||||| :::::::||||:|||||||||||||:::
Db   AlaLysAlaValAspHisAlaLeuAsnArgThrGlnPheGlyGluLysIleHisAsnPhe  376

Qy   GGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATG   1077
     |||||||||||||||||||||||||||||:|| :::|||
Db   GlyLeuIleGlnGluLysPheLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet  396

Qy   ACCTACCTCACCAGCAGGATGCTGGCACCAACCTGGCTTCCCGACTGCTCCATCGAGCA   1137
     :::||| ||| :::|||| :||||||||||||||| |||
Db   AlaTyrMetValSerAlaAsnMetAspGln---GlySerThrAspPheGlnIleGluAla   415

Qy   GCCATGTGTGAAGGTGTTCAGCTCGAGCCGCCGGCCGTGTGTGAGTGGCGGCTGCAG     1197
     :::::::||| ||||||||||||||:::          ||| ::||||
Db   AlaIleSerLysIlePheGlySerGluAlaValAlaTrpLysValThrAspGluCysIleGln  435

Qy   ATCCTCGGGGCTTGGCTACACAAGGAGCTACATCCGAGCGCATCTGCTGACACC        1257
     :::::||| :::||||||||||||||| :|||| :::||||||||||||||
Db   IleMetGlyGlyPheMetLysGluProGlyValGlnArgValLeuArgAlaHisLeu    455

Qy   CGGATCCTCCTCATCTTGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACG   1317
     |||||| ||| ||| :::||||||||||||:||| |||||:||||
Db   ArgIlePheArgIlePheGlyGluGlyThrAsnGluArgIleLeuArgPheValLeuGln    475

Qy   GGTCTGCGAGCATGCCGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG-------  1371
     || |||||||| :||| ||||||||||||| ::|||||||
Db   GlyCysMetAspLysLysGlyGluSerGlyLeuLeuLysGlyAsnAlaLeuAsnProPhe   495

Qy   GCCAAAGTGAGGCACAGTGCATGATGAATACCCGTTGGCCGAGGCTTCGGGACTCCCTGGGCCGA  1431
     ||| :::::|||||||||:||| ||| |||||||||:::|||||||||||||||
Db   GlyAsnAlaGlyLeuLeuLeuGluValGlyAlaGlyLysGlnLeuGlnArgArgAlaGlyLeu   515

Qy   ACTGTGGACCTCGGGGCTGACACCAGTGTCAGCCAGAGTCTTGCGGACAGT          1491
     :::||| |||| |||||||||||||:||||||||||| :::
Db   LysGluValHisGlnGluLeuArgSer                                532

Qy   GCCAACAAGTTGAGGAGAACACTACTGCTGCCAAGGGATCATCTCTGCTGCTGAGGAG     1551
     ||| ||||||||||||| :::|||||||||||||||:::|||||||||||||||||
Db   GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValGlaAlaLysLeuIle   552

Qy   CGCTTTGCAAGACCATCATGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTC    1611
     ::: ||||||||||||||||:::|| :::|||||||||||
Db   LysHisLysLysAspIleIleAsnGluGlnLeuPheLeuAspIleArgLeuLeuAspSerAla  572
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```
Qy  67   TCTACCGGACCGGCGGCTACTGCGCCACCAGCCCGCCTGTACGAGCTTTCGCCAAAGAG        126
          ||| :::||||||||| |||           ::::            ::::||||||||||
Db  57   SerGluAlaSerThrArgGluLysArgAlaAlaAsnSerValSerLysSerPheAlaValGly   76

Qy  127  CTTTTCCTAGGCAAAATCAAGAAGAAGAAGTTTCCATTTCCAGAAGTT--AGCCAA         183
          ||| ||||| ::::||||||||||:::|||||||||||||::|||||||  ||||||
Db  77   ThrPheGlyGlnLeuThrThrAspGlnValPheProSerValLeuAsnGlu           96

Qy  184  GATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAG    243
          ||||:: ::: |||||:||||::::||||||||||||||:||:::|| :||||
Db  97   AspGlnThrGlnPheLeuGluLeuValGlyLeuValGlyProValThrArgPheArgPheGluGluVal  116

Qy  244  GTGGACTCCCGAAAAATTGACCAGGAAGGAAAATCCCAGATGAAACTTTGGAGAAATTG    303
          || |||||||:::||||||||||| ||| :::||||:::|||||||||||||
Db  117  AsnAspAlaAlaLysAspAspAspMetLeuGlnArgValGluGluThrMetGlyInLyLeu   136

Qy  304  AAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGCCTTCTCC   363
          |||||| ::||| |||||||||||||||||||||||:::|| :::|||||
Db  137  LysGluLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyValGlyLeuCys  156

Qy  364  AACACCATGTACTCAAGACTAGGGGGAGATCATCAGCATG---GATGGTCATCACTGTG    420
          |||||:: ||||||:::|||||| |||||||         |||
Db  157  AsnThrGlnPheTyrAlaArgLeuGlyGlyIleValGlyIleValMetThrArgAspValValGlyIle  176

Qy  421  ACCCTGGCAGGCGCACCAGGCTATTGCGCCTCAAGGGGATCATCTCTGCTGCTGAGGAG     480
          |||| ||||| ||||| :::|||||| :::||:::|||
Db  177  ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyLeuLeuLeuPheGlyThrLysAla    196

Qy  481  CAGAAGCCAAAATACTTGCCTAAACTGGGCTCCGGGGAGCACATTGCAGCCTTCTGCCTC   540
          ||||||: :::||||| :::|||||||||| :::||||||
Db  197  GlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThrIleAlaAlaPheCysLeu   216
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```
Qy   1612 ATCAACCTGTATGGCATGGCGCCGTGCTGTCGCGGGGCCAGCCGCTCCATCCGCATTGGG 1671
          ||:::::|||||    |||      |||||||||||||||||||:::
Db    573 IleAsnLeuTyrAlaMetValValLeuSerArgAlaSerArgSerLeuSerGluGluGly  592

Qy   1672 CTCCGCAACCACGACCACGAGGTTCTCTTGGCCAACACCTTCGCGTGGAAGCT------- 1725
              |||||      ::|||      :::::::::|||:||||||
Db    593 HisProThrAlaGlnHisGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaAla  612

Qy   1726 ---TACTTGCAGAATCTCTTCAGCCCTCTCAGCTGACAGTATGCTCCAGAAAACCTA 1782
             :::||||||:::   :::|||    |||       |||       |||
Db    613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlu---Leu  630

Qy   1783 GATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC 1842
             |||      :::|||::: ::::::||||:::  ::: :::
Db    631 PheArgAsnPheLysSerIleSerLysAlaLeuValGluArgGlyValGlyValThrSer  650

Qy   1843 CACCCTCTG 1851
          :::|||||
Db    651 AsnProLeu  653
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Job time : 285.121 secs

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        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    May  2, 2005, 14:33:24 ; Search time 48.5718 Seconds
                                    (without alignments)
                                    5726.413 Million cell updates/sec

Title:          US-09-945-326-3
Perfect score:  3423
Sequence:       1 atgagcggctgcgggctcct........acccctggacaggacatgc 1863

Scoring table:  BLOSUM62
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Searched:       513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:   1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN_1_1_120 @runat_02052005_135411_22376 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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            6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	824	24.1	164	4	US-09-621-976-5565	Sequence 5565, Ap
2	816	23.8	601	4	US-09-902-540-11184	Sequence 11184, A
3	783	22.9	336	4	US-09-270-767-44314	Sequence 44314, A
4	691.5	20.2	390	4	US-09-252-991A-26058	Sequence 26058, A
5	666	19.5	389	4	US-09-328-352-6380	Sequence 6380, Ap
6	650	19.0	384	4	US-09-648-004-6	Sequence 6, Appli
7	650	19.0	384	4	US-10-272-419-6	Sequence 6, Appli
8	623	18.2	387	4	US-09-328-352-6442	Sequence 6442, Ap
9	618.5	18.1	403	4	US-09-252-991A-27960	Sequence 27960, A
10	608	17.8	382	4	US-09-328-352-4850	Sequence 4850, Ap
11	604	17.6	432	4	US-09-949-016-6098	Sequence 6098, Ap
12	603.5	17.6	419	4	US-09-252-991A-31097	Sequence 31097, A
13	596	17.4	394	4	US-09-328-352-6801	Sequence 6801, Ap
14	595.5	17.4	409	3	US-09-364-230-30	Sequence 30, Appl
15	592	17.3	459	4	US-09-949-016-10443	Sequence 10443, A
16	588.5	17.2	427	3	US-09-364-230-32	Sequence 32, Appl
17	559.5	16.3	383	4	US-09-328-352-7081	Sequence 7081, Ap
18	547.5	16.0	610	4	US-09-949-016-7708	Sequence 7708, Ap
19	546.5	16.0	421	4	US-09-949-016-5872	Sequence 5872, Ap
20	538.5	15.7	331	4	US-09-902-540-15531	Sequence 15531, A
21	514.5	15.0	402	4	US-09-328-352-4281	Sequence 4281, Ap
22	501	14.6	424	4	US-09-252-991A-24653	Sequence 24653, A
23	499	14.6	399	4	US-09-328-352-4360	Sequence 4360, Ap
24	495	14.5	464	4	US-09-252-991A-33108	Sequence 33108, A
25	479	14.0	415	4	US-09-806-536A-13	Sequence 13, Appl
26	479	14.0	444	4	US-09-949-016-10163	Sequence 10163, A
27	472	13.8	282	4	US-09-252-991A-29144	Sequence 29144, A
28	467.5	13.7	404	4	US-09-328-352-6854	Sequence 6854, Ap
29	465	13.6	408	4	US-09-328-352-5575	Sequence 5575, Ap
30	456	13.3	270	3	US-09-364-230-28	Sequence 28, Appl
31	443.5	13.0	467	4	US-09-949-016-11236	Sequence 11236, A
32	440	12.9	279	4	US-09-902-540-10571	Sequence 10571, A
33	437	12.8	309	4	US-09-902-540-10954	Sequence 10954, A
34	434.5	12.7	863	4	US-09-252-991A-19574	Sequence 19574, A
35	427	12.5	383	4	US-09-902-540-16004	Sequence 16004, A
36	422.5	12.3	415	4	US-09-328-352-4699	Sequence 4699, Ap
37	422	12.3	379	4	US-09-902-540-12816	Sequence 12816, A
38	416.5	12.2	393	4	US-09-252-991A-23105	Sequence 23105, A
39	394.5	11.5	683	4	US-09-252-991A-26189	Sequence 26189, A
40	392	11.5	413	4	US-09-252-991A-22542	Sequence 22542, A
41	391	11.4	227	4	US-09-270-767-32675	Sequence 32675, A
42	391	11.4	384	4	US-09-543-681A-6433	Sequence 6433, Ap
43	391	11.4	826	4	US-09-543-681A-5053	Sequence 5053, Ap
44	390	11.4	998	4	US-09-252-991A-21058	Sequence 21058, A
45	383.5	11.2	440	4	US-09-949-016-8372	Sequence 8372, Ap

ALIGNMENTS

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RESULT 1
US-09-621-976-5565
; Sequence 5565, Application US/0962197
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Jobert, S.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 5565
;  LENGTH: 164
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -16..-1
US-09-621-976-5565

Alignment Scores:
Pred. No.:               3.64e-68      Length:            164
Score:                   824.00        Matches:           164
Percent Similarity:      100.00%       Conservative:      0
Best Local Similarity:   100.00%       Mismatches:        0
Query Match:             24.07%        Indels:            0
DB:                      4             Gaps:              0

US-09-945-326-3 (1-1863) x US-09-621-976-5565 (1-164)

Qy    1 ATGAGCGGCTGCGGGCTCCTTCCTCGCGCACCACGGCTGCCGCTCGTCGGCCGGGGTCTG  60
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Db    1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu  20
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Qy  199 ATCAATCAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAAGAGGTG------GACTCC 252
             ||||                              :::||||            |||
Db   39 GlnArgLeuPheLysThrAlaLeuLeuGlnPheSerArgGluGlnValLeuProLeuSer  58

Qy  253 CGAAAAATTGAC---CAGGAAGGGAAAAATCCCAGATGAAACTTGGAGAAATTGAGAGC 309
             :::||||| ::::::                    ::  :::      |||     :::
Db   59 GluArgIleGluAlaLysAspAsnAlaLeuLeuArgGlnLeuLeuArgGlnAlaGlyGlu  78

Qy  310 CTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGCTTCCTCCCACACC 369
             |||||                              :::            ||||||||
Db   79 LeuGlyLeuLeuSerValAspIleProGluProGlnAlaTyrGlyGlyLeuGlyPhePheThr  98

Qy  370 ATGTACTACTAGGGAGATCATCAGCATGATGGTCCATCACTGTGACCCTGGCA 429
             |||||||                    :::::||||||||||
Db   99 ThrSerLeuLeuLeuAlaGluAlaMetSerLeuAsnGlySerValThrPheGly 118

Qy  430 GCGCACCAGGCTATTGGCCTCCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCC 489
             |||||||                    |||||:::            ||||||
Db  119 AlaHisThrGlyIleGlyThrLeuProIleValTrpPheGlyAsnAlaGluGlnLysAla 138

Qy  490 AAATACTTGCCTAAACTGGGCTCCGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCA 549
             ||||||||||||||||                        |||||||||
Db  139 LysTyrLeuProLysLeuAlaThrGlyLeuGluTrpValAlaAlaTyrAlaLeuThrGluGln 158

Qy  550 GCCAGTGGGAGGCGATGGCAGCCTCAATCCGGAGCAGAGCCCACTAGTGAAGACAAGAAG 609
             |||||                    :::::::::||||
Db  159 GlySerGlySerAspAlaAlaLeuGlyAlaLeuLysThrLysAlaValLeuSerProAspGlyLys 178

Qy  610 CACTACATCCTCAATGGCTCCAAGTCTCGATTACTAATGGAGGACTGGCCAATATTTTT 669
             |||:::                    :::|||||||
Db  179 HisTrpIleLeuLeuAsnGlySerLysLeuTyrIleThrAsnAlaAlaPheAlaAspValPhe 198

Qy  670 ACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGATCGATCAGTGAAAGACAAAATCACA 729
             :::                        ---------AspGly--------
Db  199 ValValPheAlaLysValAsp------AspGly--------AspLysPheThr 210

Qy  730 GCATTCATAGTAGAAAGACAGACTTTCGTGGAGTCACTAATGGAAACCCGAAGATAAATTA 789
             |||||||||||:::||                    :::||
Db  211 GlyPheIleGluValGlyLysAspThrArgValGlyLeuThrValGlyLeuProGluHisLysMet 230

Qy  790 GGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAA 849
             |||||||:::                        :::||||||
Db  231 GlyIleIleArgGlySerSerProLeuTyrPheCysProLeuTyrPheGluAspAlaAlaArgValProValGlu 250

Qy  850 AACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGC 909
             ||||||                    :::|||:::
Db  251 AsnGlnLeuAsnLeuGlyGluValGlyLysGlyHisLysLysIleAlaPheAsnIleLeuAsnTyrGly 270

Qy  910 CGGTTCAGCATGGGAGCAGCGTCGTGTGGCTGGGCTCTCAAGAGATTGATTGAAATGACTGCT 969
             |||                    :::|||                ::::::
Db  271 ArgLeuLysLeuGlyLeuGlyValLeuGlyMetLysGlyLysGlnLeuLeuGlnLeuAsnAlaLeu 290

Qy  970 GAGTACGCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGATTGATTCAG 1029
             |||||||||||:::|||||||                    ||||||:::
Db  291 ArgPheThrGlnGluGlnArgLysMetGlnPheAsnAlaProIleValGlnPheProLeuSerArg 310

Qy 1030 GAGAAAATTTGCACTGATGCTCAGAAGGTCTTACGTGCAGGATGACCTACCTACCTACCTCACA 1089
             |||||                    |||||::||||||
Db  311 GluGluLysLeuAlaLeuArgGlyMetAlaAlaLeuValTyrAlaValAlaGluSerIleMetThrTyrArgThr 330

Qy 1090 GCAGGGATGCTG-----------------GACCAACCTGGCTTT------ 1116
             ||||||:::::                    |||  :::
Db  331 AlaGlyLeuValAlaAspAlaAlaArgLeuGlyGlnGlyLysAspLysAspTyrGluAla 350

Qy 1117 ------------------CCCGACTGCTCTCAGGAGCCACTGGTAGCAGCCATGGTGAAGGTGTTCAGC 1158
                                                  :::|||
Db  351 ArgLeuLeuAlaLeuValGluGluTyrArgAlaLeuValTyrAlaIleAlaValGluSerSerIleMetLysValHisGly 370

Qy 1159 TCCCGAGGGCCGCCTGGCCAGTGTGTGAGTGAGTGGCCTGCAGATCCTCGGGGCTGGCGTAC 1218
             ||||||:::                    :::|||
Db  371 SerGluSerPheGlyHisLeuValAspAspLysAspAlaValGlnIleLeuHisGlyGlyGlyAlaGlyTyr 390

Qy 1219 ACAAGGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGCATCCTCCTCATCTTCGAG 1278
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Qy   61 GTGGTCTCTACCGCGAACCGGCGGCTACTCGCGACCAGCCCGCTGTACGAGCTTTCGCC 120
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Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla  40

Qy  121 AAAGAGCTTTTCCTAGGCAAATCAAGAAGAAAGAAGTTTCCCATTCCAGAAGTTAGC 180
             |||||||||||||||  |||||||||||
Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer  60

Qy  181 CAAGATGAACTTAATGAACATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 240
             ||||||||||||||||  ::::|||
Db   61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThr  80

Qy  241 GAGGTGGACTCCCGAAAAATTGACCAGGAAGGGAAAAATCCCAGATGAAACTTGGAGAAA 300
             |||||||||
Db   81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100

Qy  301 TTGAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGCTTC 360
             ||||||||||||||||
Db  101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGlyTyrGlyGlyLeuGlyPhe 120

Qy  361 TCCAACACCATGTACTCTCAAGACTAGGGAGATCATCAGCATGATGGTCCATCACTGTG 420
             ||||||||||||||||
Db  121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy  421 ACCCTGGCACGCGCACCAGGCTATTGGCCTCCAAGGGGATCATCTTGGCTGGCACTGAGGAG 480
             ||||||||||||
Db  141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLeuIleGlyLysLeuLeuSerGlyLeuGluGlyThrGluGlu 160

Qy  481 CAGAAAGCCAAA 492
             ||||||||||
Db  161 GlnLysAlaLys 164
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Alignment Scores:

Length:	601	
Matches:	214	
Conservative:	92	
Mismatches:	197	
Indels:	90	
Gaps:	16	

Pred. No.:	4.73e-67
Score:	816.00
Percent Similarity:	51.60%
Best Local Similarity:	36.09%
Query Match:	23.84%
DB:	4

US-09-945-326-3 (1-1863) x US-09-902-540-11184 (1-601)

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Qy  160 TTCCCATTCCAGAAGTTAGCCAAGATGAACTT------------------AATGAA 198
             ||| |||||                              :::
Db   19 PheLeuPheGluValGlySerAlaArgIleLeuThrProGluThrPheThrGluGlu  38
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Db     3  GlyIleAlaGluIleMetThrValPheAlaGlnThrGluGlnValAspProLysThrGly    22
          |||||||
Qy   709  TCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGGAGTCACTAAT      768
          ||||||||:|||||:|||||||||||||||||||||||:::
Db    23  GluLysLysAspLysValThrAlaPheIleValGluArgSerPheGlyValThrAsn       42

Qy   769  GGGAAACCCGAAGATAAATAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAA     828
          |||||||||||:::
Db    43  GlyThrProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheGlu    62

Qy   829  AACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGAGATGGGTTAAGGTGGCC    888
          :::          |||||::|||||||||||||||
Db    63  AspValLysIleProIleGluAsnValLeuGlyLysGluLysAspGlyPheLysLysValAla  82

Qy   889  ATGAACATCCTCAACAGCGCCGGTTCAGCATGGGCAGCGTCGTGGCTGGCGTGCTCAAG     948
          |||||::::|::          :::::|||
Db    83  MetAsnIleLeuAsnArgAlaGlyPheGlyMetGlyAlaThrLeuSerGlyThrMetLys   102

Qy   949  AGATTGATTGAAATGACTGCTGAGTACGGCCTGCACAAGGAACAGTTTAACAAGAGGCTC   1008
          :::
Db   103  LysCysIleGluGlnAlaThrGluHisAlaLysAlaAsnArgValGlnPheGlyLysLysLeu  122

Qy  1009  AGTGAATTTGGATTGATTCAGGAGAAATTTGCCACTGATGGCTCAGAAGGCTTACGTCATG   1068
          :::                  |||||||||
Db   123  LysAsnTyrGlySerIleGlyIleGluLysAlaGlnIleMetAsnIleLeuGlnTyrAlaThr  142

Qy  1069  GAGAGTATGACCTACCTCACAGCAGGGATGCTGACCAACCTGGCTTCCCGACTGCTCC    1128
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Db   143  GluSerMetAlaPheThrIleSerGlnAsnMetAsp---AlaGlySerLysAspTyrHis  161

Qy  1129  ATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCGCTGGCAGTGTGTGAGTAG   1188
          |||||                ::: |||||:|||||:|||
Db   162  LeuGluAlaIleAlaIleSerLysLysLysLeuTyrAlaSerGluSerAlaTrpTyrValCysAspGlu  181

Qy  1189  GCGCTGCAGATCCTCGGGGGCTTGGGCTACACAAGGACTATCGTACGAGGCCGCATACTG   1248
          |||||||          |||||:||
Db   182  AlaIleGlnIleLeuGlyGlyMetGlyTyrMetValAspThrGlyLeuGluArgValLeu  201

Qy  1249  CGTGACACCCGCCATCCTCCATCTTCGAGGAACCAATGAGATTCTCCGGATGTACATC   1308
          |||||||          ::::||||:|||||:|||||||
Db   202  ArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheIle  221

Qy  1309  GCCCTGACGGGTCTGCAGCATGCCGCGGCCCATCCTGACTACCAGGATCCATGAGCTTAAA   1368
          :::                                    SerHisLeuLysGluLeuGln  237
Db   222  AlaLeuThrGlyTyrIleGlnTyrAlaGly---------

Qy  1369  CAG------------------------GCCAAAGTGAGCACAGTCATGGATACCGTTGCCGCGGAGG   1410
          :::          :::
Db   238  ArgAlaPheLysAsnProSerAlaAlaAsnLeuGlyLeuIlePheLysGluAlaSerArgArg  257

Qy  1411  CTTCGGGACTCCCTGGCCGAACTGTGGACCTGGGGCTGACAGGCAACCATGAGTGTG   1470
          |||||||          ||||||:||||
Db   258  ----------AlaAlaSerThrValGlyLeuGlyThrAspLeuSerGlyHisVal   273

Qy  1471  CACCCCAGTCTTGCGACAGTGCCAACAAGTTTGAGGAGAACACCTACTGCTTCGGCCGG   1530
          |||||||          |||
Db   274  ValGlyGlyGluLeuProTyrAlaLysThrAlaHisCysIleAspLeuPheGlyGln   293

Qy  1531  ACCGTGGAGACACTGCTCCTCCCGTTTGGCCAAGACCATCATGGAGGAGCAGCTGGTACTG   1590
          :::|||||          ::|::::|||
Db   294  SerValGluGluLeuLeuArgTyrAsnGluLysAsnIleValAlaAsnGluGlnIleLeuLeu  313

Qy  1591  AAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGGGGTCGTCGCGGGCC   1650
          |||:::||          |||
Db   314  ThrArgLeuAlaAsnAlaAlaIleAspIlePheTyrAlaMetValThrGlnSerArgSer  333

Qy  1651  AGCCGCTCC   1659
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Db   334  SerArgAla   336
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RESULT 4
US-09-252-991A-26058
; Sequence 26058, Application US/09252991A

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Qy   391  IleGluGluTyrProValGlySerTyrArgAspAlaArgIleAsnArgIlePheGlu
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Db   410

Qy  1279  GGAACCAATGAGATTCTCCGGATGTACATCGACTTGAAGGTCTGCGACATGCCGGCCGC   1338
          ||||||||||||      |||
Db   411  GlyThrAsnGluIleLeuAsnArgMetLeuIleThrLeuLysGlyMetLeuLysLeuArgAlaValArg  430

Qy  1339  ATCCTGACTACCAGGATCCAGAGCTTAAACAG--GCCAAAGTGAGCACAGTCATGGAT    1395
          :::||||      ||||||
Db   431  ----------------GlyAspLeuProLeuPheAlaMetAlaGlyAsnValAlaAlaGlu  444

Qy  1396  ACCGTTGGCCG------------AGGCTTCGGGACTCCCTGGCCGAACTGTG   1437
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Db   445  GluLeuSerArgGlyGluArgProArgAlaArgValGlnAspAlaLeuAlaProGlnEnd  464

Qy  1438  GACCTGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAAC   1497
          |||||
Db   465  ValAlaAlaGluAlaAlaLysHisLeuAlaLeuHis------------------  476

Qy  1498  AAGTTTGAGGAGAACACCTACTGCTTCGGCCGACCGTG------GAGACACTGCTC   1551
          |||||          :::          :::|||
Db   477  --------------------------GlyLeuArgValAlaAlaGluThr--------  484

Qy  1552  CGCTTTGGCCAAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTC   1611
          |||||          ::: |||          :::::::::
Db   485  ---PheGlyProGluLeuGlnHisGlnIleLeuGluValLeuAlaLeuAlaLeuAlaLeuSerAspValVal  503

Qy  1612  ATCAACCTGTATGGCATGGGGTCGTCGCGGGCCAGCCGCTCC----------   1659
          :::::|||          ::::::
Db   504  MetAspAlaPheAlaLeuArgSerMetValThrArgThrArgGlnAlaAlaThrSerGly  523

Qy  1660  ----ATCCGCATTGGGCTC------------------------CGC   1677
          ::::||:|          ||||||
Db   524  AlaLeuAspProValArgValAlaMetThrGlnLeuTyrAlaAlaLeuAspAlaIleProArg  543

Qy  1678  AACCACGACCAC---GAGGTTCTTGCCCAACACTTCTGCGTGGAAGCTTACTTGCAG   1734
          :::|||          |||
Db   544  AlaTyrAspArgThrArgArgAlaLeuCysAlaLeuThrLeuLysGlyGlyValAlaLeuAspGln  563

Qy  1735  AATCCTTCAGCCTCCTCTCAGCTGACAAGTATGCTCCA   1773
          |||          ::: |||
Db   564  GluLeuGluArgLeuGlyThrLeuAspValPheThrPro   576
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RESULT 3
US-09-270-767-44314
; Sequence 44314, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 44314
;   LENGTH: 336
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-44314

Alignment Scores:
Pred. No.:   336
Score: 3.8e-64   Length: 336
Percent Similarity: 65.01%   Matches: 169
Best Local Similarity: 49.27% Conservative: 54
Query Match: 22.87%   Mismatches: 104
                              Indels: 16
                              Gaps: 5

US-09-945-326-3 (1-1863) x US-09-270-767-44314 (1-336)

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Qy   652  GGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGAT---TCTGATGGA   708
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Qy   808 ACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGCGAGAGTC 867
         |||||:::|||   |||   ||||   ||||:|   :|||||   |||
Db   215 ThrCysAspValIlePheAspAspCysArgValProAlaSerGlnLeuIleGlyGlyVal 234

Qy   868 ---GGAGATGGTTAAGGTGCCATGAACATCCTCAACAGCGCGCCGGTTCAGCATGGGC 924
            ||||||   ::::   ::   ||||||
Db   235 GluGlyValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgLeuHisIleAla 254

Qy   925 AGCGTCGTGGCTGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACA 984
         ::|||   |||:   :|||   |||   :|:   |||||   ||||||
Db   255 AlaValCysValGlyValAlaGlyValMetLeuGluArgMetLeuAspAlaLeuArgTyrAlaLeuGlu 274

Qy   985 AGGAAACAGTTAACAGAGGCTCAGTGAATTGGATTGATTCAGGAGAAATTTGCACTG 1044
         |||||||||||   :::::|||||   |||||   ||||||
Db   275 ArgLysGlnPheGlyGlnProIleAlaGluPheGlnLeuIleGlnIleAlaMetLeuAlaAsp 294

Qy  1045 ATGGCTCAGAAGGCTTACGTCATGGAGGATGACCTACCTCACAGCAGGATGCTGGAC 1104
         :::||||||   |||   |||||||||
Db   295 SerLysAlaGluAlaTyrAlaAlaArgCysMetValIleAspAlaAlaArgGlnArgAsp 314

Qy  1105 CAACCTGGCTTTCCCACTGCTCCATCGAGCGACCATGGTGAAGGTGTTCAGCTCCGAG 1164
         :::   |||||   :   |||||:|||||
Db   315 GluGly------ArgAspValGlyThrGluAlaSerCysAlaLysLeuPheAlaSerGlu 332

Qy  1165 GCGGCCTGGCAGTGTGTGAGTGAGGGCGCTCGAGATCCTCGGGGGCTACACAGG 1224
         |||   ||||||   |||   ||||||
Db   333 MetCysGlyArgValAlaAlaAspArgAlaValGlnIlePheGlyGlyAlaGlyTyrIleGly 352

Qy  1225 GACTATCCGTACGAGCGCATACTGCGTGCGACACCGGCCATCCTCCTCATCTTCGAGGGAACC 1284
         |||   ||||||:|||||   :|||
Db   353 AspTyrGlyIleGluArgPheTyrArgAspValArgArgIleThrTyrGluGlyThr 372

Qy  1285 AATGAGATTCTCCGGATGTACATCGCC 1311
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Db   373 ThrGlnIleGlnInLeuLeuIleAla 381
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RESULT 5
US-09-328-352-6380
; Patent No. 6552958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6380
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6380

Alignment Scores:
Pred. No.:   Length: 389
Score: 3.5e-53   Matches: 150
Percent Similarity: 666.00   Conservative: 79
Best Local Similarity: 58.27%   Mismatches: 148
Query Match: 38.17%   Indels: 16
DB: 19.46%   Gaps: 8
                         4

US-09-328-352-6380 (1-389) x US-09-328-352-6380 (1-389)

```
Qy   172 GAAGTAGCCAAGATGAACTAATGAAATCAATCAGTTCTTGGGACCCGTGTGGAAAAATTC 231
         |||:::   ||:|||||
Db     5 GlnMetIleArgAspGlu---GlyMetLeuGluGlnLeuLeuSerThrIleArgAspPhe 23

Qy   232 TTCACTGAAGAGGTGGACTCCCGA-----AAAATTGACCAGGAAGGAAAATCCCAGAT 285
         |||||   :::::   ||||||:
Db    24 ValLysAsnGluLeuIleProArgGluAsnGluValValGluLysAspLysIleProAsp 43

Qy   286 GAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAAGTGCCAAGAGAATAT 345
```

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us-09-945-326-3.rai

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 26058
; SEQ ID NO 26058
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26058

Alignment Scores:
Pred. No.:   Length: 390
Score: 1.46e-55   Matches: 147
Percent Similarity: 691.50   Conservative: 82
Best Local Similarity: 58.87%   Mismatches: 121
Query Match: 37.79%   Indels: 39
DB: 20.20%   Gaps: 8
                         4

US-09-945-326-3 (1-1863) x US-09-252-991A-26058 (1-390)

```
Qy   199 ATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTG-----GACTCC 252
         |||   |||||   ||||   ||   :::
Db    14 LeuAsnLeuLeuLeuAspSerIleArgGlnPheValArgGluSerLeuValProHisGlu 33

Qy   253 CGAAAAATTGACCAGGAAGGGAGAAATCCAGATGAAACTTTGGAGAAATTGAAGAGCCTA 312
         :::::::||   ::   :|||||   :::   :::
Db    34 GlnGluValAlaGluThrAspArgIleProGluAlaIleIleIleAlaArgMetArgGluMet 53

Qy   313 GGGCTTTTTGGGCTGCAAGAGATATGTGGCCTGGCTTCTCCAACACCATG 372
         |||||||||   ||||||   |||
Db    54 GlyLeuPheGlyLeuSerIleProGluAlaTyrGlyLyGlyLeuGly--- 68

Qy   373 TACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTGACC---------- 423
         ::::   ||||   |||   :::::::
Db    69 --------------ValThrMetGluGluGluValSerIleAlaPheGluLeu 81

Qy   424 --------------CTGCAGCGCCACCAGGCTATTGGCCTCAAG 453
                       |||   |||||   ||||||
Db    82 GlyArgThrSerProAlaPheArgSerLeuLeuGlyThrAsnAsnGlyIleGlySerGln 101

Qy   454 GGGATCATCTGGCTGCCACTGAGGAGCAGAAGCCAAATACTTGCCTAAACTGGCGTCC 513
         |||||::::   |||   ||   :::   |||   |||:||
Db   102 GlyIleValIleAspGlyThrGluGluGlnLysArgArgTyrLeuProArgLeuAlaSer 121

Qy   514 GGGGAGCACATTGCAGCCTTCTGCCTCACGGAGGCCAGTGGGAGCGATGCAGCCTCA 573
         |||||||||   |||||:::|||
Db   122 GlyGluLeuLeuSerSerPheCysLeuThrGluProAspSerGlySerAspAlaAlaSer 141

Qy   574 ATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTTCCAAG 633
         |||   ::|||||:::   ||||||:::||
Db   142 LeuLysThrThrAlaVal-----ArgAspGlyHisTyrValLeuAsnGlyThrLys 159

Qy   634 GTCTGGATTACTAATGAGGAGACTGGCCAATAATTTTACTGTGTTTGCAAAGACTGAGGTC 693
         :::|||   |||||   :::::|||
Db   160 ArgPheIleThrAsnAlaProGlnAlaGlyIleTyrThrValMetAlaArgThr------ 177

Qy   694 GTTGATTCTGATGGATGGTCAGTGAAAGACAAA-----ATCACAGCATTCATAGTAGAAAGA 747
         |||:::   :::||||   |||||
Db   178 ------AspProAlaIleArgGlyAlaAlaGlyIleTyrIleSerArgAlaPheValValGlnArg 194

Qy   748 GACTTTGGTTGGAGTCACTAATGGAAATGGAAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAC 807
         |||||||   |||   :::   ::::::
Db   195 GlyThrProGlyPheLeuSerLeuGlyLysProAspArgLysMetGlyLysMetGlyLysMetGlyLyGlnLysMetGlyLysAlaHis 214
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Qy   286 GAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAAGAGAATAT 345

; Sequence 6, Application US/09648004
; Patent No. 6498242
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL-1341-A
; CURRENT APPLICATION NUMBER: US/09/648,004
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-09-648-004-6

Alignment Scores:
Pred. No.:   1.08e-51   Length: 384
Score: 650.00   Matches: 154
Percent Similarity: 57.89%   Conservative: 77
Best Local Similarity: 38.60%   Mismatches: 132
Query Match: 18.99%   Indels: 36
DB: 4   Gaps: 11

US-09-945-326-3 (1-1863) x US-09-648-004-6 (1-384)

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Qy    181  CAAGATGAACTTAATGAA------------ATCAATCAGTTCTTGGGACCCCTGTGAAAAAA  228
               | |||||     :::                    |||||||
Db      5  GlnAspThrLeuAsnGlnLeuValAspGlyPheValAsnGlyVal---Leu           23

Qy    229  TTCTTCACTGAAGAGGTGGACTCCCCAAAAATTGACCAGGAAGGAGAAATCCAGATGAA    288
               |||||||                    ::: |||||
Db     24  IleProAsnGluGluIle------------ValAlaGluThrAspGluIleProAlaGlu   39

Qy    289  ACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAGAAATATGGT  348
               ::::::|||||||||:::    :|: ::||||||
Db     40  IleValGlnGlnMetLysGluLeuGlyLeuPheGlyLeuThrIleProGluGlyTyrGlu   59

Qy    349  GGGCTGGGCTTCTCCAACACCATGTACTCAAGACTA--------GGGGAGATCATCAGC  399
               ::|||                    |||||||||
Db     60  GlyLeuGlyLeu------ThrMetGluGluValTyrIleAlaPheGluLeuGlyArg     77

Qy    400  ATGGATGGGTCCATCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATC  459
               ::: ||||||                    ::: ||||||
Db     78  ThrSerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerSerGlyLeu   97

Qy    460  ATCTTGGCTGGCACTGAGGAGGCAGAAAGCCAAATACTTGCCTAAACTGGCTCCGGGGAG  519
               ::::::||||||::|||                    |:|||||||
Db     98  IleIleIleProHisAlaProHisAlaGlyLysGlnTyrPheLeuProArgLeuAlaSerGlyGlu  117

Qy    520  CACATTGCAGCCTTCTGCCTCACGGAGCCCAGTGGGAGCGATGCAGCCTCAATCCGG  579
               ||||||    :||::|||||                    |||||||
Db    118  IleIleGlySerPheCysLeuThrGluProSerGlySerAspAlaAlaSerLeuLys    137

Qy    580  AGCAGAGCCACACTAAGTGAAGACAAGAAGCCACTATCCTCAAGGGCTCGG  639
               :::                    ||||||||||:::||
Db    138  ThrSerProAlaArgVal-----LysAspGlyAspHisTyrIleLeuAsnGlyThrLysArgTyr  155

Qy    640  ATTACTAATGGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAG------ACTGAGGTC  693
               |||||||||||    ||| |||||                    :::::
Db    156  IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrSerThrGlnIle  175

Qy    694  GTTGATTCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAGAGACTTT  753
               ||||||    :::                    |||::::||
Db    176  LysGlyThrGlyGly------IleSerAlaPheIleValAspSerLysThr    190

Qy    754  GGTGGAGTCACTAAGTGGAAACCCGAAGATAAATTAGGCATTCGGGCGTCCAACACTTGT  813
               ||||||    :::                    |||:::||||
```
```
Db     44  AspIleValGlnGlnMetArgGluLeuGlyLeuPheGlyLeuThrIleProGluGlyTyr   63

Qy    346  GGTGGCCTGGGCTTCTCCAACACCATGTACTCAAGACTAGGG---GAGATCATCAGCATG  402
               |||||||                    |||:::
Db     64  GlyGlyLeuGlyIleThrMetGluGluValGluValAlaArgValAlaPheAlaGluLeuGlyGlnThr   83

Qy    403  GATGGGTCCATCATCACTGTGACCCTGGCAGCCCAGGCTATTGGCCTCAAGGGGATCATC  462
               |||||||    :::    :::
Db     84  SerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerSerAlaIleLeu  103

Qy    463  TTGGCTGGCACTGAGGAGGCAGAAAGCCAAATACTTGCCTAAACTGGCTCCGGGGCAC  522
               ||||||||||    :::||    |||:::|||||||
Db    104  IleAspGlyThrGluGluGluGlnGlnLysLysGlnLysLysTyrLeuProArgTyrAlaSerGlyIleIle  123

Qy    523  ATTGCAGCCTTCTGCCTCACGGAGGCCAGTGGGAGCGATGCAGCCCTCAATCCGGAGC  582
               |||    :::    :::||||||||||
Db    124  IleGlySerPheCysLeuThrGluProGluSerGlyThrAspAlaAlaSerLeuLysThr  143

Qy    583  AGAGCCACAAGTGAAGACAAGAAGCCACTACATCCTCAATGGCTCCAAGGTCTGGATT  642
               :::                    |||:::    |:|
Db    144  SerAlaVal------LysAspGlyPheTyrValLeuAsnGlyThrLysArgPheIle  161

Qy    643  ACTAATGGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACT------GAGGTCGTT  696
               ||||||||||    |:|                    ||
Db    162  ThrAsnAlaProHisAlaThrPheThrValMetAlaArgThrAsnProGluIleLeuLys  181

Qy    697  GATTCTGATGGATCAGTGAAAGACAAAATCACAGCCATTCATAGTAGAAGAGACTTTGGT  756
               |||||||    ::||||:::||
Db    182  GlySerGlyGly----------IleSerAlaPheLeuValGluAlaGluAsnThrPro  196

Qy    757  GGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTAGGCATTCCAACACTGTGAA  816
               ||||||    :::                    |||
Db    197  GlyIleThrLeuGlyLysGlnLysLysGlnLysMetGlyLysGlnLysGlySerHisThrCysAsp  216

Qy    817  GTCCATTTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTC---GGAGAT  873
               |||||||    :::|||||||||
Db    217  ValIlePheGluAsnCysArgValProAlaSerArgValAlaLeuIleGlyGlyValGluGlyIleGlyVal  236

Qy    874  GGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTCGTG  933
               ||||||:::    :::||||||||
Db    237  GlyPheLysValThrAlaMetLysLysValLeuValAspLysAspLysGlyArgLeuHisIleAlaTyrSer  256

Qy    934  GCTGGGCTGCTCAAGAGATTGATTGAATGAACTGACTGACTACGGCCTGACCAAGGAAACAG  993
               |||||||    ::|    |||
Db    257  ValGlyValAlaGluAlaArgMetLeuAsnAsnAspAlaLeuAsnTyrAlaIleGluGluArgLysGln  276

Qy    994  TTTAACAAGGCTCAGTGAATTTGGATTGATTCAGGAGGAAAATTGCACTGATGGCTCAG  1053
               :::    ||||||||||
Db    277  PheGlyLeuGlnProIleAlaAsnPheGlnIleLeuGlnLeuGlnAlaMetLeuAlaMetLeuAspSerLysAla  296

Qy   1054  AAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGATGCTGACCAACCTGGC  1113
               :::    :::||
Db    297  GluIleTyrAlaAlaLysCysSerMetValArgLeuAspArgAlaArgArgAspAsnGly--  315

Qy   1114  TTTCCCGACTGCTCCATCGAGGCAGCCATGTGAAGGTGTCAGCTCAGGGCCCTGG  1173
               |||||||    |||
Db    316  --GluAsnIleSerThrGlnAlaSerCysAlaLysThrGluMetCysGly       334

Qy   1174  CAGTGTGTGAGTGAGGGCGCTGCAGATCTCTCGGGGCTTGGGCTACACAAGGGACTATCCG  1233
               :::    ||||||||||:::||
Db    335  ArgValAlaAlaAspArgCysValGlnIleHisHisGlyValGlyAlaGlyTyrIleSerGlyThrTyrArgAla  354

Qy   1234  TACGAGGCCATACTGCGTGACACCCGACATCCTCCATCTTCGAGGGGAACCAATGAGATT  1293
               :::    ||||||    |:|
Db    355  IleGluArgPheTyrArgAspValArgLeuPheArgLeuTyrGluGlyThrThrGlnIleVal  374

Qy   1294  CTCCGGATGTACATCGCCCCTGACCGGGTCTGCAGCATGCC  1332
               |||    ||||||
Db    375  GlnGlnLeuLeuIleIleAlaAlaLysAsnMetIleArgGluAla  387
```

RESULT 6
US-09-648-004-6

```
Db      5 GlnAspThrLeuAsnGlnLeuValAspMetIleArgGlnPheValAspGlyVal---Leu  23

Qy    229 TTCTTCACTGAGAGTGGACTCCCGAAAAACTGACCAGGAGGAAAATCCCAGATGAA  288
          |||||     |||   :::     ::     ||| |||||
Db     24 IleProAsnGluGluIle------------ValAlaGluThrArgGluIleProAlaGly  39

Qy    289 ACTTTGGAGAAATTGAAGAGCTAGGGCTTTTGGGCTGCAAGTCCCAGAGAAATATGGT  348
          |||||||||:::::||| |||||   :::  :||||||
Db     40 IleValGlnGlnMetLysGluLysGlyLeuLeuGlyLeuPheGlyLeuThrIleProGluGluTyrGlu  59

Qy    349 GGCCTGGGCTGTCTCAAGACCACCATGGACTACTCAAGACTA--------GGGGAGATCATCAGC  399
          |||||           :::  ::              ||:|:
Db     60 GlyLeuGlyLeu------ThrMetGluGluGluValTyrIleAlaPheGluGluGlyArg  77

Qy    400 ATGGATGGGTCCATCACTTGGCACGCCCTGGCCTATTGGCCTCAAGGGGATC  459
          ||||       ::       ||||     |||||
Db     78 ThrSerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerGlyLeu  97

Qy    460 ATCTTGCTGGACTGGAGGAGCAGAAAGCCCAAATACTTGCCTAAACTGGCTCCGGGGGAG  519
          ::::     ||||||||||:::     ::  :||||||||
Db     98 IleIleAspGlySerGluGluGlnLysGlnLysTyrPheLeuProArgLeuAlaSerGlyGlu  117

Qy    520 CACATTGCAGCCTTCTGCCTCACGGACCAGCCAGTGGGAGCGATGCAGCCTCAATCCGG  579
          ||||      |||    ||:::   ||  ::||||||
Db    118 IleIleGlySerPheCysLeuThrGluProSerGlySerAspAlaAlaSerLeuLys  137

Qy    580 AGCAGACCCACACTAAGTAGACAAGAAGCACTACAATCCCAATGGCTCCAAGGTCTGG  639
          |||||   ||||   ||||||||:::  :||||||
Db    138 ThrThrAlaVal------LysAspGlyAspHisTyrIleLeuAsnGlyThrLysArgTyr  155

Qy    640 ATTACTAATGAGGACTGGCCAATATTTTTACTGTTGTTGCAAAG--------ACTGAGGTC  693
          ||||||       :::||||      :::   :::||||||
Db    156 IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrSerThrGluIle  175

Qy    694 GTTGATTCTGATGGATCAGTGAAAGACAAAATCCATAGTGAGAAAGAGACTTT  753
          |||||||       |||||||||   ::::||||||||||
Db    176 ------IleSerAlaPheIleValAspSerLysThr  190

Qy    754 GGTGGAGTCACTAATGCAATAAATAGGCATTCGGGCTCCAACACTTGT  813
          ||||||:::        ||||||||  :::||||||
Db    191 ProGlyIleSerLeuGlyLysAspLysMetGlyGlnLysGlyAlaHisThrCys  210

Qy    814 GAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGAGAGGTC---GGA  870
          :::||| |||||||||     |||   ||:::   ||||||
Db    211 AspValIleProAlaSerArgIleProAlaSerAlaLeuIleGlyGlyValGluGly  230

Qy    871 GATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTC  930
          |||||||||:::||| |||||   :::  :||||||
Db    231 ValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgIleHisIleAlaAlaLeu  250

Qy    931 GTGGGCTGGGCTGCTCAAGAGATTGATTGAAATGACTGCGTACGCCTGCACAAGGAAA  990
          |||||       ::: ||||||||:::  :||||||
Db    251 SerValGlyAlaAlaThrArgMetLeuGluAspSerLeuGlnTyrAlaValGluArgLys  270

Qy    991 CAGTTTAACAAGAGGCTCAGTGAATTTGGATTGATTCAG--------GAGAAA  1035
          |||||||       :::     |||   ||:::||||||
Db    271 GlnPheGlyGlnAlaIleAlaAsnPheGlnLeuIleGlnLeuGlyMetLeuAlaAspSerLys  290

Qy   1036 TTTGCACTGATGGCTCAGAAGGCTTACGTTCATGAGAGTATGACCTACCTCACAGCAGG  1095
          ::: ||||||:::     ||:::  :||||||
Db    291 AlaGluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgLeuArgAspAlaGly  310

Qy   1096 ATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCCATGGTGAAGTGTTC  1155
          |||       :::   ||:::   ||||||
Db    311 Gln------AsnValSerThrGluAlaSerValAlaSerArgAlaLysMetPhe  323

Qy   1156 AGCTCCGAGGCGCCTGCCAGTGTGGAGTGAGCGCTGCAGATCCTGCGGGGGCTTGGGC  1215
          |||||||       ::: ||||||||:::||||||
Db    324 AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyAlaGly  343

Qy   1216 TACACAAGGACTATCCGTACGAGCGCATACTGCGTGACACCCGCATCCTTCCTCATCTTC  1275
          |||       :::     ||||||||:::||||||
Db    344 TyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgPheArgLeuTyr  363
```

```
Db    191 ProGlyIleSerLeuGlyLysAspLysMetGlyGlnLysGlyAlaHisThrCys  210

Qy    814 GAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGAGAGGTC---GGA  870
          :::||| |||||||||     |||   ::||||||
Db    211 AspValIleProAlaSerArgIleProAlaSerAlaLeuIleGlyGlyValGluGly  230

Qy    871 GATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTC  930
          |||||||||:::||| |||||   :::  :||||||
Db    231 ValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgIleHisIleAlaAlaLeu  250

Qy    931 GTGGGCTGGGCTGCTCAAGAGATTGATTGAAATGACTGCGTACGCCTGCACAAGGAAA  990
          |||||       ::: ||||||||:::  :||||||
Db    251 SerValGlyAlaAlaThrArgMetLeuGluAspSerLeuGlnTyrAlaValGluArgLys  270

Qy    991 CAGTTTAACAAGAGGCTCAGTGAATTTGGATTGATTCAG--------GAGAAA  1035
          |||||||       :::     |||   ||:::||||||
Db    271 GlnPheGlyGlnAlaIleAlaAsnPheGlnLeuIleGlnLeuGlyMetLeuAlaAspSerLys  290

Qy   1036 TTTGCACTGATGGCTCAGAAGGCTTACGTTCATGAGAGTATGACCTACCTCACAGCAGG  1095
          ::: ||||||:::     ||:::  :||||||
Db    291 AlaGluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgLeuArgAspAlaGly  310

Qy   1096 ATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCCATGGTGAAGTGTTC  1155
          |||       :::   ||:::   ||||||
Db    311 Gln------AsnValSerThrGluAlaSerValAlaSerArgAlaLysMetPhe  323

Qy   1156 AGCTCCGAGGCGCCTGCCAGTGTGGAGTGAGCGCTGCAGATCCTGCGGGGGCTTGGGC  1215
          |||||||       ::: ||||||||:::||||||
Db    324 AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyAlaGly  343

Qy   1216 TACACAAGGACTATCCGTACGAGCGCATACTGCGTGACACCCGCATCCTTCCTCATCTTC  1275
          |||       :::     ||||||||:::||||||
Db    344 TyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgPheArgLeuTyr  363

Qy   1276 GAGGGAACCAATGAACAATTCCGGATGTACATCGCCGGGGTCTGCAGCATGCC  1332
          |||||           :::     ::::||||||
Db    364 GluGlyThrThrGlnIleGluGlnValIleIleAlaAlaArgAsnMetIleArgGluAla  382
```

RESULT 7

US-10-272-419-6
; Sequence 6, Application US/10272419
; Patent No. 6794165
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-10-272-419-6

Alignment Scores:

Pred. No.:	7		Length:	384
Score:	650.00		Matches:	154
Percent Similarity:	57.89%		Conservative:	77
Best Local Similarity:	38.60%		Mismatches:	132
Query Match:	18.99%		Indels:	36
DB:			Gaps:	11

US-09-945-326-3 (1-1863) x US-10-272-419-6 (1-384)

```
Qy    181 CAAGATGAACTTAATGAA----------ATCAATCAGTTCTTGGACACCCGTGGAAAAA  228
          ||||||                      |||  |||||||:::
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RESULT 8
US-09-328-352-6442
; Sequence 6442, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6442
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6442

Alignment Scores:
Pred. No.:   3.57e-49   Length: 387
Score: 623.00   Matches: 145
Percent Similarity: 56.85%   Conservative: 79
Best Local Similarity: 36.80%   Mismatches: 130
Query Match: 18.20%   Indels: 40
DB: 4   Gaps: 10

US-09-945-326-3 (1-1863) x US-09-328-352-6442 (1-387)

Qy 181 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 240
             ||||: :||||||||:::   :::   ::: ||
Db   9 GlnGluThrLeuAsnGlnLeuValAspMetIle--------------ArgIlnPheValGlu 24

Qy 241 GAGGTG----------GACTCCCGAAAAATTGACCAGGAAGGAGGAAAAATCCCAGATGAAACT 291
         ||||| :: :::   ::
Db   25 GlyValLeuIleProHisGluValAlaGluThrAspGluIleProAspProAspProAspPPIle 44

Qy 292 TTGGAGAAATTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGC 351
         :::||||:::||:|||||| ::: ||||||||
Db   45 ValGluGlnMetLysAlaLeuGlyLeuPheGlyLeuThrIleProGluGluTyrGluGluGly 64

Qy 352 CTGGGCTTCTCCAACACCATGTACTCCAAGACTAGTACTAGGGGGAGATCATCAGCATGGATGGTGGTCC 411
         ||||| ::::||||:
Db   65 LeuGly-----------------------------LeuThrMetGluGluGlu 72

Qy 412 ATCACTGTGACC----------CTGGCAGCG 432
          ::: ||
Db   73 ValTyrValAlaAspPheGluLeuGlyArgThrSerProAlaPheSerGlyLeuIleGlyThr 92

Qy 433 CACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGGCGAGGAGGAGAAAGCCAAA 492
          ||| |||||||| :::||||
Db   93 AsnAsnGlyIleGlySerSerGlyLysLeuIleIleAspGlyThrGluAlaGlnLysSerPhe 112

Qy 493 TACTTGCCTAAACTGCGCGTCCGGGGAGCACATTGCAGCCTTCGCTGCCTTCCGCCGGAGCCAGCC 552
          :::||| ||::: ||||| ||||||
Db 113 PheLeuProArgLeuAlaArgGlyLeuAlaArgGlyIleGlyValIleSerSerGlyThrGluProAsp 132

Qy 553 AGTGGGAGCGGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAGCAC 612
          ||||||| ::||||
Db 133 AlaGlySerAspAlaAlaSerLeuLysThrSerAlaVal------LysAspGlyAspPhe 150

Qy 613 TACATCCTCAATGGCTCCAAGGTCTCGGATTACTAATGGAGGACTGGCCAATATTTTTACT 672
           ||:::|||||:|| ::|||||
Db 151 TyrValLeuAsnGlyThrLysArgPheIleThrAsnAlaProHisAlaGlyValPheThr 170

Qy 673 GTGTTTGCAAAGACTGAGGTGCGTTCGTTGATTCTGATCGATCAGTGAAAGACAAAATCACACAGCA 732
          |||:::||||:|| :::||||||
Db 171 ValMetAlaArgThrAsn--PheAspIleLysPheGlyAla------SerGlyIleSerSerAla 187

Qy 733 TTCATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAGCATCCCAAGAGATAAATTAGGC 792
          ||||||| ::||:::
Db 188 PheIleValAspSerGlnThrProGlyIleSerLeuGlyLysArgAspLysLysMetGly 207

Qy 793 ATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAAC 852
          :::||| ||||||||||||||
Db 208 GlnLysGlyValHisThrCysAspValIlePheGluAsnCysArgIleProAlaSerAla 227

Qy 853 ATCCTTGGAGAGGTC---GGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCCGC 909
          :::::||| ||| ||::||||||||||
Db 228 LeuIleGlyIleGlyValGluGluGlyValGlyPheLysThrAlaMetLysValLeuAspLysGly 247

Qy 910 CGGTTCAGCATGGGCAGCGCTCGTGGCTGGCTGCTCAAGACGATTGATTGAAATGACTGCT 969
          ||| |||:   ::||||||||||
Db 248 ArgLeuHisIleAlaAlaLeuSerValGlyAlaAlaThrArgMetLeuAspAspSerLeu 267

Qy 970 GAGTACGCCTGCACAAGAGAAACAGTTAACAGAGAGCTCAGTGAGTTTGGATTGATTGATTCAG 1029
           ||||| :: :||||||||||||
Db 268 AsnTyrAlaIleGluArgLysGlnPheGlyLnProIleAlaGluPheGlnLeuIleGln 287

Qy 1030 GAGAAATTTGCACTGATGGCTCAGAGAGGCTTACGTCATGGAGAGTGACCTACCTCACA 1089
           ||| ::: ||| |||||
Db 288 AlaMetLeuAlaAspSerLysAlaGluIleTyrAlaAlaLysCysMetVal---LeuAsp 306

Qy 1090 GCAGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGCGGCAGCCATGGTGAAG 1149
           ||||||:|||||||| ::||:
Db 307 AlaAlaArgLeuArgAspAlaGly--GlnAsnValSerThrGluAlaSerCysAlaLys 325

Qy 1150 GTGTTCAGCTCCGAGCGCCGCTGGCCAGTGTGGTGAGTGGGCGGCTGCAGATCCTCGGGGGC 1209
           ::|||:|||||||| ::|||||||
Db 326 MetPheAlaThrGluMetCysGlyArgValAlaAlaAspArgCysValGlnIleHisGlyGly 345

Qy 1210 TTGGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGCATCCTCCTC 1269
           |||||| ||||||
Db 346 AlaGlyTyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgLeuPheArg 365

Qy 1270 ATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCC 1311
           ::||||||||| ::||:
Db 366 LeuTyrGluGlyThrAsnGluIleLeuGlnGlnValIleIleIleAla 379

Qy 1276 GAGGGAACCAATGAATTCTTCCGGATGTACATCGCCGATGTGCTACGCCGGGTCTGCAGCATGCC 1332
           |||||| ::::||||||
Db 364 GluGlyThrThrGlnIleGluGlnLnValIleIleAlaIleAlaArgAsnMetIleArgGluAla 382

RESULT 9
US-09-252-991A-27960
; Sequence 27960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27960
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27960

Alignment Scores:
Pred. No.:   9.64e-49   Length: 403
Score: 618.50   Matches: 149
Percent Similarity: 55.42%   Conservative: 71
Best Local Similarity: 37.53%   Mismatches: 148
Query Match: 18.07%   Indels: 29
DB: 4   Gaps: 8

US-09-945-326-3 (1-1863) x US-09-252-991A-27960 (1-403)

Qy 154 GAAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTG 213

Db   358 IleLeuLeuGlyGlyTyrIleAsnGlyTyrIleGluPheProThrGlyArgLeuLeuArgAspAla 377

Qy   1258 CGCATCCTCCTCATCTTCGAGCGAACCAATGAGAATTCTCCGATGTACATC 1308
           ::::: ||| ::: AAAAТТGACCAG   ::|||||||||
Db   378 LysLeuTyrGluIleGlyAlaGlyThrSerGluIleArgArgMetLeuIle 394

RESULT 10
US-09-328-352-4850
; Sequence 4850, Application US/09328352
; Patent No. 6552958
; GENERAL INFORMATION:
;   APPLICANT: Gary L. Breton et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;   TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC99-03PA
;   CURRENT APPLICATION NUMBER: US/09/328,352
;   CURRENT FILING DATE: 1999-06-04
;   NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4850
;   LENGTH: 382
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-4850

Alignment Scores:
Pred. No.:   Length: 382
Score: 8.88e-48   Matches: 142
Percent Similarity: 608.00   Conservative: 71
Best Local Similarity: 56.20%   Mismatches: 154
Query Match: 37.47%   Indels: 12
DB: 17.76%   Gaps: 6

US-09-945-326-3 (1-1863) x US-09-328-352-4850 (1-382)

Qy   187 GAACTTAATGAAATCAATCAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAGAG--- 243
           |||:::   ::::||||||| :::||||| ::: |||
Db   9 GlnPheThrGluGluGlnLeuLeuIleLeuArgAspMetAlaLysSerPheAlaGlnGluGln 28

Qy   244 -----GTGGACTCCCGAAAAATTGACGAGGAGGAAATCCAGATGAAACTTTGGAG 297
           ::: ||||||||||||||||
Db   29 IleLysProGlnAlaSerAspTrpAspArgAspArgGlyThrPheProLysGluThrLeuThr 48

Qy   298 AAATTGAAGAGCCTAGGGCTTTTTCGGCTGCCAAGTCCCAAGAGAATATGGTGGCCTGGC 357
           ::::: |||||| ::|||||
Db   49 GlnMetGlyGlnPheMetGlyMetLeuValSerGluGluTrpGlyGlySerAsp 68

Qy   358 TTCTCCAACACCATGTAC---TCAAGACTAGGGGAGATCATCAGCATGATGGGTCCATC 414
           :::||| |||:::
Db   69 ThrGlyAsnLeuAlaTyrValLeuAlaLeuGluGluValAlaAlaAlaAspGlyAlaThr 88

Qy   415 ACTGTGACCCTGGCAGCGCCCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCCACT 474
           :::   ::::|||||||||
Db   89 SerThrIleMetSerValHisAsnSerValGlyCysValProIleLeuLysPheGlyThr 108

Qy   475 GAGGAGCAGAAAGCCAAATACTTGCTAAACTGGCGTCCCGGGAGCACATTGCAGCCTTC 534
           ::::||||||| ::::|||||
Db   109 AspGluGlnLysProLeuAlaGlnGlyGluGlyMetIleGlyAlaPhe 128

Qy   535 TGCCTCACGGAGCCAGCCAGCGATGCGAGCCTCAATCCGGAGCAGCAGACCACACTA 594
           :::|||||| |||||||:::
Db   129 AlaLeuThrGluProHisThrGlySerAspAlaAlaIleLysThrArgAlaVal--- 147

Qy   595 AGTGAAGACAGAAGACACTACATCCTCAATGGCTCCAAGGTCTCGGATTACTAATGGAGGA 654
           :::   ::::|||||||
Db   148 --LysAspGlyAspTyrIleLeuAsnGlyLysPheIleThrSerGlyAsn 166

Qy   655 CTGGCCAATATTTTTACTGTGTTGCAAAGACTTGAGGTCGTTGATTCTGATGATCAGTG 714
           ::: |||||||
Db   167 AsnAlaGlyValIleIleValPheAlaValThrAsp------ProSerAlaGly 182

Qy   715 AAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCAATGGGGAAA 774
           ||| :::::|||||||
Db   183 LysLysGlyIleSerAlaPheLeuValProArgGluThrProGlyTyrGluValIleArg 202

```
Db     3  |||||||  |||                         ArgLeuLeuArgGlySerArgLeuLeuArg-- 16
             GlyLeuAlaVal-------

Qy   115  TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAGAAGAGTTTTCCCA---TTTCCA 171
             |||::::|||||||                          :::          ||||
Db    17  -------ArgAsnPheLeuThrCysLeuSerSerTrpLysIleProProHisValSer 33

Qy   172  GAAGTTAGCCAAGATGAA------CTTAATGAAATCAATCAG-----TTCTTGGGACCC 219
             :::  |||||||  |||                  |||||:::                |||
Db    34  LysSerSerGlnSerGluAlaLeuLeuAsnIleThrAsnAsnGlyIleHisPheAlaPro 53

Qy   220  GTGGAAAAATCTTCACTGAGAGGTGGACTCCCGAAAA------------------- 258
             ::::::|||      |||:::                       :::
Db    54  LeuGlnThrPheThrAspGluGluMetMetIleLysSerLysValLysPheAlaGln 73

Qy   259  -----------------ATTGACCAGGAAGGAGAAATCCCAGATGAAACT 291
                               ::::|||
Db    74  GluGlnIleAlaProLeuValSerThrMetAspGluAsnSerLysMetGluLysSerVal 93

Qy   292  TTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCCAAGTCCCAGAAGAATATGGTGGC 351
             :::::  |||                              ||||||||
Db    94  IleGlnGlyLeuPheGlnGlnGlyLeuMetGlyIleGluValAspProGluTyrGlyGly 113

Qy   352  CTGGGC------TTCTCCAACACCATGTACTACAAGACTAGGGGAGATCATCAGCATGAT 405
             |||                            :::|||                      :::|||
Db   114  ThrGlyAlaSerPheLeuSerThrValLeuVal--IleGluGlyLeuAlaLysValAsp 132

Qy   406  GGGTCCATCACTGTGACCCTGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTG 465
             |||:::|||                            ||||||
Db   133  AlaSerValAlaValPheCysGluIleGlnAsnThrLeuIleAsnThrLeuIleArgLys 152

Qy   466  GCTGGACTGGAGGACGAGAAAGCCAAATACTTGCCTAAACTGGCCTCGGGGAGCACATT 525
             |||                  :::|||                      |||:::
Db   153  HisGlyThrGluGluGlnLysAlaThrTyrLeuProGlnLeuThrThr---GluLysVal 171

Qy   526  GCAGCCTTCTGCCTCACGGAGCAGCCAGCCATGTGGAGGATGCAATCCGAGCAGAGA 585
             ::::|||||:::|||                      |||||
Db   172  GlySerPheCysLeuSerGluAlaGlyAlaAlaGlySerAspSerPheAlaLeuLysThrArg 191

Qy   586  GCCACACTAAGTGAAGACAAGAAGACTACATCCTCAAGGTCTCGGATTACT 645
             |||                   |||
Db   192  AlaAspLysGluGlyAsp-------TyrTyrValLeuAsnGlySerLysMetTrpIleSer 209

Qy   646  AATGGAGGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGATTCTGAT 705
             :::                      |||                               ---Asp 224
Db   210  SerAlaGluHisAlaGlyLeuPheLeuValMetAlaAsnVal-------

Qy   706  GGATCAGTGAAAGACAAA---ATCACAGCATTCATAGTAGAAGAAGACTTTCGTGGAGTC 762
             :::::::                |||                  :::|||
Db   225  ProThrIleGlyTyrIleThrSerPheLeuValAspArgAspThrProGlyLeu 244

Qy   763  ACTAATGGCAAACCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCAT 822
             :::                  ::::|||||:::|||
Db   245  HisIleGlyLysProGluAsnLysGluLysGlyLeuArgAlaSerSerThrCysProLeuThr 264

Qy   823  TTTGAAAACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAG 882
             |||||||||||                   |||
Db   265  PheGluAsnValLysValProGluAlaAsnIleLeuGlnIleLeuGlyHisGlyTyrLys 284

Qy   883  GTGGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGCGTCGTGGGCTG 942
             |||:::                   :::  |||||||||
Db   285  TyrAlaIleGlySerLeuAsnGluGlyArgIleGlyIleAlaAlaGlnMetGluGlyLeu 304

Qy   943  CTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCAAGGAAACAGTTTAACAAG 1002
             |||              :::  |||  ||||||          ||||||
Db   305  AlaGlnGlyCysPheAspTyrThrIleProTyrIleLysGluArgGlnPheGlyLys 324

Qy  1003  AGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTAC 1062
             |||  |||       ||||||||||||
Db   325  ArgLeuPheAspPheGlyLeuGlnHisValAlaHisValAlaThrGlnLeuLeuGlu 344

Qy  1063  GTCATGGAGAGTATGACCGCAACCGGCGGGATGCTGACCAGGCAGGATGCCGCCTGTACGAGCT 1122
             :::  ||||||||                      :::  |||      |||
Db   345
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Qy   775  CCCGAAGATAAATTAGGGGCTTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACC 834
             |||:::|||||:::                       |||:::
Db   203  ValGluGluLysLeuGlyLeuHisAlaSerAspThrCysGlnIleAlaLeuThrAspVal 222

Qy   835  AAGATACCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAAC 894
             :::::::|||||||:::                      ||||||
Db   223  ArgIleHisLysSerLeuMetLeuGlyLysGlyGluGluGlyLysIleAlaLeuAla 242

Qy   895  ATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTCGTGGGCTGCTGGGCTGCTCAAGAGATTG 954
             :::|||||                 :::
Db   243  AsnLeuGlyGlyGlyArgIleGlyIleAlaAlaAlaGlnAlaValGlyLeuAlaArgAlaAla 262

Qy   955  ATTGAAATGACTGCTGAGTACGCCCTGCACAAGGAAACAGTTTAACAGAGGCTCAGTGAA 1014
             |||:::|||                 |||      :::
Db   263  LeuGluGluAlaThrArgTyrAlaLysGluArgIleThrPheGlyLysProIlePheGlu 282

Qy  1015  TTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGT 1074
             |||                      :::
Db   283  HisGlnThrIleAlaPheArgLeuAlaSerMetAlaThrGlnIleGluLeuAlaAlaArgGln 302

Qy  1075  ATGACCGCAACCGGCGGGATGCTGACCAGGCAGGATGCCGCCTGTACGAGCTGCTCCATCGAG 1134
             :::                   |||          |||
Db   303  LeuValHisTyr---AlaAlaArgLeuLysGluLysGluGlyAlaLeuGlyAlaGlyPro 320

Qy  1135  GCAGGCCATGGTGAAGGTGTTCAGCTTCGAGCGCCGCCTCGAGCAGTGTGGAGGCGCTG 1194
             |||||:::|||
Db   321  AlaSerMetAlaLysAlaGlyLeuPheAlaSerGluMetThrGluArgValCysSerSerAlaLeu 340

Qy  1195  CAGATCCTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGGCCATACTGCGTGAC 1254
             |||||||                      :::  :::|||||||
Db   341  GlnValPheGluGlyGlyTyrGlyTyrLeuArgAspPheProIleGluArgIleTyrArgAsp 360

Qy  1255  ACCCGCCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCC 1311
             |||||          :::|||        ||||
Db   361  AlaArgIleCysGlnIleTyrAspIleGlyThrSerAspIleGlnArgLeuValIleAla 379
```

RESULT 11
US-09-949-016-6098

; Sequence 6098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 6098
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6098

Alignment Scores:
Pred. No.:   432
Score: 2.27e-47   Length: 432
                    604.00   Matches: 157
Percent Similarity: 54.46%   Conservative: 81
Best Local Similarity: 35.93%   Mismatches: 155
Query Match: 17.65%   Indels: 44
DB: Gaps: 14
                    4

US-09-945-326-3 (1-1863) x US-09-949-016-6098 (1-432)

```
Qy    55  GGTCTGGTGGTGTCTCACCGGCGAACCGGCCGACTACGGCCACCAGCCGCCTGTACGAGCT 114
             :::  ||||||                    |||          :::  |||
```

Db   345 AlaAlaArgLeuLeuThrTyrTyrAsnAlaAlaArgLeuLeu---GluAlaGlyGlyLysProPhe 363

Qy   1123 TGCTCCATGCGAGGCAGCCATGTGAGAGGTGTTCAGCTCAGCTCCGAGGCCCCTGGCAGTGTGTG 1182
          |||||:|| ::::: ||||||||||||:|| ::||| ||| ||||||
Db   364 IleLys--GluAlaSerMetAlaLysTyrTyrAlaSerGluIleAlaGlyGlnThrThr 382

Qy   1183 AGTGAGGCGCTGCGATCCTCCGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGC 1242
          ||||:|| ::::: ||||||||||||:::||||||:::||
Db   383 SerLysCysIleGluTrpMetGlyGlyValGlyValTyrGlyValGlyTyrAspTyrProValGluLys 402

Qy   1243 ATACTGCGTGACACCCGCCATCCTCCATCTTCGAGGGAACCAATGAGATT 1293
          ||||||||| :|| :::
Db   403 TyrPheArgAspAlaLysIleGlyThrIleTyrIleGluGlyAlaSerAsnIle 419

RESULT 12
US-09-252-991A-31097
; Sequence 31097, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31097
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31097

Alignment Scores:
Pred. No.:   2.48e-47   Length: 419
Score: 603.50   Matches: 136
Percent Similarity: 57.83%   Conservative: 67
Best Local Similarity: 38.75%   Mismatches: 139
Query Match: 17.63%   Indels: 9
                         4   Gaps: 6

US-09-945-326-3 (1-1863) x US-09-252-991A-31097 (1-419)

Qy   262 GACCAGGAGGGAAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTTAGGGCTTTTT 321
          |||||||| :: |||||| ::::: |||||
Db   74 AspArgGluHisArgPheProAlaGlyAlaIleArgGluMetAlaAspLeuGlyPheLeu 93

Qy   322 GGGCTGCAAGTCCCAGAAAGAATATGTGGCCTGGCTTCTCCAACACCATGTACTCA--- 378
          ||||:|| ::: ||||||||||||:||||
Db   94 GlyMetLeuValProGluGlyValTrpProGlyValGlyAlaGlyHisLeuAlaTyrAlaMet 113

Qy   379 AGACTAGGGGAGATCATCAGCATGGGATCCATCACTGTGACACCTGCAGCCGCACCAG 438
          ||||||| :: ::::: ||||| ||
Db   114 AlaLeuGluGluIleAlaAlaLysAlaAspAlaGlyAlaCysSerThrIleMetSerValHisAsn 133

Qy   439 GCTATTGGCTCAAGGGGGATCATCCTGGCTGGCACTGAGGAGGCAGAAAGCCAAATACTTG 498
          ::::: ||||||||||||||||||||||||||||||
Db   134 SerValGlyCysMetProIleHisGlyPheGlySerAlaGluGluGlnLysGluArgPheLeu 153

Qy   499 CCTAAACTGCGCGTCCGGGAGCACATTGCAGCCTTCTGCCTCACGGAGGCCAGTCGGG 558
          ::: ::: ||||||||
Db   154 ArgProLeuAlaGlnGlySerMetLeuGlyAlaPheAlaLeuThrGluProGlnAlaGly 173

Qy   559 AGCGATGCAGCCTCAATCCGGAGCAGCCACTAAGTGAAGACAAGAAGCACTACATC 618
          ::::: ::::: |||||
Db   174 SerAspAlaSerPheLeuLysThrArgAla-----ArgArgAspGlyAspHisTyrVal 191

Qy   619 CTCAATGGCTCCAAGGTCTGGATTACTAATGACGAGTGGCCAATATTTTTACTGTGTTT 678
          ||| |||||| ||:::: ||||||
Db   192 LeuAsnGlyAlaLysGlnPheIleThrSerGlySerHisAlaGlyMetValIleIleValPhe 211

Db   679 GCAAAGACTGAGGTCGTTGATTCTGATGCAGTGAAAGACAAAAATCACAGCATTCATA 738
          ||| ||| ||||||||||:::
Db   212 Ala--------ValThrAspProAspAlaGly--LysArgGlyIleSerAlaPheIle 227

Qy   739 GTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCGG 798
          ||| ::: ||||||||||||||||:::
Db   228 ValProThrAspThrProGlyThrGluValValArgIleGluAspLysLysGlyLeuGlyGlnHis 247

Qy   799 GGCTCCAACACTGTGAAGTCCATTTTGAAAACACCAGAGTACCGTGGAAAAACATCCTT 858
          |||||| ::: ::::: |||||||
Db   248 AlaSerAspThrCysGlnLeuAlaPheAsnAspLeuArgIleProAlaThrLeuArgLeu 267

Qy   859 GGAGAGGTCGGAGATGGTTAAGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGC 918
          ::: ||||||||||||:||::: |||
Db   268 GlyGluGlyGluGlyTyrTyrArgIleAlaLeuAlaAsnLeuGluGlyGlyArgIleGly 287

Qy,   919 ATGGGCAGCGTCGTGGCTGCGTCGTCGGGCTGTCAAGAGATTGATTGAAAATGACTGCTGAGTACGCC 978
          ::: ||||| ::: ||||||:::
Db   288 IleAlaAlaGlnAlaValGlyMetAlaAlaArgAlaAlaPheGluAlaAlaAlaArgAspTyrAla 307

Qy   979 TGCACAAGGAAACAGTTAACAAGAGGCTCAGTGATTGATTCAGGAGAAATTT 1038
          |||||| ::: ||||| :::
Db   308 HisGluArgGluThrPheGlyLysProIleIleGluHisGluHisGlnAlaValAlaPheArgLeu 327

Qy   1039 GCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGGGATG 1098
          ||| ::: ||||||||||||:::
Db   328 AlaAspMetAlaThrArgIleAlaAlaArgGlnMetValHis--HisAlaAlaSer 346

Qy   1099 CTGGACCAACCTGGCTTCCCGACTGCTCTCCGACTGGTCCAGCCATGGTGAAGGTGTTCAGC 1158
          ||| ::: |||||| ::: |||
Db   347 LeuArgGluAlaGlyLeuPro---CysLeuThrGluAlaSerMetAlaLysLeuPheAla 365

Qy   1159 TCCGAGGCCCGCCTGCCAGTGTGTGAGTGAGGCGCTGCGAGATCCTGGGGCTGTTGGGCTAC 1218
          ||| ::: |||||| :::
Db   366 SerGluMetAlaGluGluValCysSerAlaAlaIleGlnThrLeuGlyGlyGlyTyrGlyTyr 385

Qy   1219 ACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGCCATCCTCCATCTTCGAG 1278
          ||||||||||||||||:::
Db   386 LeuLysAspPheProValGluArgIleTyrArgAspValArgValCysSerGlnIleTyrGlu 405

Qy   1279 GGAACCAATGAGATTCTCCCGGATGTACATCGCC 1311
          |||||||||| ::: |||
Db   406 GlyThrSerAspValGlnArgLeuValIleAla 416

RESULT 13
US-09-328-352-6801
; Sequence 6801, Application US/09328352
; Patent No. 6662958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6801
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6801

Alignment Scores:
Pred. No.:   1.19e-46   Length: 394
Score: 596.00   Matches: 140
Percent Similarity: 57.10%   Conservative: 73
Best Local Similarity: 37.53%   Mismatches: 138
Query Match: 17.41%   Indels: 22
                         4   Gaps: 9

US-09-945-326-3 (1-1863) x US-09-328-352-6801 (1-394)

RESULT 14
US-09-364-230-30
; Sequence 30, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-364-230-30

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  Percent Similarity: 595.50   Conservative: 64
  Best Local Similarity: 54.87%   Mismatches: 143
  Query Match: 38.46%   Indels: 33
  DB: 17.40%   Gaps: 13
                                3

US-09-945-326-3 (1-1863) x US-09-364-230-30 (1-409)

Qy   184 GATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAGAG 243
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Db   32 AspAspThrGlnGlu------GlnPheLysGluSerValHisLysPheAlaGlnGluThr   49

Qy   244 GTG------GACTCCCGAAAAATTGACCAGGAAGGAAGGGAAAATCCCA---GATGAAACTTTG 294
            ::: ||| :: |||| :|| ||| ||| |||||
Db   50 IleAlaProHisAlaAlaAlaIleAspAlaSerAsnHisPheProLysAspValAsnLeu   69

Qy   295 GAGAAATTGAAG---AGCCTAGGGCTTTTGGGCTGCAAGTCCAGAGAAGAATATGGTGGC 351
            ||||||||||| ||| |||| ||||||| ||| ||
Db   70 TrpLysLeuMetGlyAspPheAsnLeuHisGlyLeuThrAlaProGluGluTyrGlyGly   89

Qy   352 CTGGGCTTCTCCAACACCATGTACTCA-----AGACTAGGGGAGATCATCAGCATGGAT 405
            :::||| |||| : |||| :|: ||| ||| |||| || |||
Db   90 MetGlyLeu--GlyTyrMetTyrHisCysIleAlaMetGluGluIleAsnArgAlaSer 108

Qy   406 GCCTCCATCATGTGACCCTGGACCCTGGCCTATTGGCTCAAGGGGATCATCTTG 465
            ||| :: ||| ::: |||: :: ||| ||: ||| :|||
Db   109 GlySerValGlyLeuSerTyrSerAlaHisSerAsnLeuCysIleAlaGlnLeuValArg 128

Qy   466 GCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGCGTCCGGGGACACATT 525
            ||| :: ||| ||||| ||| ||| |:| :||
Db   129 HisGlySerProAlaGlnLysLeuLysPheLeuProLysSerLeuIleThrGlyHisVal 148

Qy   526 GCAGCCTTCGTGCCTCCACGGGAGCAGCCTCAATCCGGAGCAGA 585
            ||| :|| ||| ||| ::| |||| |||
Db   149 GlyAlaLeuAlaMetSerGlySerAspValSerMetLysCysLys 168

Qy   586 GCCACACTAAGTGAAGACAAGAAGCAC-----TACATCCTCAATGGCTCCAAGGTCTGG 639
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Db   169 Ala------------GluLysValTyrGlyGlyTyrValIleAsnGlyAsnLysMetTrp 184

Qy   640 ATTACTAATGAGGACGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTC---GTT 696
            |||| :::| ||||||
Db   185 CysThrAsnGlyProSerAlaGlnThrLeuGlyValTyrArgAspIleThrAla 204

Qy   697 GATTCTGATGATCAGTGAAAGACAAAATCACAGCATTCATTAGTAGAAGAGACTTTGGT 756

Qy   220 GTGGAAAAATTCTTCACTGAGAGAGGG 273
            |||||| |||||
Db   373 IleGlyAlaGlyThrSerGluIleArgArgMetLeuIle 385

Qy   220 GTGGAAAAATTCTTCACTGAGAGAGGG 273
            |||||::::||||| :::||||||
Db   25 ValAlaAlaPheCysAlaLysGluIleAlaProIleAlaGlnIleAspGlnAspAsn   44

Qy   274 AAAATCCCAGATGAAACTTTGGAGAAATTTGAGAGCCTAGGGGCTTTTGGGCTGCAAGTC 333
            ||| :::   :||:
Db   45 LysPheProAlaHisLeuTrpLysPheGlyAspMetGlyLeuLeuGlyMetThrVal   64

Qy   334 CCAGAGAATATGGTGGCCTCGGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGATC 393
            |||||||||||||||| ::| || ||
Db   65 SerGluGluTyrGlyGly--------AlaAsnMetGlyTyr------LeuAlaHisIle   79

Qy   394 ATCAGCATG-----------------GATGGCTCCATCACTGTGACCCTGGCCAGCGCGCAC 435
            |||:::   ::::::: |||||| ||||| |||
Db   80 IleAlaMetGlnIleLeuSerGlyLeuGluTyrValGlyLeuSerTyrGlyValAlaHis   99

Qy   436 CAGGCTATTGCCTCCAAGGGGATCATCTTGCCTGCTGGCCACTGAGGAGGAGCAGAAAGCCAAATAC 495
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Db   100 SerAsnLeuCysValAsnGlnIleAsnArgAsnGlyAspGlnGlnLysGlnLysLysTyr 119

Qy   496 TTGCCTAAACTGGGCTCCGGGGAGCACATTGCAGCCTTCGTGCCTCCACGGAGCCAGCAGT 555
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Db   120 LeuProLysLeuIleSerGlyValGluTyrValGlyTyrValAlaLeuAlaMetSerGluProAsnAla 139

Qy   556 GGGAGCCGATGCAGCGCTCAATCCGGACAGAGCCCACCACTAAGTGAAGACAAGAAGCACTAC 615
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Db   140 GlySerAspValValSerMetLysSerLeuArgAlaGluGlnLysLysGlyGlyAsp------HisPhe 157

Qy   616 ATCCTCAATGGCTCCAAGGTCTGGAGATTACTAATGAGGACGGCCAATATTTTTACTGTG 675
            :::||||||||||||||| ||| || |:||:: |||||
Db   158 ValLeuAsnGlySerLysMetTrpIleThrAsnGlyProAlaGlnLeuValVal 177

Qy   676 TTTGCAAAGACTGAGTCGTTGATTCTGATGGATCAGTGAAAGACAAAATCACAGAGATTC 735
            |||||| ::: |||||||||
Db   178 TyrAlaLysThr--------AspProGlnAlaGlyProLysGly--MetThrAlaPhe 193

Qy   736 ATAGTAGAAAGAGACTTTGGTGTGGAGCTCACTAATGGGAAACCCGAAGATAAATTAGGCATT 795
            ||| ||||||:::||||||| ::: |:||: |:| |::
Db   194 LeuIleGluLysGlyMetLysGlyMetLysGluIleSerGlyPheSerHisGlyLeuAsnHisGlyLeuAsnHisGlyLeuMet 213

Qy   796 CGGGGCTCCAACACTTGTGAAGTCTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAACATC 855
            ||||| |||| ::: |||| :| ||| |:| |||||| ||| || |||
Db   214 ArgGlySerAsnThrTyrProLeuPheAsnValGluValProAlaGluAsnVal 233

Qy   856 CTTGGAGAGGTCGGAGATGGTTTAAGGTCGCCATGAACATCCTCAACACGCGGCCGGTTC 915
            ||| |||||:::|||||||| || || ||||
Db   234 LeuGlyGlyValGlyValGlyAsnGlyValIleGlyValLeuLysAspTyrGlnArgAla 253

Qy   916 AGCATGGGCAGCGCTGCTGGCTGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTAC 975
            |||||||||:::   :::||| |:: ||:| | :|| ||| || |||
Db   254 ValLeuSerAlaGlyProLeuGlyIleTyrIleMetAspAlaAlaCysLysLeuAspAspValValIleProTyr 273

Qy   976 GCCTCCACAGGAAACAGTTAACAAGAGGCTCAGTGAATTTGGAATTGATTCAGGAGAAA 1035
            ||| :::   ::: |:| ||||| ||: ||||||
Db   274 LeuHisGlnArgGluGluLeuGlyGlnLysPheGlyIleAspLeuPheGlnLeuMetGlnGlyLeuLys 293

Qy   1036 TTTTGCGATGATGGCTCAGAGAGGCTTACGTCAGAGAGTATGACCTACCTCACCTCACAGAGG 1095
            ||| :::||:|| ||| ||| || ||:: |||| |||
Db   294 LeuAlaAspMetTyrSerThrProLeuAlaCysLysAlaLeuAlaLeuValTyrAlaValGlyAla 313

Qy   1096 ATGCTGGACCAACCTGGCTTCCCGACTGCTCCATC-----GAGGCAGCCATGTGTGAAG 1149
            ||| :::|| ||| ::| :: ||| ||||||| ::|
Db   314 AlaCysAspLysAlaAspHis--AspArgSerLeuArgLysAspAlaAlaSerAlaIle 332

Qy   1150 GTGTTCAGCTCCGAGGCCGCTGGCAGTGTGTGAGTGAGGACGATCCTCCGGGGGGC 1209
            |||||||| :::   ::: |||||| |||
Db   333 LeuTyrAlaAlaGluLysGlyAlaThrTrpMetAlaGlyGluAlaIleGlnThrLeuGlyGly 352

Qy   1210 TTGGGCTACACAAGGACTACTACGAGCGCATACTGCGTGACACCCGATCTCCTC 1269
            |||||:::   :::::||||
Db   353 AsnGlyTyrIleAsnGluProAlaGlyLeuTrpArgAspAlaLysTyrArgAspAlaLysTyrArgGlu 372

Qy   1270 ATCTTCGAGGGAACCAATGAGAGTTCTCCGGATGTACATC 1308

Query Match: 17.29%   Indels: 46
DB: 4   Gaps: 13

US-09-945-326-3 (1-1863) x US-09-949-016-10443 (1-459)

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Qy      8  GCTGCGGGGCTTCTGCGCACCACGGCTGGGGCTCGTGCCCGTGGGGTCGGTGCTGCTGCT  67
                :::||||||||||::| ||| |||||:::|||:||||||
Db     28  SerAlaGlySerCysMetAlaGlyMet--AlaThrAlaThrArgLeuLeuGlyTrpA  47

Qy     68  CTACCCGGAACCGGCCTACTGCGCCGGTTCGCCACCAGCCCGCTGTACGAGCTTTCGCCAAAGAGC  127
                ||||:::  |||     |||    ||||:|
Db     47  rgValAlaSerTrpArgLeu------------ArgProProLeuAlaGlyPheValSerGln-  63

Qy    128  TTTTCCTAGGCAAATCAAGAAGAGAGTTTTCCCATTTCCAGAAGTTAGCCAAGATG  187
                                     :::       |||
Db     64  --------------ArgAlaHisSerLeuLeuProValAspAlaAlaIleAsnGlyL  78

Qy    188  AACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTG-  246
                :::               ||||||||||||||||||
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Qy    247  ----GACTCCGAAAAATTGACCAGGAAGGGAAAATCCCAGAT-----GAAACTTTGG  295
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Db     98  laProLysAlaGlnGlyIleLeuGlnIleAspSerArgAsnLeuArgGluPheTrpL  118

Qy    296  AGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAGAAGAATATGGTGGCCTGG  355
                :::||||||||||||
Db     118  ysGlnLeuGlyAsnLeuGlyValLeuGlyIleThrAlaProValGlnTyrGlyGlySerG  138

Qy    356  GCTTCTCCAACACCATGTACTCAAGACTAGGGGACGATCATCAGC---ATGGATGGGTCCA  412
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Db     138  lyLeuGlyTyrLeuGlyHisValMetGluGlyIleLeuSerArgAlaSerGlyAlaV  158

Qy    413  TCACTGTGACCCTGCAGCGCCACCAGGCTATTGGCTCAAGGGGACATCATCTGGCTGGCA  472
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Db     158  alGlyLeuSerTyrGlyAlaHisSerAsnLeuCysIleAsnGlnLeuValArgAsnGlyA  178

Qy    473  CTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCCACATTGCAGCCT  532
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Qy    533  TCTCGCCTCACGGAGCCAGCCAGTGGAGGGATGCAGCGCCTCAATCCGGAGCAGAGCCACAC  592
                |||||||||||                  :::::::
Db     198  euAlaMetSerGluProAsnAlaGlySerAspValSerMetLysLeuLysAla----  216

Qy    593  TAAGTGAAGACAAGAAG------CACTACATCCTCAATGGCTCCAAGGTCTGGATTACTA  646
                ::||||||         ||   ::|||||
Db     217  --------GluLysLysGlyAsnHisTyrIleLeuAsnGlyAsnLysPheTrpIleThrA  234

Qy    647  ATGGAGGAGCTGGCCAATATTTTACTGTGTTGCAAAGACTGAGTCGTTGATTCTGATG  706
                ||||                ||||||||||||||
Db     234  snGlyProAspAlaAspValLeuIleValThrArgAlaLysThrAspLeuAlaAlaValProA  254

Qy    707  GATCAGTCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAAGAAGACTTTGGTGGAGTCACTA  766
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Db     254  laSer------ArgGlyIleThrAlaPheIleValGluLysGlyMetProGlyPheSerT  272

Qy    767  ATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTG  826
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Db     272  hrSerLysLysGlyLeuGlyMetArgGlySerAsnThrCysGluValProPheG  292

Qy    827  AAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTTGAAGATGGGTTTAAGGTGG  886
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Db     292  luAspCysLysIleProAlaAlaAlaAsnIleLeuGlyHisGluAsnLysGlyValValL  312

Qy    887  CCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGCAGCGCTGTGGCTGCTCTCA  946
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Qy    220  GlyPheSerThrAlaGlnLysLeuAspLysGlyMetArgGlySerAspThrCysGlu  239
Qy    817  GTCCATTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGG  876
Db    240  LeuValPheGluAsnCysPheValProHisGluValLeuGluGlyGlyGlyLysGly  259
Qy    877  TTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGCAGCGCTGTCGTGGCT  936
Db    260  ValTyrValMetMetSerGlyLeuAsnLeuGluArgPheValLeuAlaAlaGlyProSer  279
Qy    937  GGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTT  996
Db    280  AlaLeuMetGlnAlaCysPheLeuAspValAlaValLeuTyrValArgGluGlnPhe  299
Qy    997  AACAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAG  1056
Db    300  GlyArgProIleGlyGluPheGlnPheIleArgGlyLysLeuAlaAspMetTyrThrSer  319
Qy   1057  GCTTACGTCATGGAGAGTATGACCTACCTCCACAGCA------------GGGATGCTG  1101
Db    320  LeuGlnSerSerArgSerPheValTyrSerValAlaArgAspCysSerValAlaAsnGlyLysVal  339
Qy   1102  GACCAAACCTGGCTTTCCCGACTGCTTCCCATCGAGGCCAGCCATGGTGAAGGTGTTCAGCTCC  1161
Db    340  AspArg------LysAspCys------------AlaGlyValIleLeuLeuPheAlaAla  352
Qy   1162  GAGGGCCGCCTCGGCAGTGTGTGAGGACGGCCTTGGGTACTCTCGAGATCCTCGGGGCTTGGGCTACACA  1221
Db    353  GluArgAlaThrGlnValAlaLeuGlnAlaIleGlnCysLeuGlyLeuGlyAsnGlyTyrIle  372
Qy   1222  AGGGACTACATCCGTAGAGCGGCATCTGCGTGACACCCGACATCCTCCATCTTCGAGGGA  1281
Db    373  AsnGluTyrProThrAlaArgLeuLeuGluArgAspAlaLeuLysAspAlaLeuuSerLeuProGluIleGlyProGly  392
Qy   1282  ACCAATGAGATTCTCCGGATGTACATCGCC  1311
Db    393  ThrSerGluIleArgArgMetIleIleAla  402
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RESULT 15
US-09-949-016-10443

; US-09-949-016-10443, Application US/09949016
; Sequence 10443, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10443
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10443

Alignment Scores:

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Best Local Similarity:	34.62%	Mismatches:	179
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Qy   1052 AGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACAGCAGGATGCTCGACCAACCTG 1111
               ::: ||||||      |||    || |||::
Db    372 ysArgGlnTyrVal------------TyrAsnValAlaLysAlaCysAspGlu----- 385

Qy   1112 GCTTTCCCGACTGCTCCATC---GAGGCAGCCATGTGAAGGTGTTCAGCTCCGAGGCCG 1168
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Db    386 -----GlyHisCysThrAlaLysAspCysAlaGlyValIleLeuTyrSerAlaGluCysA 404

Qy   1169 CCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTGGGGGCTTGGCTACCACAGGGACT 1228
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Db    404 laThrGlnValAlaLeuAspGlyIleGlnCysPheGlyGlyAsnGlyTyrIleAsnAspP 424

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Qy   1289 AGATTCTCCGGATGTACATCGCCCCTGACGGGTCTCTGCAGCATGCCCGCCGCCATCCTGACTA 1348
               ||:||| |||::|||      |||||
Db    444 luValArgLeuValIle-------------------------GlyArgAlaPheAsnA 456

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Job time : 75.5718 secs

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          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:     May  2, 2005, 14:49:52 ; Search time 206.808 Seconds
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                                     6001.474 Million cell updates/sec

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Scoring table:  BLOSUM62
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                Fgapop   6.0 , Fgapext   7.0
                Delop    6.0 , Delext    7.0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched:        1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters:        2852064

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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                      SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Result   Query

No.	Score	Match	Length	DB	ID	Description
1	3153	92.1	621	9	US-09-945-326-2	Sequence 2, Appli
2	3153	92.1	621	14	US-10-168-274-24	Sequence 24, Appl
3	3153	92.1	621	15	US-10-112-944-420	Sequence 420, App
4	3153	92.1	621	16	US-10-408-765A-1059	Sequence 1059, Ap
5	3153	92.1	621	16	US-10-408-765A-2053	Sequence 2053, Ap
6	3129	91.4	628	15	US-10-112-944-869	Sequence 869, App
7	1360	39.7	655	15	US-10-362-537-10	Sequence 10, Appl
8	1356.5	39.6	653	15	US-10-362-537-9	Sequence 9, Appli
9	1345	39.3	653	15	US-10-362-537-11	Sequence 11, Appl
10	1308	38.2	655	15	US-10-362-537-1	Sequence 1, Appli
11	1308	38.2	655	16	US-10-408-765A-534	Sequence 534, App
12	1299	37.9	655	16	US-10-408-765A-320	Sequence 320, App
13	1210.5	35.4	613	15	US-10-369-493-5444	Sequence 5444, Ap
14	954	27.9	188	16	US-10-408-765A-1442	Sequence 1442, Ap
15	954	27.9	188	16	US-10-408-765A-2052	Sequence 2052, Ap
16	844.5	24.7	594	15	US-10-369-493-16704	Sequence 16704, A
17	821	24.0	594	15	US-10-369-493-17429	Sequence 17429, A
18	816	23.8	581	15	US-10-369-493-19424	Sequence 19424, A
19	815.5	23.8	594	15	US-10-369-493-23285	Sequence 23285, A
20	799	23.3	585	15	US-10-369-493-9765	Sequence 9765, Ap
21	795.5	23.2	583	15	US-10-369-493-9771	Sequence 9771, Ap
22	765	22.3	583	15	US-10-369-493-10383	Sequence 10383, A
23	704	20.6	373	15	US-10-369-493-16614	Sequence 16614, A
24	699	20.4	382	15	US-10-369-493-16795	Sequence 16795, A
25	690	20.2	379	15	US-10-369-493-17460	Sequence 17460, A
26	686.5	20.1	377	15	US-10-369-493-9826	Sequence 9826, Ap
27	682	19.9	378	15	US-10-369-493-23196	Sequence 23196, A
28	678	19.8	381	15	US-10-369-493-16918	Sequence 16918, A
29	675.5	19.7	379	15	US-10-369-493-16613	Sequence 16613, A
30	663	19.4	646	14	US-10-156-761-10104	Sequence 10104, A
31	658	19.2	380	15	US-10-369-493-17459	Sequence 17459, A
32	652.5	19.1	379	15	US-10-369-493-23337	Sequence 23337, A
33	652	19.0	387	15	US-10-369-493-577	Sequence 577, App
34	650	19.0	384	14	US-10-272-419-6	Sequence 6, Appli
35	644.5	18.8	370	15	US-10-369-493-14087	Sequence 14087, A
36	641	18.7	375	15	US-10-369-493-8807	Sequence 8807, Ap
37	640	18.7	378	15	US-10-369-493-16449	Sequence 16449, A
38	633	18.5	375	15	US-10-369-493-17779	Sequence 17779, A
39	630.5	18.4	387	15	US-10-369-493-13698	Sequence 13698, A
40	629.5	18.4	381	15	US-10-369-493-546	Sequence 546, App
41	629	18.4	374	15	US-10-369-493-9830	Sequence 9830, Ap
42	626	18.3	373	15	US-10-369-493-11638	Sequence 11638, A
43	626	18.3	377	15	US-10-369-493-14685	Sequence 14685, A
44	625.5	18.3	379	15	US-10-369-493-10412	Sequence 10412, A
45	624	18.2	378	15	US-10-369-493-9086	Sequence 9086, Ap

ALIGNMENTS

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RESULT 1
US-09-945-326-2
; Sequence 2, Application US/09945326
; Patent No. US20020127680A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel
;  APPLICANT:  Hunter, John Joseph
;  TITLE OF INVENTION:  62112, A NOVEL HUMAN DEHYDROGENASE AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: MNI-187
;  CURRENT APPLICATION NUMBER: US/09/945,326
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: 60/229,831
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  LENGTH: 621
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-945-326-2
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Alignment Scores:
Pred. No.:
Score:                   1.29e-251        Length:          621
Percent Similarity:      3153.00          Matches:         621
Best Local Similarity:   100.00%          Conservative:    0
Query Match:             100.00%          Mismatches:      0
DB:                      92.11%           Indels:          0
                         9                Gaps:            0

US-09-945-326-3 (1-1863) x US-09-945-326-2 (1-621)
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US-09-945-326-3

Qy      1  ATGAGCGGGCTGCGGGCTCTTCCTGCGCACCACGGCTGCGGCTGCGTGCCTGCCGGGGTCTG   60
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Db      1  MetSerGlyGlyLeuArgLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyGlyLeu   20

Qy     61  GTGGTCTCTACCGGCCGACCGGCTACTGCGCACCAGGCCCTGGCACGCCTTTCGCC      120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21  ValValSerThrAlaAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla   40

Qy    121  AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAGAAGTTTCCATTTCCAGAAGTTAGC      180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41  LysGluLeuPheLeuGlyLysIleLysLysLysLysPheProPheProGluValSer   60

Qy    181  CAAGATGAACTTAATGAAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA      240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GlnAspGluLeuAsnGluAsnGlnSerValLeuGlyProValGluLysPhePheThrGlu   80

Qy    241  GAGGTGGACTTCCCGAAAAATTGACCAGGAGGGAAAATCCAGATGAAACTTGGAGAAA      300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81  GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys  100

Qy    301  TTGAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATGGTGGCCTCGGCTTC      360
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Db    101  LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe  120

Qy    361  TCCAACACCATGTACTACCAAGACTAGGGAGATCATCAGCATGATGGGTCCATCACTGTG      420
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Db    121  SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetMetAspGlySerIleThrVal  140

Qy    421  ACCCTGGCCAGCGCACCAGGCTATTGCCTCAAGGGGATCATCTTGCCTGCACTGAGGAG      480
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Db    141  ThrLeuAlaAlaAlaHisGlnAlaIleGlyTyrIleLeuLeuLysGlyIleIleLeuAlaGlyLeuAlaGlyThrGluGlu  160

Qy    481  CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCCACATTGCAGCCTTCTGCCTC      540
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Db    161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyAlaHisIleAlaAlaPheCysLeu   180

Qy    541  ACGGAGCCAGCCAGTGGGAGGAGGCGATGCAGCCTCAATCCAGAGCAGAGCCACACTAAGTGAA      600
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Db    181  ThrGluProAlaSerGlySerAspAlaAlaSerArgIleArgSerArgAlaThrLeuSerGlu   200

Qy    601  GACAAGAAGGACTACTACCATCCTCAAATGGCTCGGATTACTAATGGGACTGGCC      660
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Db    201  AspLysLysHisTyrIleLeuLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla  220

Qy    661  AATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGAATCTGATGGATCTAGTGAAAGAC      720
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Db    221  AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp   240

Qy    721  AAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGGAGTCACTAATGGGAAACCCGAA      780
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Db    241  LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu   260

Qy    781  GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATA      840
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Db    261  AspLysLeuGlyIleArgGlyGlySerAsnThrCysGluValHisPheGluAsnThrLysIle  280

Qy    841  CCTGTGGAAAAACAATCCTTGGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTC      900
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Db    281  ProValGluAsnIleLeuGlyValAlaGlyGluValAspGlyPheLysValAlaMetAsnIleLeu   300

Qy    901  AACAGCGGCCGGTTCAGCATGGGCACCGGCCGTGCGGCTGCGCTCCAAGAAGTTGATTGAA      960
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Db    301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuArgLeuLeuArgLeuIleGlu  320
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Qy   1021  TTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCGAGAGTATGACC      1080
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Qy   1081  TACCTCACAGCAGGAGATGCTGACCAACCTGGCTTCCCGACTGCTCCATCGAGCAGCC    1140
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Db    361  TyrLeuThrAlaGlyMetLeuAspProGlyPheProThrAlaProSerIleGluGlnAlaAla  380

Qy   1141  ATGGTGAAGGTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC    1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381  MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle  400

Qy   1201  CTCGGGGGCTTGGGCTACAACAGGACTACTCCGTACGAGGCCATACTGGTGACACCCGC    1260
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Db    401  LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg  420

Qy   1261  ATCTCCTCCATCTTCCGAGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT    1320
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Db    421  IleLeuLeuIlePheArgGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly  440

Qy   1321  CTGCAGCATGCGCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG    1380
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Db    441  LeuGlnHisAlaArgArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal  460

Qy   1381  AGCACCATGATGGATACCGTTGGCCGGAGCTCCCTGGGACTCCTGGCCGAACTGTGGAC    1440
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Db    461  SerThrValMetAspThrValGlyArgArgSerLeuGlyArgGlyArgThrValAsp  480

Qy   1441  CTGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCCGGACAGTGCCAACAAG    1500
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Db    481  LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys  500

Qy   1501  TTTGAGGAGAACACCTACTGCTTCGGCCCGGACCGTGGAGAACACTGCTGCTCCGCTTTGGC    1560
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Db    501  PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly  520

Qy   1561  AAGACCATGATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTG    1620
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Db    521  LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu  540

Qy   1621  TATGCATGACGGCCGTGCTGTCGCCGGGGCTCATCCGCATTGGGCTCCGCAAC    1680
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Db    541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgIleArgSerIleArgGlyLeuArgArgAsn  560

Qy   1681  CACGACCACCAGAGTTCTCTTGCCAACACCTTCTGCGTGGAAGCTTACTGCAGAATCTC    1740
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Qy   1741  TTCAGCCTCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA    1800
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; Sequence 24, Application US/10168274
; Publication No. US2003012410A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: YUE, Henry
;  APPLICANT: LAL, Preeti
```

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; APPLICANT:  TANG, Y. Tom
; APPLICANT:  HILLMAN, Jennifer
; APPLICANT:  BAUGHN, Mariah R.
; APPLICANT:  AZIMZAI, Yalda
; APPLICANT:  LU, Dyung Aina M.
; TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
; FILE REFERENCE: PF-0754 PCT
; CURRENT APPLICATION NUMBER: US/10/168,274
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/172,367
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 24
;  LENGTH: 621
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc feature
;  OTHER INFORMATION: Incyte ID No. US2003012106A1 5540437CD1
US-10-168-274-24

Alignment Scores:
Pred. No.:
Score:                1.29e-251          Length:          621
Percent Similarity:   3153.00            Matches:         621
Best Local Similarity: 100.00%           Conservative:    0
Query Match:          100.00%            Mismatches:      0
DB:                   92.11%             Indels:          0
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US-09-945-326-3 (1-1863) x US-10-168-274-24 (1-621)
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Qy 181 CAAGATGAACTAATGAAATAAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA   240
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Db   61 GlnAspGluLeuAsnGluIleLeuAsnGlnPheLeuGlyProValGluGluIleLysPhePheThrGlu   80

Qy 241 GAGGTGGACTCCCCGAAAAAATTGACCAGGAAGGGAAAAATCCCAGATGAAACTTTGGAGAAA   300
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Db   81 GluValAspSerProLysLysLeuThrArgLysGlyLysIleProAspGluThrLeuGluLys   100

Qy 301 TTGAAGAGCCTAGGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGGCCTGGGCTTC   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 LeuLysSerLeuGlyAlaPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyLeuGlyPhe   120

Qy 361 TCCACACCATGTACTCAAGACTGGCGAGCAGATCATCAGACATGGGATCATCATCACTGTG   420
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Db 121 SerAsnThrMetTyrSerArgLeuGlyLeuGlnIleIleIleIleSerMetAspGlySerIleThrVal   140

Qy 421 ACCCTGGCAGCGCCACCAGGCTATTGCTGCCTCAAGGGGGATCATCTTCGCTGGCACTGAGGAG   480
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Db 141 ThrLeuAlaAlaHisHisGlyIleIleLeuGlyIleLeuAlaGlyThrGluGlu   160

Qy 481 CAGAAAGCCAAATACTTGCCTAAACTGGCCTCCGGGGAGCACATTGCAGCCTTCTGCCTC   540
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Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu   180

Qy 541 ACGGAGCCAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCCACCTAAGTGAA   600
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Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu   200

Qy 601 GACAAGAAGCACTACATCCTCAATGCTCAATGGTTCTGGATTACTAATGGAGGACTGGCC   660

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Qy 721 AAAATCACAGCATTCATAGTAGAAAAAGAGACTTGGTGAGTCACTAATGGGAAACCCGAA   780
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Qy 781 GATAAATTAGGACATTGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA   840
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Qy 901 AACAGGCGGCCGGTTCAGCATGGGCAGCGTCGGCTGGCGTCTGCTCAAGAGATTGATTGAA   960
         AsnSerGlyArgPheSerMetGlySerValAlaGlyLeuLeuLysLeuLeuGlu   320

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Qy 1021 TTGATTCAGGAGAAAATTGACTGCTGATGGCTCAGAAGGCTTACGTCACTGGAGTATGACC 1080
         LeuIleGlnGluLysLeuAspCysSerLysAlaTyrValMetGluSerMetThr   360

Qy 1081 TACCTCCACAGCAGGATGCTGACAACACCTGGCTTCCCGACTGCTCCATCCAGCCAGCC 1140
         TyrLeuThrAlaGlyMetLeuAspAsnGlnProGlyPheProAspCysSerIleGluAlaAla   380

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         MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerValSerGluGluIle   400

Qy 1201 CTCGGGGCTTGGCTGTACAACAAGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGC 1260
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Qy 1261 ATCCCTCATCTTCGAGGACCAATGAGATTCTCCGGATGATCATCGCCCTGACGGGT 1320
         IleLeuLeuIleLeuPheGluGlyGlyThrArgAsnGluIleLeuLeuArgMetTyrIleAlaLeuThrGly   440

Qy 1321 CTGCAGCATGCCGCGGCCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
         LeuGlnHisAlaAlaGlyArgIleLeuThrThrArgIleHisGluGluLeuLysGlnAlaLysVal   460

Qy 1381 AGCACAGTCATGGATACCGTTGGCCGGAGGCTTCGGACTGGCGAGGAGACTGTGAC 1440
         SerThrValMetAspThrValGlyArgArgLeuArgThrGlyArgThrValAsp   480

Qy 1441 CTGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG 1500
         LeuGlyLeuThrGlyAsnHisGlyValAlaHisProSerLeuAlaAspSerAlaAsnLys   500

Qy 1501 TTTGAGAGACAACCTACTGCTTCTCGGCGACACGCCGTCTCCCCGCTTTTCGGC 1560
         PheGluGluAsnThrThrCysPheSerAlaThrProLeuLeuLeuArgProPheGlyGly   520

Qy 1561 AAGACCATCATGGAGGAGCAGCTGGTACTGGCGCGGTGGCCAACATCCTCATCAACCTG 1620
         LysThrIleMetGluGluGlnLeuValLeuAlaArgValAlaAsnIleLeuIleAsnLeu   540

Qy 1621 TATGGCATGACGGCCCGTCGTGCCGGCGCTCCATTCGAGCAGCAGCACCTAAGTGAA 1680
         TyrGlyMetThrAlaValLeuSerArgArgAlaSerArgIleGlyLeuArgAsn   560

Qy 1681 CACGACCAGAGGTTCTTCTTGCCAACCAGTGCCTCTGCTGGAAGCTTACTTGCAGAATCTC 1740

Db   561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy   1741 TTCAGCTCTCCAGCTGGACAAGTATGCTGCTGCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
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Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaAlaProGluAsnLeuAspGluGlnIleLysLys 600

Qy   1801 GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCACCCCTCTGGACAGGACA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaThrProLeuAspArgThr 620

Qy   1861 TGC 1863
          |||
Db   621 Cys 621

RESULT 3
US-10-112-944-420
; Sequence 420, Application US/10112944
; Publication No. US20040048249A1
GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040004249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 420
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-112-944-420

Alignment Scores:
Pred. No.:   1.29e-251   Length: 621
Score: 3153.00   Matches: 621
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 92.11%   Indels: 0
DB: 15   Gaps: 0

US-09-945-326-3 (1-1863) x US-10-112-944-420 (1-621)

Qy   1 ATGAGCGGCTGCGGGCTCTTCCTGCGCACCACGGCTGCGGCTGCCTGCCGCGGGGTCTG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20

Qy   61 GTGGTCTTCTACCGGCCGAACCGGCGCTACTGCCGCACCAGCCCCCCTGCGAGCTTTCGCC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40

Qy   121 AAAGAGCTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTCCATTTCCAGAAGTTAGC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60

Qy   181 CAAGATGAACTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGlnIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80

Qy   241 GAGGTGGACTCCCGAAAAATTGACCAGGAAGGGAAAATCCAGATGAACTTTGGAGAAA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerArgLysIleAspGlnGluGlyLysIleGlnMetAsnPheGlyGluLys 100

Qy   301 TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGCCTGGGCTTC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGlnTyrGlyGlyLeuGlyPhe 120

Qy   361 TCCAACCATGTACTCAAGACTAGGGGAGTCATCAGCATGGATGGTCCATCACTGTG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140

Qy   421 ACCCTGGCAGCGCACCAGGTATTGGCCTCAAGGGGGATCATCTTGCTGGCACTGAGGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuLeuAlaGlyThrGluGlu 160

Qy   481 CAGAAAGCCAAATACTTGCCTAAACTGGCTCGGCGGCACATTGCAGCCTTCTGCCTC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180

Qy   541 ACGGAGCCCAGCCAGTGGAGGCGGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200

Qy   601 GACAAGAAGCACTACATCCTCAATGCTCCAAGGTCTGATTACTAATGAGGACTGGCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 AspLysLysHisTyrIleLeuAsnGlySerLysSerAspTyrThrAsnGluGlyLeuAla 220

Qy   661 AATATTTTTACTGTGTTGCAAAGACTGAGGTCGTGATTCTGATGAAGAC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240

Qy   721 AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGAGTCACTCAATGGGAAACCCGAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAlaPheIleValGluArgAspPheGlyGluSerLeuAsnGlyLysProGlu 260

Qy   781 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluLysThrLysIle 280

Qy   841 CCTGTGGAAAACATCCTTGGAGATGGTTAAGGTGGCCATGAACATCCTC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ProValGluAsnIleLeuGlyGluValGlyAlaGlyLeuLeuLysArgLeuIleLeuGlu 300

Qy   901 AACAGCGGCCGGTTCAGGATGGCCATGGGTTCAGCGTGGCTGGCTGTTGCTCAAGAGATTGATTGAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlySerValAlaGlyLeuLeuLysLeuArgLeuLeuGlu 320

Qy   961 ATGATGCTGCTGAGTACGCCTGCACAAGGAGAAACAGTTAACAGAGGCTCAGTGAATTTGGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrArgAlaGluTyrAlaCysThrArgLysGlnPheAsnLysSerGluGluPheGly 340

Qy   1021 TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAGGGCTTACGTCATGGAGAGTATGACC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnArgAlaTyrValMetGluSerMetThr 360

Qy   1081 TACCTCACAGCAGGGATGCTGGACCAACTGGCTTTCCGACTGCTCCATCGCAGGCAGCC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380

```
;      TYPE: PRT
;      ORGANISM: Homo sapiens
US-10-408-765A-1059

Alignment Scores:
Pred. No.:                  1.29e-251          Length:           621
Score:                      3153.00            Matches:          621
Percent Similarity:         100.00%            Conservative:       0
Best Local Similarity:      100.00%            Mismatches:         0
Query Match:                92.11%             Indels:             0
DB:                                            Gaps:              16

US-09-945-326-3 (1-1863) x US-10-408-765A-1059 (1-621)

Qy    1 ATGAGCGGCTGCGGGCTTCTGCTGCCGCCACCACGGCTGCGGCTTCGTGCCGCCTGCCGGGCTCTG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetSerGlyCysGlyLeuLeuLeuProLeuProProThrAlaAlaAlaArgAlaCysArgLeuProGlyLeu   20

Qy   61 GTGGTCTCTACCGGCAACCGGCGGCTACTGCGCACCAGCCCGCCTGCACGAGCTTTCGCC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla   40

Qy  121 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTTCCCATTTCCAGAAGTTAGC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer   60

Qy  181 CAAGATGAACTAATGAAATCAATCAGTTCTTGGGAACCCGTGGAAAAATTCTTCACTGAA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuMetLysSerIleSerSerTrpGluProValGluLysPhePheThrGlu   80

Qy  241 GAGGTGACTCCGAAAAATTGACCAAGGAAGGAAATCCAGATGAAACTTTGGAGAAA  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerArgLysIleAspProGluGlyLysIleProGluLysLeuGluLys   100

Qy  301 TTGAAGAGCCTAGGGCCTTTTGGCCTGCAAGTCCCAAGAAGAAGAATATGGTGGCCTGGGGCTC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProLysLysAsnMetValAlaTrpGlyLeuPhe   120

Qy  361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCACTGTG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal   140

Qy  421 ACCCTGGCAGCGCACCAGTCATTGGCCTATTGCCTCAAGGGGATCATCTTGGCACTGAGGAG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrLeuAlaAlaHisGlnAlaIleAlaTyrLeuLeuLysGlyIleIleLeuAlaLeuArgArg   160

Qy  481 CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGGCACTAATGGGAAACCCGAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu   180

Qy  541 ACGGAGCAGCCAGTGGAGCCAGTGGAGCGATGCAGCCCAATCCGAGCGCACACTAAGTGAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu   200

Qy  601 GACAAGAAGACTACATCCTCAAGGTCTCGGATTACTAATGGGAGGACTGCGCC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 AspLysLysLysAspTyrIleLeuLysGlySerLysValTrpIleThrAsnGlyGlyLeuAla   220

Qy  661 AATATTTTACTGTGTTGCAAAGACTGAGTCGTTGATTCGATGATCAGTGAAAGAC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221 AsnIlePheThrValPheAlaLysThrGluValValAspSerSerValLysAsp   240

Qy  721 AAAATCACAGACATTCATGATAGAAAGGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAA  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyIleLysProGlu   260

Qy  781 GATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCATTTTGAAAACACCAAGATA  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 AspLysArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle   280

Qy  841 CCTGTGGAAAACATCCTTGGAGAGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTC  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 ProValGluAsnIleLeuGlyGluValGlyValGlyAspGlyPheLysLysValAlaMetAsnIleLeu   300

Qy 1141 ATGGTGAAGTGTTCAGCTCCGAGCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 MetValLysValPheSerSerGluSerGluAlaAlaTrpGlnCysValSerValAlaLeuGlnIle   400

Qy 1201 CTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCCTGACACCCGC  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg   420

Qy 1261 ATCCTCCATCTTCGAGGGAACCAATGAGATTCCGGATGTACATCGCCCTGACGGGT  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 IleLeuLeuIlePheGluGlyThrAsnGluIleProAspValHisIleAlaLeuThrGly   440

Qy 1321 CTGCAGCATGCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal   460

Qy 1381 AGCACAGTTCATGGATACCGTTGGCCGGGAGGCTTCGGGAGACTTCCCTGGCCGCGAACTGTGAC  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  461 SerThrValMetAspThrValGlyArgGluGlyGlyPheGlyArgLeuArgGlyThrValAsp   480

Qy 1441 CTGGGGCTGACAGGGCAACCATGAGTGTGTGCACCCAGTCTGCGGACAGTGCCAACAAG  1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 LeuGlyLeuThrGlyGlnAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys   500

Qy 1501 TTTGGAGGAGAACACCTACTGCTTCGGCCGGAACCGTGGGAGACACTGCTGCTCCGCTTTGGC  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly   520

Qy 1561 AAGACCATCATGGAGCAGCTCGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTG  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  521 LysThrIleMetGluGlnLeuGlyLeuLysArgValAlaAsnIleLeuIleAsnLeu   540

Qy 1621 TATGCGATGACGGCCGTGCTGTCGCGGGCCAGCCGCCCTCCATCCGCATTGGCCTCCGCAAC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerArgIleSerIleArgLeuGlyLeuArgAsn   560

Qy 1681 CACCACCAGAGTTCTCTTGGCCAACAACTTCTGTGCTGGAAGTTACTTGCAGAATCTC  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  561 HisHisGlnSerLeuLeuAlaAsnThrPheCysAlaGlySerTyrLeuGlnAsnLeu   580

Qy 1741 TTCAGCCTCTCTCAGCTGACAAGTAATGCTCCAGAAAAACCTAGATGAGCAGATTAAGAAA  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  581 PheSerLeuSerGlnLeuThrSerAsnAlaProGluLysProArgAspGluGlnIleLysLys   600

Qy 1801 GTGTCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCTCTGGACAGGACA  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 ValSerGlnGlnIleLeuGluLysGlyArgAlaTyrIleCysAlaHisProLeuAspArgThr   620

Qy 1861 TGC  1863
          |||
Db  621 Cys  621
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RESULT 4
US-10-408-765A-1059
; Sequence 1059, Application US/10408765A
; Publication No. US2004010 1874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1059
; LENGTH: 621

Alignment Scores:
Pred. No.:
Score: 1.29e-251   Length: 621
Percent Similarity: 3153.00   Matches: 621
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 92.11%   Indels: 0
                                              Gaps: 0

US-09-945-326-3 (1-1863) x US-10-408-765A-2053 (1-621)

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Qy        1 ATGAGCGGCTGCGGGCTCTTCCTGCGCACCAGGCTGCGGCTCGTGCCTCGTGCCTGGCGGGGTCTG    60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MetSerGlyCysGlyLeuPheLeuArgThrArgLeuArgLeuValAlaAlaCysArgGlyLeu     20

Qy       61 GTGGTGCTCTACCGCGAACCGGCGGCTACTGCCGCCACCAGCCCGTACGAGCTTTCGCC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgProValArgAlaPheAla   40

Qy      121 AAAGAGCTTTTCCTAGGCAAAATCAAGAGAAGAAAGAGTTTCCATTTCCAGAAGTTAGC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       41 LysGluLeuPheLeuGlyLysIleLysLysLysLysGluValPhePheProPheProGluValSer   60

Qy      181 CAAGATGAACTTAATGAAATCAATCAGTTCTTGGACACCGGTGGAAAAATTCTTCACTGAA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuAspThrGlyGlyLysIleLeuHisGluLeuThr   80

Qy      241 GAGGTGGACTCCGAAAAATTGACCAGGAGGAAAATCCAGATGAAACTTTGGAGAAA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 GluValAspSerArgLysIleAspIleLysLysLysIleProAspGluThrLeuGluLys       100

Qy      301 TTGAAGAGCCTAGGGCTTTTTGGGCTGGCAAGTCCAGAGAATATGGTGGCTGGGCTTC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe      120

Qy      361 TCCAACACCATGTACTCAAGACTAGGGAGACATCAGCATGGATGGTCCATCACTGTG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 SerAsnThrMetTyrSerArgLeuGlyLeuGluIleIleSerMetAspGlySerIleThrVal    140

Qy      421 ACCCTGGCAGCGCACCAGCTATTGGCTCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuGlyLeuLeuLysGlyIleIleLeuLeuLysGluGlu  160

Qy      481 CAGAAAGCCAAATACTTGCCTAAACTGGCCTCCGGGGAGCACATTGCAGCCTTCTGCCTC   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu      180

Qy      541 ACGGAGCCAGCCAGTGGGAGCGATGCGATCCAATCCGAGGGCAACCTCAATCCGAGAGTGAA    600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuuSerGlu     200

Qy      601 GACAAGAAGACACTACATCCTCAATGGCTCAATGGCTCTGGATTACTAATGGAGGACTGGCC   660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   901 AACAGCGGCCGGTTCAGCATGGGCGAGCGTCGTGGCTGGCTGCTCAAGAGAGATTGATTGAA   960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlyGluArgValAlaGlySerValAlaGlyLeuLeuLysArgLeuIleGlu   320

Qy   961 ATGACTGCTAGCTACGCCCTGCACAAGGAAACAGTTTAACAAGAGCTCAGTGAATTTGGA   1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrAlaGluTyrAlaCysThrArgLysThrArgLysGlnPheAsnLysArgSerGlnPheGlyGly   340

Qy   1021 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAGAGGCTTACGTCATGGAGGAGTATGACC   1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysLeuHisPheAlaLeuMetAlaGlnArgGlyLeuArgValMetGluSerMetThr   360

Qy   1081 TACCTCACAGCAGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCATCGAGGCAGCC   1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrAlaGlyMetLeuAspPheGlnProGlyPhePheProAspCysSerIleGluAlaAlaAla   380

Qy   1141 ATGGTGAAAGTGTTCAGTTCGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCCTGACACCCGC   1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 MetValLysValPheSerSerGluAlaLeuSerGluAlaAlaLeuGlnIle   400

Qy   1201 CTCGGGGGGCTTGGGCTACACAAGGGGACTATCCGTACGAGCGCATACTGCCTGACACCCGC   1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyGlyLeuGlyLeuTyrThrArgAspTyrProTyrGluArgIleIleLeuArgAspAspThrArg   420

Qy   1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTTCCGGATGTAACCATCGCCCTGACGGGT   1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGluThrAsnGluIleLeuArgMetTyrIleAlaLeuThrArgGly   440

Qy   1321 CTTGCAGCATGCCGGCCGCCATCGACTACTACGGATCCATCATGAGCTTAAACAGGCCAAAGTG   1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuGlnHisAlaGlyArgIleLeuThrArgIleHisGluLeuThrArgIleHisGluLysGlnAlaLysVal   460

Qy   1381 AGCACAGTCATGGATACCGGTTGGCCGGAGGCTTCGGGACTCCCTGGCCCGGAACTGTGAC   1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrArgLeuArgGluArgLeuArgGlyLeuArgArgLeuArgAspAspThrVal   480

Qy   1441 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG   1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrGlyAsnHisGlyValValHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys   500

Qy   1501 TTTGAGGAGACACCTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGCTTGGC   1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGluAspThrThrTyrCysPheGlyArgThrValGluThrArgLeuLeuArgGlyPheGly   520

Qy   1561 AAGACCATCATGGAGGAGCAGCTGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTG   1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrIleMetGluGluGlnLeuTyrTrpSerGlyTrpSerGlyAlaAsnIleLeuIleLeuAsnLeu   540

Qy   1621 TATGGCATGACGGCCGTGCTGTCGCGGGCCAGCCGCTCATCCGCATTGGGCTCCGCAAC   1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn   560

Qy   1681 CACGACCAGCAGGTTCTCTTGGCCAACACCCTCTGCGCTGGAAGCTTACTTGCAGAATCTC   1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 HisAspGlnGlnValLeuLeuAlaAsnThrLeuCysAlaGlyGluAlaTyrLeuGlnAsnLeu   580

Qy   1741 TTCAGCCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA   1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLysLys   600

Qy   1801 GTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCCCACCCTCTGGACACGGACA   1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnGlnIleLeuGluLysAlaArgAlaTyrIleCysAlaHisProLeuAspThrArgProThr   620

Qy   1861 TGC   1863
            |||
Db   621 Cys   621
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RESULT 5
US-10-408-765A-2053
; Sequence 2053, Application US20040101874A1
; Publication No. US20040101874A1

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Qy   1741 TTCAGCCTCCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLysAsp 600

Qy   1801 GTGTCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTCCACCCTCTGACACAGGACA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ValSerGlnGlnIleLeuGluGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy   1861 TGC 1863
          ||
Db    621 Cys 621
```

RESULT 6
US-10-112-944-869
; Sequence 869, Application US/10112944
; Publication No. US20040048249A1
GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249Ale1 Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 869
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(628)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fort
; OTHER INFORMATION: in Example 2
US-10-112-944-869

Alignment Scores:
Pred. No.:   Length: 628
Score: 1.25e-249   Matches: 616
Percent Similarity: 3129.00   Conservative: 2
Best Local Similarity: 99.52%   Mismatches: 3
Query Match: 99.19%   Indels: 0
DB: 91.41%   Gaps: 0
                     15

US-09-945-326-3 (1-1863) x US-10-112-944-869 (1-628)
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Db   201 AspLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy   661 AATATTTTACTGTGTTCGAAAGACTGAGGTCGTTGATTCTGATCAGTGAAAGAC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 AsnIlePhePheThrValPheAlaLysThrGluValValAspSerAspValValLysAsp 240

Qy   721 AAAATCACAGCATTCATAGTAGAAAGAGAACTTGGTGGAGTCACTAATGGGAAACCCGAA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260

Qy   781 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy   841 CCTGTGGAAAACATCCTTGAGAGAGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 ProValGluAsnIleLeuGluArgValGlyAspGlyPheLysValAlaMetAsnIleLeu 300

Qy   901 AACAGCGCCGGTTCAGCATGGCCAGCCTCGTCGCTGCTGGGCTGCTCAAGAGATTGATTGAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AsnSerGlyArgPheSerMetGlySerValAlaAlaValAlaGlyLeuLeuLysArgLeuGlu 320

Qy   961 ATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTAACAAGAGGCTCAGTGAATTGGA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340

Qy  1021 TTGATTCAGGAGAAATTGCACTGATGGCTCAGAGAGGCTTACGTCATGAGAGTATGACC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuIleGlnGluLysLeuHisPheAlaLeuMetAlaGlnArgGlyLeuArgValMetGluSerMetThr 360

Qy  1081 TACCTCACAGCAGCAGGGATCCTGGACCAACCTGGCTTCCCGACTCGCTCCATCGAGGCAGCC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TyrLeuThrAlaAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380

Qy  1141 ATGTGAAGGTGTTCAGTTCCGAGGCCGGCTGGAGTGTGAGTGAGGCGCTGCAGATC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 MetValLysValPheSerSerGluAlaGlyTrpGlnCysValSerGluAlaLeuGlnIle 400

Qy  1201 CTGCAGCGGGCTGGCTACACAAGGACTATCCGTACGAGGCGCATACTGCGTGACACCCGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyLeuGlyLeuGlyTyrThrArgThrIleArgThrArgGluLeuLeuArgAspThrArg 420

Qy  1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCCGGATGTGAATCATCGGCTGTCGACGGGT 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGluGlyThrAsnGluIleLeuAspLeuLeuArgMetCysIleAlaLeuThrGly 440

Qy  1321 CTGCAGCATGCCGGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluHisGluLeuLysGlnAlaLysVal 460

Qy  1381 AGCACAGTCATGGATACCGTTGGCGGAGGCTTCGGAGACTCCCGGAGCCGAACTGTGGAC 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrValGlyGlyGlyPheGlyAspSerArgSerArgThrValAsp 480

Qy  1441 CTGGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTGTGCGACAGTGCCAACAG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrGlyGlnProTrpSerLeuValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy  1501 TTTGAGGAGACAACACCTACTGCTTCGGCCCGACCGTGGAGACACTGGTTCCGCTTTGGC 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuLeuArgPheGly 520

Qy  1561 AAGACCATCATGGAGGAGCAGCTGGTACTGGAAGCGGGTGGCCAACATCCTCATCAACCTG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrIleMetGluGluGlnLeuValLeuGluAlaGlyGlyGlnHisProHisGlnProAla 540

Qy  1621 TATGGCATGACGACGCCCGTGTCCGGGGGCCAGCCCTCCATCCGCATTGGGCTCCGCAAC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TyrGlyMetThrArgAlaValLeuSerArgAlaSerArgIleArgSerIleAlaSerArgAsn 560

Qy  1681 CACGACCACCAGAGTTCTCTTGGCCAACACCTTCTGCGTGCAGAATCTCAGAAATCTC 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 HisAspHisGlnValLeuLeuLeuAlaAsnThrPheCysValGlnAlaTyrLeuGlnAsnLeu 580
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Qy   1081 TACCTCACAGCAGGAGGATGCTGACCAACCTGGCTTTCCGACTGCTCCATGAGGCAGCC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 TyrLeuThrAlaGlyPheLeuArgThrArgMetLeuAspGlnProGlyPheProAspCysProSerIleGluAlaAla 387

Qy   1141 ATGGTGAAGGTGTTCAGCTCCGAGGCCGCTGGCAGTGTGTGAGTGTGAGGGCCTGCGAGATC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 407

Qy   1201 CTCGGGGGCTTGGCTACACAAGGACTATCCGTACGAGCGCCATACTGGTGACACCCGC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    408 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 427

Qy   1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 447

Qy   1321 CTGCAGCATGCCGGCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 LeuGlnHisAlaGlyAlaIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 467

Qy   1381 AGCACAGTCATGGATACCGTTGGCCGAGGCTTCGGACTCCCTGGCCGGCTTGCGGACTGTGGAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    468 SerThrValMetAspThrValGlyArgArgAspSerLeuGlyArgThrValAsp 487

Qy   1441 CTGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 LeuGlyLeuThrGlyAsnHisGluLeuCysThrProSerLeuAlaAspSerAlaAsnLys 507

Qy   1501 TTTGAGGAGAACACCTACTGCTTCGGCCCGATGGAGACCACTGCTGCTCCGTCCGCTTTGGC 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 PheGluGluAsnThrTyrCysPheGlyAlaThrValGluThrGluGlyAlaPheGly 527

Qy   1561 AAGACCATCATGAGGAGGAGAGCCTGGTACTGGAGCGGGTGGTGCCAACATCCTCATGAACCTG 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 LysThrIleMetGluGluGluSerLeuValLeuGluArgValAlaAsnIleLeuIleAsnLeu 547

Qy   1621 TATGGCATGACGGCCGTGCTGTCCGGGCCCAGCCGCCTCCATCCGCCATTGGGCTCCGCAAC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 TyrGlyMetThrAlaValLeuSerGlyProSerArgLeuHisProProLeuGlyLeuArgAsn 567

Qy   1681 CACGACCACGAGGTTCTCTTGGCCAACACACCTTCTGCGTGGAAGTTACTTGCAGAATCTC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 HisAspHisGluValLeuLeuAlaAsnThrProPheCysValGluValLeuGlnAsnLeu 587

Qy   1741 TTCAGCCCTCTCAGCTGACAAGCTGATGCTCCAGAAAACCTAGTGAGCAGATTAAGAAA 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGlnIleLeuLysLys 607

Qy   1801 GTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCACCCTCGGACAGGACA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaThrLeuProLeuAspArgThr 627

Qy   1861 TGC 1863
          |||
Db    628 Cys 628
```

RESULT 7

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Qy   1   ATGAGCGGCTGCGGGCTCTTCCTGCGCACCACGGCTGCGGCTGCGCTGGCGGGGTCTG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8   MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 27

Qy   61  GTGGTCTCTACCGGCGAACCGGCTACTGCGCCGACCACGGCCGCCGTACTGAGCGTTTCGCC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28  ValValSerThrArgAlaAsnArgLeuLeuArgThrSerProProValArgAlaPheAla 47

Qy   121 AAAAGCTTTCCTAGGCAAAATCAAGAAGAAGAAGTTTCCCATTCCAGAAGTTAGC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   48  LysGluLeuPheLeuGlyLysLysLysLysGluValPheProPheProGluValSer 67

Qy   181 CAAGATGAACTTAATGAAATCAATCAGTTCTTTGGACCCCTGGAAAAATTCTTCACTGAA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68  GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 87

Qy   241 GAGGTGGACTCCCGAAAAATTGACCAGGAGGGAAAATCCAGATGAAACTTTGGAGAAA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88  GluValAspSerArgArgLysIleAspGlnGluGlyLysIleProAspGluValGluLys 107

Qy   301 TTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTCCCAGAAGAATATGTCGCCTGGGCTTC 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe 127

Qy   361 TCCAACACCATGTACTCAGAGTACTAGGGGGATCATCAGCATGGGTCCATCACTGTG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 SerAsnThrMetTyrSerArgLeuGlyGluThrMetAspGlySerIleThrVal 147

Qy   421 ACCCTGGCCAGCGCCACCAGGTCATTGGCCTCAAGGGGATCATCTTGGCTGCACTGAGGAG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 ThrLeuAlaAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 167

Qy   481 CAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGCAGCCTTCTGCCTC 540
         :::|||||||||||||||||||||||||||||||||::|||||||||||||||||||||
Db   168 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyAspAlaAla***IleArgSerGlyAlaLeuAlaAlaLeuAlaAlaPheCysSerLeu 187

Qy   541 ACGGAGCCAGCCAGCGGATGCAGCTCAATCCGAGCAGAGCCACACTAAGTGAA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 ThrGluProAlaAlaAsnGlySerAspAlaAla***IleArgSerArgAlaThrLeuSerGlu 207

Qy   601 GACAAGAAGCTACTACATCCTCAAGTGTCTGGATTACTAATGGAGGAGACTGGCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 AspLysLysHisTyrIleLeuLysValSerValTrpIleIleThrAsnGlyGlyLeuAla 227

Qy   661 AATATTTTTACTGTGTTTGCAAAGACTGAGGTGGTCGTTGGATTCTGATGGATCAGTGAAAGAC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 247

Qy   721 AAAAATCACAGCATTCATAGTAGAAAGAACTTTGGTGAGTCACTAATGGGAAACCCGAA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 LysIleThrAlaPheHisSerArgArgAsnProPheGlyGlyValThrAsnGlyLysProGluGlu 267

Qy   781 GATAAATTAGGCATTCGGGCTCCAAACTTGTGAAGTCCATTTGAAAACACCAAGATA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 287

Qy   841 CCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAGTGGCCATGAACATCCTC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   288 ProValGluAsnIleLeuGluValGlyGluValGlyPheLysValAlaMetAsnIleLeu 307

Qy   901 AACAGCGGCCGGTTCAGCATGGGCAGCCAGCGGCTCGTCGTGGCTGCTCAAGAGATTGATTGAA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   308 AsnSerGlyArgPheSerMetGlySerGlnArgLeuValValAlaGlyLeuLeuLysArgLeuIleGlu 327

Qy   961 ATGACTGCTGAGTACGCCCTGCACAAGGAAACAGTTAACAAGGACTCAGTGAATTTGA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 MetThrAlaGluTyrAlaCysThrArgLysThrArgLysAsnLeuArgGlnLeuArgLeuValSerGluLeuGlnLeuPheGly 347

Qy   1021 TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCACTGGAGAGTATGACC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   348  LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValThrGlyGluSerMetThr 367
```

```
; TYPE: PRT
; ORGANISM: Mouse
US-10-362-537-10

Alignment Scores:
Pred. No.:          2.8e-103
Score:              1360.00
Percent Similarity: 66.05%
Best Local Similarity: 48.24%
Query Match:        39.73%
DB:

Length:        655
Matches:       287
Conservative:  106
Mismatches:    184
Indels:        18
Gaps:          9

US-09-945-326-3  (1-1863) x US-10-362-537-10  (1-655)
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Qy    103  CCTGTACGAGCT----------------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAG  150
                |||  ||||                 ||||||  |||:::::     ||||
Db     66  ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrIle  85

Qy    151  AAAGAAGTTTTCCATTCCAGAAGTT---AGCCAAGATGAACTTAATGAAATCAATCAG  207
                ::::||||||||||||||:|||    |||       ::: :::
Db     86  AspGlnValPhePraSerValLeuSerGluGluGlnAlaGlnPheLeuLysGlu  105

Qy    208  TTCTTGGGACCCGTGAAAAATCTTCACTGAAGAGGTGGACTCCCGAAAAAATTGACCAG  267
               |||||||||   :|||:|||  |||||  |||||||  ||||||||||||
Db    106  LeuValGlyProValAlaArgPhePheGluGlnValAlaAspProAlaLysAsnAspAla  125

Qy    268  GAAGGGAAAATCCCAGAAGAAACTTGAGAAATGAAGAGCCTAGGGCTTTTGGGCTG  327
               ::|:||||||||   |||:| ||||||:::|       ||||
Db    126  LeuGluLysValGluAspAspThrLeuGlnIleLeuLysGluLeuGlyLeuGlyLeu  145

Qy    328  CAAGTCCCAGAAGAATATGTGGCCTTCTCCAACACCATGTACTTCAAGACTAGGGG  387
               ||||||||||||    |||   |:|||||||||||   |:|||
Db    146  GlnValProSerGluLeuGlyLeuGlyLeuGlyLeuSerAsnThrGlnTyrArgLeuAla  165

Qy    388  GAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGCAGCCAGGCTATT  444
                |||||||||||   |||:  ||||||||  |||||  ||||||||
Db    166  GluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSerIle  185

Qy    445  GGGCCTCAAGGGGATCATCTTGGCTGCCACTGAGGAGCAGAAAGCCAAATACTTGCTAAA  504
               ||  ||||||||||||:::|||||| ::: ||||||||||||:::
Db    186  GlyPheLysGlyGlyIleLeuLeuTyrGlyThrArgAlaGlnArgGluGluTyrLeuProArg  205

Qy    505  CTGGCGTCCGGGGAGCACATTGCAGCCTTGCAGCCGAGCCAGTGGAGGCGAT  564
              ::|||||||||    :::  |||||||||||||  ||||||||||||
Db    206  ValAlaSerGlyValGlnAlaLeuAlaAlaPheCysAsnCysLeuSerGlySerAsp  225

Qy    565  GCAGCCTCAATCCGGGAGCAGCAGCCACACTAAGTGAAGACAAGAAGCCACTACATCCTCAAT  624
               ||||| :::|||||||||||||||  |||:: ||||||||||
Db    226  ValAlaSerIleArgSerSerAlaIleProSerProCysGlyThrLysTyrThrThrLeuAsn  245

Qy    625  GGCTTCCAAGGTCTGATTACTAATGAGGACTGGCCAATATTTTACTGTGTTTGCAAAG  684
               |||||||||||:::|||||    ||||||||:::|||||||||||||
Db    246  GlySerLysIleTrpIleSerAsnGlyGlyLeuAlaLeuThrValPhePheValPheAlaLys  265

Qy    685  ACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAGAAACAAAATCACAGCATTCATAGTA  741
               |||   ||   |||    ::|  ||   |||||||||||||||:::
Db    266  ThrProIleLysAspAlaThrAlaThrGlyAlaAlaLysLysIleGluLysThrIleThrGlyAla  285

Qy    742  GAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGGC  801
               |||||||||||||||||||    ||||||||||:::||||||:::
Db    286  GluArgSerPheGlyGlyValThrProGlyPheLeuProGluLeuLysMetGlyIleLysAla  305

Qy    802  TCCAACACTTGTGTGAGTCCATTTTGAAAACACCAAGATACCTGTGAAAACATCCTTGA  861
               ||||||||||:::||||     ::::    ||||||||||:::||||||||
Db    306  SerAsnThrSerGluValTyrPheGluAspSerGlyValLysValLysProSerGluAsnValLeuGly  325

Qy    862  GAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATG  921
               ||||||||||||||||||||||||||||  |||||||||||||:::|||
Db    326  GluValGlyAspGlyPheLysPheGlyValAlaLeuAsnIleLeuAsnAlaAsnGlyArgPheGlyMet  345

Qy    922  GGCAGCGTCGTGGGCTGCTCAAGAGATGATTGAAGATGACTGCTGAGTACGCCCTGC  981
               ||||||||||||||||||||||||||||||||||:::|||:::||||||
Db    346  AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysAlaAlaLysAlaValAspHisAlaThr  365
```

```
Qy    982  ACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTGGATTGATTCAGGAGAAATTTGCA  1041
              |||||| |||||||||||||||||||||||||||||||||:::::
Db    366  AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValValIleGluGlnLysLeuAla  385

Qy    1042  CTGATGCTCAGAAGGCTTACGTCATCGAGAGTATGACCACTCACTCACAGCAGGGATGCTG  1101
               |||||| ||||||||||||||:::  :::  ||| ::: :::
Db    386  ArgMetAlaLeuLysAlaTyrValIleGluSerMetAlaTyrMetLeuSerAlaAsnMet  405

Qy    1102  GACCAACCTGGCTTTCCCGACTGTCTCCATCGAGGGCAGCCATGGTGAAGGTGTTCAGCTCC  1161
               ||||||||||||||| ||||||||||||||||||||:::||||||||||
Db    406  AspGln---GlyPheLysLysAspPheGlnIleGluAlaAlaIleSerLysLysIlePheCysSer  424

Qy    1162  GAGGCCGGCCTGCAGTGTGTGAGTGAGGCGCGTCAGATCCTCGGGGGCTTGGGCTACACCA  1221
              ||||||||||||||||||||||||||||||||||:::||||||  :::
Db    425  GluAlaAlaTrpValAlaAspGlyCysIleGlnIleMetGlyMetGlyMetPheMet  444

Qy    1222  AGGGACTATCCTACGAGCGCATACTGCGTGACACCCGCCATCTCCTCATCTTCGAGGGA  1281
              :::::  ||||||||||:::||||||||||||||||||||  ||||||
Db    445  LysGluProGlyValGluArgValLeuArgAspThrArgIleArgIleArgPheGluGly  464

Qy    1282  ACCAATGAGATTCTTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCCGCATC  1341
               |||||||||||||||||  :::||||||||||||||||||||||||||
Db    465  AlaAsnAspIleLeuArgLeuPheValAlaLeuPheValAlaLeuGlnCysMetAspLysLysGlu  484

Qy    1342  CTGACTACCAGCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGTCATGGAT  1395
              ||||||||||||||:::         |||:::||||
Db    485  LeuThrGlyLeuGlyLysAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly  504

Qy    1396  ACCGTTGGCCGGAGGTTCGGGACTCTTGGTGCCGCCGAACTGTGGACCTGGGGCTGACAGGC  1455
              ||||||:::||||||||||||||||||  ||||||||||||:::--
Db    505  GluAlaGlyIleGlnLeuArgArgArgArgThrGlyLyIleGlyLySerGlyLySerLeuSer--  523

Qy    1456  AACCATGGAGTTGTGCACCCCAGTGTGCGACAGTGCCAACAAGTTTGAGGAGAACACC  1515
              :::      |||||
Db    524  ------GlyIleValHisProGlyLeuSerArgSerGlyGluLeuValAlaValGlnAlaLeu  541

Qy    1516  TACTGCTTCGGCGCCGTGGAACGTGCTGCTGCCGTTGGCAAGACCATCATGGAG  1575
              |||||||||||||||||  ||||||||||||||||||||:::||||||
Db    542  AspGlnPheAlaThrValGluAlaValLeuAlaLeuValLysHisLysLysValIleValAsn  561

Qy    1576  GAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACCGCC  1635
              ||||| :::||||||||||||||  ||||||||||||||||||||:::
Db    562  GluGlnPheLeuLeuLeuGlnArgLeuArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValVal  581

Qy    1636  GTGCTGTCGCGGGGCCAGCCGCTCCATCCGAATTGGGCTCCCCAACCACGACCAGAGTT  1695
              |||||||||||||  ||||||||||  ||||||||||||:::
Db    582  ValLeuSerArgArgAlaSerArgLeuSerGluGluGlyLyTyrProThrAlaGlnHisHisGluLys  601

Qy    1696  CTCTTGGCCAACACCTTCTGCGGTGAAGCT--------TACTTGCAGAATCCTTCAGC  1746
              :::||     |||||||||||||| ------  ::: :::||||||
Db    602  MetLeuCysAspSerTrpCysIleArgGluAlaAlaThrArgIleArgGluAsnMetAlaSer  621

Qy    1747  CTCTCTCAGCTGGACAAGATGTCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCC  1806
              |||   :::||||||||||||||||||||||||  :::  ||:::
Db    622  LeuGlnSerProGlnHis------GlnGluLeuPheArgAsnPheArgSerIleSer  639

Qy    1807  CAGCAGATCCTTGAGAAGGCAGCCTATATCTGTGCCCACCCTCTG  1851
              :::  :::||||||||||||||||||  ::::|||||
Db    640  LysAlaMetValGluAsnGlyGlyLeuValThrGlyValAsnProLeu  654
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```
RESULT 8
US-10-362-537-9
; Sequence 9, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: IRAP Binding Protein
FILE REFERENCE: 2774 USOP
CURRENT APPLICATION NUMBER: US/10/362,537
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: JP 2000-254263
PRIOR FILING DATE: 2000-08-21
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; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Rat
US-10-362-537-9

Alignment Scores:
Pred. No.:           5.45e-103      Length:          653
Score:               1356.50        Matches:         295
Percent Similarity:  63.36%         Conservative:    108
Best Local Similarity: 46.38%       Mismatches:      192
Query Match:         39.63%         Indels:          41
DB:                                 Gaps:            12
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US-09-945-326-3 (1-1863) x US-10-362-537-9 (1-653)

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Qy    25  CGCACCACCGGCTGCGGCTCGTGCCTGCCCGGGGTCTTGGTGCTGTCTCTACCCGCGAACCGGCGG   84
          |||    |||||||     ||||:
Db    32  ArgProThrSerAlaGlnArg---------------LeuTyrAlaSerGluAlaThrGlnAla   47

Qy    85  CTACTGCGC-----------------------------------------ACCAGCCGCCTGTACGA   111
          :::||||
Db    48  ValLeuLeuLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAlaArg   67

Qy   112  GCT----------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAGAGAAAGAAGTT   159
          |||                ||||||     |||     ::|||
Db    68  AlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnVal   87

Qy   160  TTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA--------------ATCAAT   204
          |||||||
Db    88  PheProTyrProSerVal---------------LeuAsnGluGlyGlnThrGlnPheLeuLys   103

Qy   205  CAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGAC   264
          :::  ||||||||||     |||     |||
Db   104  GluLeuValGlyProValAlaArgPheAlaGluPheGlnIleGluValAlaLeuAsnAsp   123

Qy   265  CAGGAGGGAAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGAGCCTAGGCTTTTTGGG   324
          :::    ::||||:||||||     ||||||||||
Db   124  SerLeuGluLysValGluGluGluAspThrLeuGlnGlyLeuLysGlyAlaPheGly   143

Qy   325  CTGCAAGTCCAGAGAGAATATGGTGGCCTGGGCTTCTCCAACACCATGTACTCAAGACTA   384
          ||||     ||||||||||     |||||||
Db   144  LeuGlnValProSerGluGlyLeuGlyLeuGlyLeuSerAsnThrGlnTyrAlaArgLeu   163

Qy   385  GGGGAGATCATCAGCATG---GATGGGTCCATCACTGACCCCTGGCACAGGCCACCAGGCT   441
          :::||||||||     |||
Db   164  AlaGluIleIleGlyMetHisAspLeuProLeuValLeuSerValThrLeuGlyAlaHisGlnSer   183

Qy   442  ATTGGCCTCAAGGGGATCATCTTGGCTGCACTGGAGAAATACTTGCCT   501
          |||||:||     ||||||     :||||     ::|||
Db   184  IleGlyPheLysGlyIleIleLeuAlaLeuTyrGlyThrLysAlaGlnLysGluLysTyrLeuPro   203

Qy   502  AAACTGGCGTCCGGGGACACATTGCAGCCTTCTGCCTCACGGAGCCCAGGTGGGAGC   561
          |||||     ::||||:     ||:
Db   204  ArgValAlaSerGlyValAlaLeuAlaLeuTyrThrGluSerSerGlySer   223

Qy   562  GATGCAGCCTCAATCCGGAGCAGCGAGAGCCACCTAAGTGAAGAAGCACTACCATCCTC   621
          |||     ||||||     ||:
Db   224  AspValAlaSerIleArgSerArgAlaProSerArgValProSerGlyCysGlyLysTyrTyrThrLeu   243

Qy   622  AATGGCTCCAAGGTCTGGATTACTAATGAAGGAGACTGGCCCAATATTTTTACTGTGTTTGCA   681
          ||||||     ||||||     |||||     |||||
Db   244  AsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPheAla   263

Qy   682  AAGACTGAGCTCGTTGAT---TCTGATGAGTCAGTGAAGAAGACAAAATCACAGCATTCATA   738
          |||||     |||     :||
Db   264  LysThrProIleLysProAspAlaAlaThrGlyAlaValAllGlyAlaValLysGluLysIleThrPheAlaPheVal   283

Qy   739  GTAGAAAGAGACTTTGGTGGAGTCACTAATGGAGAAACCCGAAGATAAATTAGGCATTCGG   798
          ||||||     :||||:||
Db         ...
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Right column (amino acid / nucleotide alignment):

```
Db   284  ValGluArgSerPheGlyGlyValThrHisGlyLeuProGluProGluLysMetGlyGlyIleLys   303

Qy   799  GGCTCCAACACTTGTGAAGTCAGTCCATTTGAAAAACACCAAGATACCTGTGGAAAACATCCTT   858
          |||||     ||||||     ::::
Db   304  AlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnValLeu   323

Qy   859  GGAGAGTCGGAGATGGTTAAGGTGCCATGAACATCCTCAACAGCGGCCGGTTCAGC   918
          ||||||||||||     |||:::|||
Db   324  GlyGluValGlyAspGlyPheLysValAlaValAlaAsnIleLeuAsnGlyArgPheGly   343

Qy   919  ATGGGCCAGCGTCGTGCTGGGCGCTGTCAAGAGATTGATTGAAATGACTGCTGAGTACGCC   978
          ||:::     :::|||     ::|||
Db   344  MetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleAlaLysAlaValAspHisAla   363

Qy   979  TGCACAAGGAAACAGTTAACAAGAGGCTCAGTGAATTGGATTGATTCAGGAGAAATT   1038
          :::     |||||||
Db   364  ThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeu   383

Qy  1039  GCACTGATGGCTCAGAGAGGCTTACGTCATGGAGAGTMATGACCTACCTCACAGCAGGGATG   1098
          |||     |||||:     :::
Db   384  AlaArgMetAlaIleLeuGlnTyrValThrGluSerMetLeuSerAlaAsn   403

Qy  1099  CTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGCAGCAGCCATGTGAAGTGTTCAGC   1158
          :::|||     |||||||||
Db   404  MetAspGln--GlyPheLysAspPheGlnIleGluAlaAlaIleAlaIleSerLysLysIleSerPheGlyIle   422

Qy  1159  TCCGAGGCCGCCGCCAGTGTGTGAGTGAGGCCGTGCAGATCCTCCGGGGCTTGGGCTAC   1218
          ||||||||||     :||||||||||
Db   423  SerGluAlaAlaTrpLysValThrArgSerIleGlnIleIleMetGlyValMetGlyPhe   442

Qy  1219  ACAAGGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGCATCCTCATCTTCGAG   1278
          |||     ||||||||||     :||
Db   443  MetLysGluProGlyValGluArgValAlaArgAspIleArgIleGlnPheGlu   462

Qy  1279  GGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGCCGGC   1338
          ||||||||||     :::
Db   463  GlyThrAsnAspIleLeuArgLeuProPheAlaAlaLeuGlnHisGlyMetAspLysGlyLys   482

Qy  1339  ATCCTGACTACCAGGATCCATGAGCTCATGAGCTCTAAACAG------GCCAAAGTGAGCAGCAGTCATG   1392
          ||||||     |||||
Db   483  GluLeuThrGlyLeuGlyLeuAsnAlaLeuLeuLysAsnProLeuGluValAsnValGlyLeuLeuIle   502

Qy  1393  GATACCCGTTGGCCGGAGGCTTCGGGACCTCCCTGGGCCGAACTGTGGACCTGGGCTGACA   1452
          |||||     |||||||
Db   503  GlyGluAlaSerLysGlnLeuArgArgArgThrGlyIleLeuGlySerGlyLeuSerLeuSer   522

Qy  1453  GGCAACCATGAGTTGTGCACCCCAGTCTTCGGACAGTGCCAACAAGTTGAGGAGAAC   1512
          ||||||     :::     |||
Db   523  --------GlyIleValHisProGluLeuSerArgSerGlyGluLeuValAlaValGlnAla   539

Qy  1513  ACCTACTGCTTCGGCCGACCGTGGAGGACACTGCTGCTCCGCCTTTGCCAAGACCATCATG   1572
          |||||||     ::|||
Db   540  LeuGluGlnPheAlaThrValValGluAlaAlaLeuMetLysHisLysGlyIleIleVal   559

Qy  1573  GAGGAGCAGCAGTCTGGTACTGGACGCGGTGGCCAACATCCTCATCAACCTGTATCGGCATGACG   1632
          ||||||     :::||:||     |||
Db   560  AsnGluGlnPheLeuGluGlnLeuAsnArgGluValAlaAspProLeuTyrAlaMetVal   579

Qy  1633  GCCGTGCTGTCGCGGGCCAGCCGCTCCATCCGCATTGGGCTGTATCCGACCACCACGAG   1692
          |||||||
Db   580  ValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGlu   599

Qy  1693  GTTCTTCTTGGCCAACACCTTCTGCGTGGAAGCT-------TACTTGCAGAATCTCTTC   1743
          :::||     |||||||||
Db   600  LysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAla   619

Qy  1744  AGCCTCTCTCAGCTGGACAAGTATGTCCAGAAAACCTAGATGAGCAGATTAAGAAGTG   1803
          ||||||     |||
Db   620  SerLeuGlnSerAsnProGln------GlnIleGluLeuPheArgAsnPheArgSerIle   637

Qy  1804  TCCCAGCAGATCCTTGAGAAGCAGACCTATATCTGTGCCCACCCCTCTG   1851
          :::|||     |||||||
Db   638  SerLysAlaMetValGluAsnGlyGlyLeuAsnGlyLeuValThrSerAsnProLeu   653
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RESULT 9
US-10-362-537-11

; Sequence 11, Application US/10362537
; Publication No. US20040008510A1
GENERAL INFORMATION:
   APPLICANT: Takeda Chemical Industries, Ltd.
   TITLE OF INVENTION: IRAP Binding Protein
   FILE REFERENCE: 2774 USOP
   CURRENT APPLICATION NUMBER: US/10/362,537
   CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Bovine
US-10-362-537-11

Alignment Scores:
Pred. No.:   4.8e-102   Length: 655
Score: 1345.00   Matches: 285
Percent Similarity: 65.51%   Conservative: 110
Best Local Similarity: 47.26%   Mismatches: 194
Query Match: 39.29%   Indels: 14
DB: 15   Gaps: 9

US-09-945-326-3 (1-1863) x US-10-362-537-11 (1-655)

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Qy    67  TCTACGGCGACCGGCGGCTACTGCGCACCAGCCCGCTGCGGAGCTTTCGCCAAAGAG    126
              |||   |  ||||||    ||   ::       |||   |||||||||||:|||
Db    57  SerGluAlaSerThrArgGlyLysArgAlaAsnSerValSerLysSerPheAlaValGly  76

Qy   127  CTTTTCCTAGGCAAAATCAAGAGAAAGAGAGTTTCCCATTTCCAGAAGTT--AGCCAA   183
              ||| |:||||    :::||||||||||||||| |||    :    :::|||
Db    77  ThrPheLysGlyGlnLeuThrThrAspProTyrProSerValLeuAsnGlu  96

Qy   184  GATGAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAG   243
              |||    ::       :::    || |||  ||||||||||||||||||||||
Db    97  AspGlnThrGlnPheLeuLysLysGluLysValGlyProValThrArgPheGluGluVal  116

Qy   244  GTGGACTCCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAAATTG   303
              :::       |||       ::|   :::     ::|   ::
Db   117  AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluGluThrMetGlnGlyGlyLeu  136

Qy   304  AAGAGCCTAGGGCTTTTGGGCTCAAGTCCCAGAAGAATATGGTGGCCTGGGCTTCTCC   363
              ||||  ||||||||  |||||||||||:     |||||:
Db   137  LysGlyLeuLeuGlyLeuAlaPheGlyLeuLysProAsnGluValGlyLeuValGlyLeuCys  156

Qy   364  AACACCATGTACTCAAGACTAGGGGAGATCATCAGCATG---GATGGTCCATCACTGTG   420
              ||||||:     :: |||      |:     |||||:   |||||||||||||
Db   157  AsnThrGlnTyrAlaArgLeuValAlaArgLeuValGlyIleValGlyMetTyrAspGlyAlaValGlyIleIle  176

Qy   421  ACCCTGGCCAGCCGCCACCAGCCTATTGCCTCAAGGGATCATCTTCGCCTGCACTGAGGAG   480
              ||||||:||||||:::||||||  ||||||||||  :::
Db   177  ValLeuGlyAlaHisGlnSerIleGlyTyrIlePheLysGlyLeuLeuPheGlyThrLysAla  196

Qy   481  CAGAAAGCCAAATACTTGCCTAAACTGGGCTCCGGGGAGCACATTGCAGCCTTCTGCCTC   540
              ||||||||||||||||||||||||||||||||||||  :|||||||||||||||||:
Db   197  GlnLysGlyLeuLysProLysLeuGlySerGlyGluHisIleAlaAlaPheCysLeu  216

Qy   541  ACGGAGGCCAGCCAGTGGGAGCCGATGCCAGCTTCAATCCGGAGCAGAGCCACACTAAGTGAA   600
              ||||||||||||||||||||||:      :: ||||||||||||||||:
Db   217  ThrGluProSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro  236

Qy   601  GACAAGAAGCAGCTACATCCTCAATGGCTCCAAGGTTCTGGATTACTAATGAAGGACTGGCC   660
              ||||||||:      ||||||||  ||||||  :::|||||||||||||||:
Db   237  CysGlyLysTyrTyrThrLeuAsnGlySerLysSerIleTrpIleSerAsnGlyLysLeuAla  256

Qy   661  AATATTTTTACTGTGTTTGCAAAGACTGAGTCGTTGAT---TCTGATGATCAGTGAA   717
              ::||||||  ||| |    |||
Db   257  AspIlePheThrValPheAlaAlaLysThrProValThrAspThrArgThrGlyAlaValLys  276

Qy   718  GACAAATCACAGCATTCATAGTAGAGAAAGAGACTTGGTGGAGTCACTAATGGGAAACCC   777
              |||||||||||||||||||    ||||||||:||||||||||||||:       :::||||||
Db   277  GluLysIleThrAlaPheValValGluArgSerPheGlyLysValThrHisGlyValThrGlyProPro  296

Qy   778  GAAGATAAATTAGGCATTCGGGGCCTCCAACACTGTGAAGTCCATTTGAAAACACCAAG   837
              ||||||:      |||:||||||     ||||||||||||||:::||||||||||||||
Db   297  GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg  316

Qy   838  ATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATC   897
              ::||||   |||     ||:     ||||||||||  |||||||||||:||||||||
Db   317  ValProAlaGluAsnValLeuGlyGluValGlyGlyTrpLeuArgTrpProMetAsnIle  336

Qy   898  CTCAACAGCGGCCGGTTCAGCATGGGCAGCCTTCGTGGCTGGCCTGCTTCAAGAGATTGATT   957
              |||||||||||||||||||||||||:      |||||||||||   :::||||||||||
Db   337  LeuAsnAsnGlyArgPheGlyMetAlaAlaAlaAlaLeuAlaGlyThrMetLysGlyIleIle  356

Qy   958  GAAATGACTGCTGAGTACGCCTGACACAAGAACAGTTAACAGAGAGCTCAGTGAATTT   1017
              ::       |||||||||||::|  ::       |||||||||||||||||::
Db   357  AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsnPhe  376

Qy  1018  GGATTGATTCAGGAGAAATTGCACTGATGGGCTCAGAAGGCTTACGTCATGGAGAGTATG   1077
              ||||||||:      ::  ||:  :||||||||:     ||||||||||||||||||
Db   377  GlyLeuIleGlnGluLysLeuAlaLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet  396

Qy  1078  ACCTACCTCACAGCAGCAGGGATGCTGGACCTTCCCGACTGCTCCATCGAGGCA   1137
              |||||:      ::    ::|||  |||||||||||||||||||||||||:
Db   397  AlaTyrMetValSerAlaAsnMetAspGln--GlySerThrAspPheGlnIleIleGluAla  415

Qy  1138  GCCATGGTGAAGGTGTTCAGTCCAGGCCGCCTGGCAGTGTGAGTGGGCCTGCAG   1197
              |||||||||||||||||    ||||||||:     ||||||||||||||:  :|||
Db   416  AlaIleSerLysIlePheGlySerGluAlaLeuAlaAlaTrpLysValThrArgAspGlyCysIleGln  435

Qy  1198  ATCCTCGGGGCCTTGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCGTGCACACC   1257
              |||::::||||||||||:     ||||  ||:      |||||||||||||||||
Db   436  IleMetGlyIleGlyPheMetLysGluGluGlyProGlyLysValLeuArgValAspLeu  455

Qy  1258  CGCATCCTCCTCATCTTCGAGGGAACCAATGAGAATTCTCCGGATGTACATCGCCCTGACG   1317
              ||||||:      ||||||||||||||||||    ::|||||||||||:
Db   456  ArgIlePheArgIleGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnLeuGln  475

Qy  1318  GGTCCAGCATGCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG------   1371
              ||||:     ::: ::       ::    :::       ||||||:||||||
Db   476  GlyCysMetAspLysLysGlyLysGluLeuSerGlyLeuAsnAlaLeuLysAsnProPhe  495

Qy  1372  GCCAAGTGACCAGCACAGTCATGGAACATCCGTGGTACTGGACTCCCGGGCCGA   1431
              ||||||||||||||||:      :::    ||||||||||:
Db   496  GlyAsnAlaGlyLeuLeuGlyLeuAlaGlyLysGlnLeuGlnLeuArgArgArgAlaGlyLeu  515

Qy  1432  ACTGTGGACCTGGGGCTGACAGGCAACCATGAGTTGTGACCCCAGTCTTGCGGACAGT   1491
              ||||||||||||||||:     ||||||||:     |||||||||||||:
Db   516  GlySerGlyLeuSerLeuSer-------GlyIleValHisGlnGluSerArgSer  532

Qy  1492  GCCAACAAGTTGAGGAGAACAACTACTGCTTCTTGGGCAACACTGCTGCTC   1551
              ||||||||||||||  :::||||||||||||||||||||||||||||||:
Db   533  GlyGluLeuAlaValGlnAlaGlnLeuGluGlnPheAlaThrValAlaLysLeuIle  552

Qy  1552  CGCTTTGCCAAGAACCATCATGGAGGAGGGGTGCCAACATCCTC   1611
              ::       :::|||     |||||||||||||||||:
Db   553  LysHisLysLysAspIleIleAsnGluGlnLeuLeuGlnLeuArgLeuGluAspSerAla  572

Qy  1612  ATCAACCTGATGCATGAACGGCCGTCGTCGGGCCGCCTCCATCCCGCCATTGGG   1671
              |||||||||||||||:      ||  |||||||||||||||||||:
Db   573  IleAspLeuTyrArgAlaMetValAlaLeuValValLeuGlnAlaSerArgSerGluGly  592

Qy  1672  CTCCGCAACCACGACCACGAGGTTCTTGGCAACACCTTCTGCGTGGAAGCT------   1725
              |||||||||||||||||||||:      ::       ||||||||||||
Db   593  HisProThrHisGlnHisGluLysMetLeuCysLysAspSerTrpCysIleGluAlaAlaAlaAla  612

Qy  1726  ---TACTTGCGAATCTTCTTCAGCCTCCTCAGCTGACAAGTATGCTGCAGAAAACCTA   1782
              :::|||    |||
Db
```

```
Db    613  ArgIleArgAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlu---Leu  630
Qy   1783  GATGACGCAGATCAGAAAGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCTGTGCC  1842
                      |||  ::::::|||||   :::::|||| :::::|||
Db    631  PheArgAsnPheLysSerIleSerLysAlaLeuValGlnArgGlyGlyValThrSer     650
Qy   1843  CACCCTCTG  1851
           ::|||||||
Db    651  AsnProLeu  653
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RESULT 10
US-10-362-537-1

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; Sequence 1, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
;  APPLICANT: Takeda Chemical Industries, Ltd.
;  TITLE OF INVENTION: IRAP Binding Protein
;  FILE REFERENCE: 2774 USOP
;  CURRENT APPLICATION NUMBER: US/10/362,537
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: JP 2000-254263
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: JP 2000-276633
;  PRIOR FILING DATE: 2000-09-07
;  NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 1
;  LENGTH: 655
;  TYPE: PRT
;  ORGANISM: Human
US-10-362-537-1
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```
Alignment Scores:
Pred. No.:        5.61e-99          Length:           655
Score:            1308.00           Matches:          276
Percent Similarity: 64.97%          Conservative:     106
Best Local Similarity: 46.94%       Mismatches:       194
Query Match:      38.21%            Indels:           12
DB:               15                Gaps:             8
```

US-09-945-326-3 (1-1863) x US-10-362-537-1 (1-655)

```
Qy    109  CGAGCTTTCCCCAAAGAGAGCTTTCCTAGGCAAAATCAAGAAGAGAAAGAAGTTTCCCATTT  168
                :::::|||||    ||||| |  :::|||  :::::|||||
Db     71  LysSerPheAlaValGlyMetPheLysGlyGlnIleuThrThrAspGlnValPheProTyr  90

Qy    169  CCAGAGAACTTAGCCAAGATGAACTTAATGAA--ATCAATCAGTTCTTGGGACCCGTGGAA  225
            |||  :::|||||||||::: :::  :::::||  :::  ::  |||||
Db     91  ProSerValLeuAsnGluGlnThrGluGlnThrGlnPheLeuLysGluValGlyProValSer  110

Qy    226  AAATTCTTCACTGAAGAGGTGGACTCCCCAGAAAAATTGACCAGGAAGGGAAAATCCAGAT  285
            ||||||||||||| |||:::|||||:::     ::: |||||||||||
Db    111  ArgPheGluGluValAsnAspProAlaLysAsnAspProAlaLeuGluMetValGluGlu  130

Qy    286  GAAACTTTGGAGAAATTGAAGAGCCTAGGCGTTTTGGGCTGCCAAGTCCCAGAAGAGAAATAT  345
                :::  |||||||||||||||:::|||||||||||||
Db    131  ThrThrTrpGlnGlyLeuLysGluLeuGlyAlaPheHisGlyLeuGlnIleuProSerGluLeu  150

Qy    346  GGTGGCCTGGGCTTCCCAACCATGTACTACCAAGACTAGGGAGGATCATCAGCATG---  402
            |||  :::|||   |||:::|||::: |||||||||
Db    151  GlyLeuGlyValGlyLeuCysAsnThrGlnThrTyrAlaArgLeuValGluValGlyMetHis  170

Qy    403  GATGGGTCCATCACTGTGACCCTGCAGCCGCACCAGGCTATTGGCCTCAAGGGGATCATC  462
            :::  ::: |||||||||||||||||||
Db    171  AspLeuGlyValGlyIleThrLeuGlnHisGlnAlaHisGlnSerIleGlyPheLysGlyIleLeu  190

Qy    463  TTGGCTGACTGAGGGACGAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCAC  522
            |||  :::|||   ||||||||||
Db    191  LeuPheGlyThrLysGluLysGlyLysTyrLeuProLysLeuAlaSerGlyLeuGluThr  210

Qy    523  ATTGCAGCCCTTCGCCTCACGGAGCCCAGTGGGAGCCATGCAGCCTCAATCCGGAGC  582
            :::|||||||||   :::::|||||
Db    211  ValAlaAlaPheCysLeuGlyProSerSerGlySerAspAlaAlaSerIleArgThr  230
```

```
Qy    583  AGAGCCACACTAAGTGAAGACAAGAGACCACTACATCCTCAATGGCTCCAAGGTCTGGATT  642
                     |||   ::::|||:::::|||||||| ||||||||
Db    231  SerAlaValProSerProCysGlyLysTyrTyrThrLeuAsnGlySerLeuTrpIle  250

Qy    643  ACTAATGGAGGACTGGCCAATATTTTACTGTGTTGCAAGACTGAGGTCGTTGAT---  699
            ||||||  :::|||||||||  ::|||||||:::
Db    251  SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysAspIleAspThrAspPro  270

Qy    700  TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATAGTGAGAAAGAACACTTGGTGGA  759
            :::  |||||||||||||||||||
Db    271  AlaThrGlyAlaValLysGluLysTyrIleThrAlaPheValGlnArgGlyPheGlyGly  290

Qy    760  GTCACTAATGGGAAACCCGAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTC  819
            ::::|||||   ||||| :::::|||||
Db    291  IleThrHisGlyProProGluLysGlyMetGlyIleLysAlaSerAsnThrAlaGluVal  310

Qy    820  CATTTTGAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTT  879
            |||||||   :::::|||||||||||
Db    311  PhePheAspGlyValArgValProSerGluAsnValLeuGlyGluValGlySerGlyPhe  330

Qy    880  AAGGTGGCCATGAACATCCTCAACGACGCGGTTCAGCATGGGCAGCGTCGTGGCTGGG  939
            |||||||||||||   :::::|||||
Db    331  LysValAlaMetHisIleLeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGly  350

Qy    940  CTGCTCAAGAGATTGATTGAAATGACTCGTGAGTACCCCTGCCCACAAGGAAACAGTTTAAC  999
            :::::  ::::|||   |||||||
Db    351  ThrMetArgGlyIleIleAlaLysAlaValAspHisAlaThrAsnArgThrGlnPheGly  370

Qy   1000  AAGAGGCTCAGTGAATTTGATTGATTCAGGAGGAAATTTGCACTGATGGCTCAGAAGGCT  1059
            :::::  :::|||   |||||||
Db    371  GluLysIleHisAsnPheGlyLeuIleGlnGlyLeuIleLysLeuAlaArgMetValMetLeuGln  390

Qy   1060  TACGTCATGGAGAGTGAAGATGACCTCACCTCACAGCAGGGATGCTGGACCAACCTGGCTTTCCC  1119
            |||||  :::::|||   :::  :::
Db    391  TyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln---GlyAlaThr  409

Qy   1120  GACTGCTCCATCGAGCGACAGCAGCCATGGTGAAGGTGTTCAGCTCGCGAGGCCGCCTGGCAGTGT  1179
            |||||||   ||||| :::||||||
Db    410  AspPheGlnIleIleGluAlaIleAlaIleSerLysIleProGlySerGluAlaAlaTrpLysVal  429

Qy   1180  GTGAGTGAGGGCGCTGCAGATCCTCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAG  1239
            :::  :::|||   ||||| |||||||
Db    430  ThrAspGluCysIleGlnIleMetGlyPheMetLysGlyMetGlyProGlyValGlu  449

Qy   1240  CGCATACTGCGTGACACCGCCATCCTCCATCTTCGAGGGGAACCAATGAGATTCTTCCGG  1299
            ::::|||||||||||||  |||||
Db    450  ArgValLeuArgAspLeuArgIlePheArgGlyThrArgAsnAspIleLeuArg  469

Qy   1300  ATGTACATCGCCCTGACGGGTTCTGCAGCATGCGCCGCCATCCTGACTACCAGGATCCAT  1359
            |||   |||   ::::||||||||||
Db    470  LeuPheValAlaLeuGlyCysMetAspLysGlyGlyLeuLeuSerGlyLeuGlySer  489

Qy   1360  GAGCTTAAACAG------GCCAAAGTGAGCACAATCATGAACATGGAAGGAGGCTT  1413
            :::  ::::::::
Db    490  AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeu  509

Qy   1414  CGGGACTCCCTGCGCCAACTGTGACCTGGGGCTGCAGCGCAACCATGAGTTGTGCAC  1473
            ||||||  ::::  :::|||
Db    510  ArgArgArgAlaGlyIleAspArgLeuLeuSerLeuSer------GlyLeuValHis  526

Qy   1474  CCCAGTCTTGCGGACAGTGCCAACAAGTTTGAGGAGAACACCTACTGCTTCGGCCGGACC  1533
            |||   :::|||||||||||
Db    527  ProGluLeuSerArgSerGlyLeuGluLeuAlaValArgAlaLeuGluThrVal  546

Qy   1534  GTGGAGACACTGCTGCTCCGCTTGGCCAAGACCATCATGGAGGAGCAGCTGTACTGAAG  1593
            ||||||:::|||||||||||
Db    547  ValGluAlaValLeuLeuIleLeuHisLysLysSerGlyIleValAsnGluGlnLeuGln  566

Qy   1594  CGGGTGGCCAACATCCTCATCAACCTGTATGCATGACGCCGTGTCCGGGCCAGC  1653
            |||||||||||||||||
Db    567  ArgLeuAlaAspGlyAlaIleAspLeuThrTyrAlaMetValValLeuSerArgAlaSer  586

Qy   1654  CGCTCCATCGCCATTGGGCTCCGCAACCACCAGACCACCGAGGTTCTCTGGCCAACACCTTC  1713
```

Db   587 ArgSerLeuSerGluGlyHisProThrAlaGlnHisGluLysMetLeuCysAspThrTrp 606
           |||||||||::: ||||| :::||||||:::
Qy   1714 TGGGTGGAA------GCTTACTTGCAGAATTCTTCAGCCTCTTCAGCTGGACAAGTAT 1767
              |||||| :::|||| ::   :::|||| :::||
Db   607 CysIleGluAlaAlaAlaArgIleArgGluGlyMetAlaAlaAlaLeuGlnSerAspProTrp 626
           |||:||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Qy   1768 GCTCCAGAAAACCTAGATGAGAGCAGATTAAGAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGA 1827
           ::|||||||| ||| |||||||||||:::||||||||||||||||||||||:::||
Db   627 GlnInGlu---LeuTyrArgAsnPheLysSerIleSerLysAlaLeuValGluArgGly 645
              ::: ||| :::||||||||||
Qy   1828 GCCTATATCTGTGCCACCCTCTG 1851
              :::::|||||||
Db   646 GlyValValThrSerAsnProLeu 653

RESULT 11
US-10-408-765A-534
; Sequence 534, Application US/10408765A
; Publication No. US2004010187A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibbon, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 534
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-534

Alignment Scores:
Pred. No.:   Length: 655
Score: 5.61e-99   Matches: 276
Percent Similarity: 1308.00   Conservative: 106
Best Local Similarity: 64.97%   Mismatches: 194
                     46.94%   Indels: 12
Query Match: 38.21%   Gaps: 8
DB: 16

US-09-945-326-3 (1-1863) x US-10-408-765A-534 (1-655)

Qy   109 CGAGCTTTGCCAAAGAGTTTTCTCTAGGCAAAATCAAGAAGAAGAAGAAGTTTCCATTT 168
           :::||||||||||| ::||||:::::
Qy   71   LysSerPheAlaValGlyMetPheLysGlyGlnLeuThrArgAspGlnValProPheProTyr 90
Qy   169 CCAGAAGTTAGCCAAGATGAACTTAATGAA---ATCAATCAGTTCTTGGGACCCGTGGAA 225
           ||| :::   :: ::: :::   :::||| |||||
Db   91   ProSerValLeuAsnGluGluGlnThrGlnPheLeuLysGluLeuValGlyProValSer 110
Qy   226 AAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAGGAGAAAATCCCAGAT 285
           ::|||||||||| ||| :::||||||||||||||
Db   111 ArgPheGluGluValAsnAspProAlaLysAsnAspAlaAlaLeuGluMetValGluGlu 130
Qy   286 GAAACTTTGAGAAATTGAGAGGCCTAGGCGTTTTTGGGCTGCAAGTCCCAGAAGAAATAT 345
           ||| ::|||||||||| |||||||||
Db   131 ThrThrTrpGlnGlyLeuLysGlyLeuLeuGlyAlaPheGlyLeuGlnLeuThrArgGluLeu 150
Qy   346 GGTGGCCTTGGCGTTCTCCAAACACCATGTACTACCAGGGGAGATCATCAGCATG--- 402
           :::||||| ||||||||| :::
Db   151 GlyLeuValGlyLeuGlyCysAsnThrGlnInTyrAlaArgLeuValGluIleValGlyMetHis 170
Qy   403 GATGGGTCCATCACTGACCCTGGCAGCCGACCAGGCTATTGGCCTCAAGGGGATCATC 462
           ||| :::||||||||| |||:::
Db   171 AspLeuGlyValGlyValGlyIleThrLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeu 190

Db   463 LeuPheGlyThrLysAlaGlnInLysGlyLeuTyrLeuProLysLeuAlaSerGlyLeuThr 210
           ||| ::
Qy   522 TTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTACTTGCCTAAACTGCGTTCCGGGGAGCAC 522
           ||| |||
Db   211 ValAlaAlaAlaPheCysPheGluThrGlySerAspAlaAlaSerIleArgThr 230
Qy   523 ATTGCAGCCTTCTGCTTCGAGACCGGGAGCGGATGCAGCCTCAATCCGGAGC 582
           :::||||||||||||||||||||:::|||||||||:::|||||||||
Db   231 SerAlaValProSerProCysGlyLysTyrTyrThrLeuAsnGlySerLysLeuTrpIle 250
Qy   583 AGAGCCACTAAGTGAAGACAAGAGACACTACATCCTCAATGGCTCCAAGGTCTGGATT 642
           ||| :::|||||||||| |||:::
Db   251 SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysAspThrValPheProVal 270
Qy   643 ACTAATTGGAGGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGAT--- 699
           :::||| |||:::   :::|||:::
Db   271 AlaThrGlyAlaValAlaLysGluLysThrAlaPheValValGluLysIleThrArgGlyPheGlyGly 290
Qy   700 TCTGATGGATCAGTGAAGACAAAATCCAGACATTCATAGTAGAAAGAGACTTTGGTGGA 759
           ::: |||||||||:::   :::|||
Db   291 IleThrHisGlyProGluGlyLysMetGlyIleIleLysAlaSerAsnThrAlaGluVal 310
Qy   760 GTCACTAATGGCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTC 819
           |||||||||||||||||::: ||||||||||||||
Db   311 PhePheAspGlyValArgValProSerGluAsnValLeuGlyLeuValGlySerGlyPhe 330
Qy   820 CATTTTGAAAACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTT 879
           ||| :::||| |||||||||
Db   331 LysValAlaMetHisIleLeuLeuAsnAsnGlyArgPheGlyMetAlaAlaAlaAlaLeuAlaGly 350
Qy   880 AAGGTGCCATGAACATCCTCAACAGCGGCGGTTCAGCATGGCAGCGTCGGCTGGCTGGG 939
           ||||||||| :::||||||||| :::
Db   351 ThrMetGlyTyrIleLeuAlaLysAlaValAlaAspHisAlaThrAsnArgThrGlnPheGly 370
Qy   940 CTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTAAC 999
           ||| :::|||||||||| |||:::
Db   371 GluLysIleHisAsnPheGlyLeuIleGlnGluLysLeuAlaArgMetValMetLeuGln 390
Qy   1000 AAGAGGCTCAGTGAATTTGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCT 1059
           ||| :::|||||||||
Db   391 TyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln---GlyAlaThr 409
Qy   1060 TACGTCATGGGAGTGATGACCTACCTCACAGCAGCGGATGCTGACCAACCTGGCTTTCCC 1119
           ||||||||||||| :::   :::||||||
Db   410 AspPheGlnIleIleValAlaLysAlaIleSerLysLysSerGluAlaIleArpLysVal 429
Qy   1120 GACTGCTCCATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCGCTGGCAGTGT 1179
           ||| ||||||||| |||:::
Db   430 ThrAspGluCysIleGlnIleMetGlyGlyLeuMetGlyPheMetLysGlyProGlyValGlu 449
Qy   1180 GTGAGTGAGGCGGCTGCAGATCCTGGGGGCTTGGGCTGGCTACACAGGGACTATCCGTACGAG 1239
           ||| :::   :::||||||
Db   450 ArgValLeuArgAspLeuArgIlePheArgIleLeuPheGluGluGlyTyrThrAsnAspIleLeuArg 469
Qy   1240 CGCATACTGCCTGACACCCGCATCCTCCTCATCTTCGAGGGGGACCAATGAGATTCTCCGG 1299
           ||||||||| ::::||||||||||
Db   470 LeuPheValAlaLeuLeuGlnIleCysMetAspLysAspLysGlyLysLeuLeuSerGlyLysSer 489
Qy   1300 ATGTACATCCGCCCTGACGCGGTCTCGACATGCCGCCATCCTGACTACCAGGATCCAT 1359
           ::: ||||||||| :::
Db   490 AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyLeuAlaGlyLysGlnLeuLeu 509
Qy   1360 GAGCTTAAACAG------GCCAAAGTGAGCACAGTCATGGATACCGTTGGCCGGAGGCTT 1413
           :::   :::||||||||||
Db   510 ArgArgArgAlaGlyLeuGlyLeuLeuSerLeuSerLeuSer------GlyLeuValHis 526
Qy   1414 CGGGACTCCCTGGCCTTCCAACTGTGACCTGGGCTGGGCAACCATGGAGTTGTGCAC 1473
           ||| :::|||||||||
Db   527 ProGluLeuSerArgSerGlyLeuValLeuValArgAlaLeuArgLeuGlnPheAlaThrVal 546
Qy   1474 CCCAGTCTTGCGGACAGTGCCAACAAGTTTGAGGAGAACACCTACTGCTTCGGCCGGACC 1533
           ||| :::|||:::

Qy   1534 GTGGAGACACTGCTGCTCCGCTTTGGCAAGACCATCATGGAGGAGCAGTCGTACTGAAG 1593
          ||||||| ||| ||| ::::|||:::
Db   547 ValGluAlaLeuLeuLeuArgPheGlyLysThrIleMetGluGluGlnSerTyrEnd   566

Qy   1594 CGGGTGCGGCCAACATCCTCATCAACCTGTATGGCATGACGGCCGGCGTGTCGCGGGCCAGC 1653
          ||||||:::|| ||||||||| |||||||
Db   567 ArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValValLeuSerAsnArgAlaSer   586

Qy   1654 CGCTCCATCCCGCATTGGGCTCCGCAACCACCACGAGGTTCTCTTGGCCAACACCTTC   1713
          ||||::: ||| ::::|||
Db   587 ArgSerLeuSerGluGlyHisProThrAlaGlnHisHisGluLysMetLeuCysAspThrTrp   606

Qy   1714 TGCGTGGAA------GCTTACTTGCAGAATCTCTTCAGCCGTCCTCTTCAGCTGGACAAGTAT   1767
          |||::::||| ||| ::: ||| :::
Db   607 CysIleGluAlaAlaArgIleArgGluGlyMetAlaAlaLeuGlnSerAspProTrp   626

Qy   1768 GCTCCAGAAAACCTAGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGA   1827
          ||||:::   :::||| |||
Db   627 GlnGlnGlu---LeuTyrArgAsnPheLeuSerIleSerLysAlaLeuValGluArgGly   645

Qy   1828 GCCTATATCTGTGCCACCCTCTG 1851
          :: :::::||||||||
Db   646 GlyValValThrSerAsnProLeu 653

RESULT 12
US-10-408-765A-320
; Sequence 320, Application US/10408765A
; Publication No. US2004010187A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660008.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-320

Alignment Scores:
Pred. No.:   Length: 655
Score: 3.12e-98   Matches: 275
Percent Similarity: 1299.00   Conservative: 106
Best Local Similarity: 64.80%   Mismatches: 195
Query Match: 46.77%   Indels: 12
DB: 37.95%   Gaps: 8
                      16

US-09-945-326-3 (1-1863) x US-10-408-765A-320 (1-655)

Qy   109 CGAGCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAGAAGTTTCCCATTT   168
          :::::::||||| ::||||||:::::   :::|||||
Db   71 LysSerPheAlaValGlyMetPheLysGlyGlnIleLeuThrThrAspGlnValPheProTyr   90

Qy   169 CCAGAAGTTAGCCAAGATGAACTTAATGAA---ATCAATCAGTTCTTGGGACCCGTGGAA   225
          ::||| || :::   :::||| |||
Db   91 ProSerValLeuAlaAsnGluGluProPheGlnPheLeuLysGluLeuValGlyProValSer   110

Qy   226 AAATTCTTCACTGAAGAGAGTGGACTCCCAGAAAATTGACCAGGAAGGAGAAAATCCCAGAT   285
          :::::::|| ||| |||||| :::
Db   111 ArgPhePheGluGluValAlaAsnAspProAlaLysAlaAsnAspAlaLeuGluMetValGluGlu 130

Qy   286 GAAACTTTGGAGAAATTGAAGAGCTTTTTGGCTGCAGTCCCAGAAGAATAT   345
          ||| ::: |||||| |||||||||||
Db   131 GluLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyLeuGlnGlyLysGlnLeuLeu 150

```
Db   32  LysLysValAlaAlaAlaAspSerPro------SerPheValMetAsnLeuPheArgGly   49

Qy  139  AAAATCAAGAAGAAAGAAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA      198
              ::|||||||::::|||      ||:::||||||
Db   50  LysAlaValThrAspGlnValPheProTyrProLeuAsnMetThrAspGlnLysGlu      69

Qy  199  ---ATCAATCAGTTCTTGGCAACCCGTGGAAAAATCTTCACTGAAGAGGTGGACTCCCGA    255
              :::|||      :|||::|||      ||::::|||
Db   70  ThrLeuGlyMetValMetSerProLeuGlyLysMetLeuValGluValAsnAspValVal    89

Qy  256  AAAATTGACCAGGAAGGAGAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGG    315
              |||:|||      ||||::::|||      ::::||||::|||
Db   90  LysAsnAspGluThrSerAspIleProArgAlaValLeuAspGlnPheAlaGluLeuGly   109

Qy  316  CTTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGCGCTGGGTTCTCCAACACCATGTAC   375
              |||||||:::      ||||||||||||
Db  110  ThrPheGlyValLeuValProGluGluGlyLeuGluGlnPheAlaAsnSerGlnMet     129

Qy  376  TCAAGACTAGGGGAGATCATC---AGCATGATGGGTCCATCACTGTGACCCTGGCCAGCG   432
              ::|||||:|||      :|:      |||
Db  130  AlaArgValAlaGluIleValGlyAlaTyrAspLeuGlyPheGlyValValMetGlyAla   149

Qy  433  CACCAGGCTATTGGCCTCAAGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAA   492
              |||::::|||      ||::::|||      ||||||
Db  150  HisGlnSerIleGlyTyrLysGlyIleIleLeuLeuGlyThrAspAlaGlnLysGlnLys  169

Qy  493  TACTTGCCTAAACTGCGTCCGGGAGCACATTGCCGCCTTCTGCCTCACGGAGCCAGCC   552
              |||||||||:::      |||::::|||
Db  170  TyrLeuProAspLeuAlaThrGlyArgLysPheAlaAlaPheAlaAlaLeuThrGluProThr  189

Qy  553  AGTGGGAGCCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAGCAC   612
              :::||||||||      |||||||||:::
Db  190  ThrGlySerAspAlaSerValArgThrArgAlaGluLeuSerValAspGlyLysHis    209

Qy  613  TACATCCTCAATGGCTTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTTACT   672
              :|||||||::::|||      ||||||||||
Db  210  TyrValLeuAsnGlyGlyLysIleTrpIleSerAsnGlyGlyPheAlaAspValPheThr  229

Qy  673  GTGTTGTCAAAGACTGAGGTCGTTGATTCTGATGATCAGTGAAGACAAAATACACAGCA   732
              ||||::::|||      |||:::||||||
Db  230  ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysAspLysMetSerAla  249

Qy  733  TTCATAGTAGAAAGAGACTTTGGTGGAGTCAATGGAAACCCGAAGATAAATTAGGC   792
              |||:::||||      ::::|||      |||||
Db  250  PheIleValGluArgAlaPheGlyGlyValThrSerGlyValProGlnGluLysLysMetGly  269

Qy  793  ATTCGGGCTCCAAACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAAC   852
              |||::::|||      ||||||      |||:::|||
Db  270  IleLysGlySerAsnThrArgThrGluValHisPheAspAsnLeuLysIleProValGluAsn  289

Qy  853  ATCCTTGGGAGAGGTCGGAGATGGGTTAAGGTGCCATGAACATCCTCAACGCGCGCGG   912
              :::|||      |||:::|||||||
Db  290  LeuLeuGlyLysGlyGluGlyPheLysLysValAlaMetAsnIleLeuAsnAsnGlyArg  309

Qy  913  TTCAGCATGGGCAGCGTCGGCGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAG     972
              |||  ::: ||||||||||:::
Db  310  PheGlyIleProAlaAlaCysThrGlyAlaMetLysHisCysGlnLysThrValAsp    329

Qy  973  TACGCCTGCACAAGAAACAGTTAACAGAGGCTCAGTGAATTGGATTCAGATTCAGGAG   1032
              ||||||||      |||      |||||
Db  330  HisIleThrArgValGlnThrProGlyGlyLysLysGlyLeuGlnPheGlyAsnIleGlu  349

Qy 1033  AAATTGACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACTACCTCACACAGCA   1092
              |||      |||::::|||      ||::::|||
Db  350  LysLeuValGluMetIleSerPheLysLeuValTyrAlaThrGlnIleIleValTyrMetLeuSer  369

Qy 1093  GGGATGCTCGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCCAGCCATGGTGAAGGTG   1152
              :::|||:::      ::|||||||||
Db  370  SerAsnMetAspArg--GlyIleLysGluTyrGlnLeuGlnLeuAlaAlaIleGlyLysVal  388

Qy 1153  TTCAGCTCCGAGGCCGCCTGGCAGTGTGTGCAGTGTGGAGTGAGGCGCTGCGAATCCTG   1212
              |||      :::||||||||::: :::|||||
Db  389  LeuAlaSerGluAsnAlaTrpLeuValCysAspAspGlyAlaIleGlyAlaIleGlyMet  408
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Db  510  ArgArgAlaGlyLeuGlyLysSerGlyLeuSerLeuSer-------GlyLeuValHis      526

Qy 1414  CGGGACTCCCTGGGGCCGAACTGTGACCTGGGCCTGACAGGCAACCATGGAGTGTGCAC   1473
              |||||      ||:|::      ||:||||

Qy 1474  CCCAGTCTTCGCGACAGTGCCAACAGTTTGAGGAGAACACCTACTGCTTCGGCCGGACC   1533
              |||:::      |||
Db  527  ProGluLeuSerArgSerGlyAlaValArgAlaValArgAlaLeuGluGluGlnPheAlaAlaThrVal  546

Qy 1534  GTGGAGACACTGCTGCTCCGCTTGCAAGACCATCATGAGGAGGAGCAGCTGGTACTGAAG   1593
              ||||||      |||      :::|::::
Db  547  ValGluAlaLysLeuHisLysHisLysLysGlyIleIleValAsnGluGlnPheLeuLeuGln   566

Qy 1594  CGGGTGGCCAACATCCTCATCAACCTGATATGGCATGGCGGCCGTGTGCTGCGGGGCCAGC   1653
              |||::::|||::::||||||
Db  567  ArgLeuAlaAspGlyAlaIleLeuAspLeuTyrAlaMetValValLeuSerArgAlaSer   586

Qy 1654  CGTCCATCCGCATTGGGCTCCGCAACCACGAGGTTCTCTTGGCCAACACCTTC       1713
              |||:::      |||      ::::|||      ::|||
Db  587  ArgSerLeuSerGluGlyHisHisProThrAlaGlnHisHisGlyLysMetLeuCysAspThrTrp  606

Qy 1714  TGGGTGGAA------GCTTACTGCAGAATCTCTTCAGCCTCTCCAGTCTGGACAAGTAT    1767
              ||:::      ||::::|||      |||      :::|||
Db  607  CysIleGluAlaAlaAlaArgIleArgGluGlyMetAlaAlaLeuGlnSerAspProTrp   626

Qy 1768  GCTCCAGAAAACCTAGATGAGACAGATTAAGAAAAGTGTCCCAGCAGATCCTTGAGAAGGA   1827
              |||      :::      |||      :::||||
Db  627  GlnGlnGlu--LeuTyrArgAspPheLysSerIleSerLysLysAlaLeuValGluValGluArgGly  645

Qy 1828  GCCTATATCTGTGCCACCCTCTG   1851
              :: ::::|||||||
Db  646  GlyValValThrSerAsnProLeu   653
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Qy   19  TTCCTGGCGACCACCGGCTGCGGCTCGTGCCTGCCGCGGGGTCGGTGGTCTCTACCGCGAAC   78
              |||:||:::|||::::|||      ::::
Db   16  PheIleArgLeuSerHisSerAlaAlaAlaLeuAlaLys-------AspAlaLysPro      31

Qy   79  CGGCGGCTACTGCCACCAGCCCGCCTGTACGAGCTTTCGCCAAAGAGCTTTTCCTAGGC    138
              ||| :::|||      ||||||
Db   79  LeuAlaSerGluAsnAlaTrpLeuValCysAspAspGlyAlaIleGlyAlaIleGlyMet
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Alignment Scores:

Pred. No.:	
Score:	6.38e-70
Percent Similarity:	954.00
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	27.87%

Length:	188
Matches:	188
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-945-326-3 (1-1863) x US-10-408-765A-1442 (1-188)

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Qy   1300 ATGTACATCGCCCTGACGGGTCTGCAGCATGCGCCGCCGCATCCTGCTGACTACCAGGATCCAT 1359
          ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db      1 MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrArgIleHis 20

Qy   1360 GAGCTTAAACAGGCCAAAGTGAGCACAGTCATGGACCATGATACCGTTGGCCGGAGGCTTCGGGAC 1419
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAsp 40

Qy   1420 TCCCTGGGCCGAACTGTGACCTGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGT 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 SerLeuGlyArgThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSer 60

Qy   1480 CTTGCGGACAGTGCCAACAAGTTGAGGAGAACACCTACTGCTTCGGCCCGACCGTGGAG 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu 80

Qy   1540 ACACTGCTGCTCCGCTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGGAAGCGGGTG 1599
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGlnLeuValLeuLysArgVal 100

Qy   1600 GCCAACATCCTCATCAACCTGTATGGCCATGACGGCCGTGCTGTCGGGCCAGCCCGCTCC 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 120

Qy   1660 ATCCGGATTGGGCTCCGCAACCACGAGGTTCTCTGGCCAACACCTTCTCGCGTG 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuLeuAlaAsnThrPheCysVal 140

Qy   1720 GAAGCTTACTTGCAGAATCTCTTCAGCCTCCTCAGCTGACAAGTATGCTCCAGAAAAC 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluAlaTyrLeuGlnAsnLeuPheSerLeuLeuSerGlnLeuAspLysTyrAlaProGluAsn 160

Qy   1780 CTAGATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAAGAGCGAGCCTATATCTGT 1839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 LeuAspGluGlnIleLysLysValSerGlnGlnIleLeuGluGluArgAlaTyrIleCys 180

Qy   1840 GCCCACCCTCTGGACAGGACATGC 1863
          ||||||||||||||||||||||||
Db    181 AlaHisProLeuAspArgThrCys 188
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RESULT 15
US-10-408-765A-2052
; Sequence 2052, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;   APPLICANT: Ghosh, Soumitra S.
;   APPLICANT: Fahy, Eoin D.
;   APPLICANT: Zhang, Bing
;   APPLICANT: Gibson, Bradford W.
;   APPLICANT: Taylor, Steven W.
;   APPLICANT: Glenn, Gary M.
;   APPLICANT: Warnock, Dale E.
;   TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;   TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;   FILE REFERENCE: 660088.465
;   CURRENT APPLICATION NUMBER: US/10/408,765A
;   CURRENT FILING DATE: 2003-04-04
;   NUMBER OF SEQ ID NOS: 3077
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2052
;   LENGTH: 188
;   TYPE: PRT
;

Left column (rotated sequence alignment):

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Qy   1213 GGCTACACAAGGACTATCCGTACGAGCCGATGCGGTGACACCCGCATCCTCCTCATC 1272
          |||:|||||   |||:::||   |:||||||||:::||:|||||||||||||||||||
Db    409 GlyPheMetArgGluThrGlyLeuGlnLeuArgValLeuArgArgAspLeuArgIlePheArgIle 428

Qy   1273 TTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCC 1332
          |||||||:|||:   |||:||:::|||||||:||::||||||||||||||||||||||||
Db    429 PheGluGlyAlaAsnAspValLeuArgLeuPheIleAlaLeuThrGlyLeuGlnHisAla 448

Qy   1333 GGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTCATG 1392
          |||:|||         :::|||||||||         |||||||||||:
Db    449 GlyLys---------HisLeuAlaGluGlnAla------SerGlyValGly 460

Qy   1393 GATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACTGTGACCTGGGCCTGACA 1452
          ::||||         |||||||||||||:         |||:
Db    461 GlyLeuIleGlyLeuAlaValSerArgValThrGly---------GlyAsnThr 475

Qy   1453 GGC---AACCATGGA--GTTGTGCACCCCAGTCTTGCGGACAGTGCCAACAAGTTTGAG 1506
          |||      ||||||    ||||||||||||||||||||||||||||||||||||||
Db    476 GlySerAsnPheGlyValGlnValValAspAlaSerLeuGlnAspSerAlaLysValLeuAsp 495

Qy   1507 GAGAACACCTACTGCTTCGGCCCGACCGTGGAGACACTGCTGCTCCGCTTGGCAAGACC 1566
          |||||||||||||||||||||||||||||||||||:
Db    496 GlnGlnIleAlaLeuPheGlyGlnThrValGlnIleGlyLeuLeuMetLysHisLysLysGly 515

Qy   1567 ATCATGGAGGAGCAGCTGGTACTGGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGC 1626
          |||::|||  ::  ||   |||   ||:||||:
Db    516 IleIleAspArgGlnTyrGluMetThrAlaValAlaAlaAlaAlaIleAsnIleTyrSer 535

Qy   1627 ATGACGGCCGTGCTGTCGGGCCAGCCCGCTCCATCCGGATTGGGCTCCGCAACCACGAC 1686
          |||||||||||||||||        :::|||||||||||||||||||||
Db    536 SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLysLysAsnSerSerAlaAsp 555

Qy   1687 CACGAGGTTCTCTGGCCAACACCTTCTCGCGTGGAAGCTTACTTGCAGAATCTCTTCAGC 1746
          |||||      :||   |||||:   |||:::   :::
Db    556 PheGluArgGlyValAla---ThrTyrTyrValAspLysAlaMetLys--------Ser 571

Qy   1747 CTCTCAGCTGACAAGTATGCTCCAGAAAAACTAGATGAGCAGATTAAGAAAGTGTCC 1806
          ||||||||||   ||:::   :::
Db    572 SerAsnArgPheLeuGlnAspAlaGlySerGlyValGlnAlaSerGlyValAlaLeuAlaThr 591

Qy   1807 CAGCAGATCCTTGAAGAGCGAGCCTATATCTGTGCC------------CAC 1845
          |||   |||   |||   |||   :::||
Db    592 IleGluSerLeuAlaLysGlu------ValCysGlyAsnGlyGlyThrLeuGlnLeuHis 609

Qy   1846 CCTCTGGAC 1854
          |||:::|||
Db    610 ProValGlu 612
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RESULT 14
US-10-408-765A-1442
; Sequence 1442, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;   APPLICANT: Ghosh, Soumitra S.
;   APPLICANT: Fahy, Eoin D.
;   APPLICANT: Zhang, Bing
;   APPLICANT: Gibson, Bradford W.
;   APPLICANT: Taylor, Steven W.
;   APPLICANT: Glenn, Gary M.
;   APPLICANT: Warnock, Dale E.
;   TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;   TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;   FILE REFERENCE: 660088.465
;   CURRENT APPLICATION NUMBER: US/10/408,765A
;   CURRENT FILING DATE: 2003-04-04
;   NUMBER OF SEQ ID NOS: 3077
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1442
;   LENGTH: 188
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-1442

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; ORGANISM: Homo sapiens
US-10-408-765A-2052

Alignment Scores:
Pred. No.:              6.38e-70        Length:         188
Score:                  954.00          Matches:        188
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            27.87%          Indels:         0
DB:                     16              Gaps:           0

US-09-945-326-3 (1-1863) x US-10-408-765A-2052 (1-188)

Qy   1300 ATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCCGATCCTGACTACCAGGATCCAT 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCCGATCCTGACTACCAGGATCCAT   20
          MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHis

Qy   1360 GAGCTAAACAGGCCAAAGTGAGACAGTCATGGATACCGTTGGCCGGAGGCTTCGGGAC   1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAsp   40

Qy   1420 TCCCTGGGCCGAACTGTGACCTGGGGCTGACAGGCAACCATGAGTTGTGCACCCCAGT   1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 SerLeuGlyArgThrValAspLeuGlyLeuThrGlyValAsnHisGlyValValHisProSer  60

Qy   1480 CTTGCGGACAGTGCCAACAAGTTGAGGAGAACACCTACTGCTTCGGCCCGGACCGTGGAG 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu   80

Qy   1540 ACACTGCTGCTCCGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTG 1599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGlnLeuValLeuLysArgVal  100

Qy   1600 GCCAACATCCTCATCAACCTGTATGGCGATGACGGCCGTGCTGCGGGCCAGCCGCTCC   1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer  120

Qy   1660 ATCCGCCATTGGGCTCCGCAACCACCAGGTTCTTGGCCAACACCTTCTGCGTG       1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal  140

Qy   1720 GAAGCTTACTTGCTGACGAATCTCTTCAGCCTCTCCAGCTGACAAGTATGCTCCAGAAAAC 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn  160

Qy   1780 CTAGATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGGCGAGCCTATATCGT  1839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 LeuAspGluGlnIleLysLysValSerGlnGlnIleLeuGluLysAlaSerArgAlaTyrIleCys 180

Qy   1840 GCCCACCCTCTGGACAGGACATGC 1863
          ||||||||||||||||||||||||
Db    181 AlaHisProLeuAspArgThrCys  188
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Search completed: May 2, 2005, 15:57:38
Job time : 256.808 secs

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              GenCore version 5.1.6
       Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:        May 2, 2005, 14:27:05 ; Search time 60.2291 Seconds
                                        (without alignments)
                                        5952.335 Million cell updates/sec

Title:         US-09-945-326-3
Perfect score: 3423
Sequence:      1 atgagcggctgcgggctctt........accctctggacaggacatgc 1863

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched :     283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:   566832

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09945326/runat_02052005_135411_22364/app_query.fasta_1.4686
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN_1_1_225 @runat_02052005_135411_22364 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     PIR_79:*
               1: pir1:*
               2: pir2:*
               3: pir3:*
               4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3149	92.0	621	2	JC7892	acyl-CoA dehydroge
2	1356.5	39.6	655	2	A54872	acyl-CoA dehydroge
3	1308	38.2	655	2	S54183	acyl-CoA dehydroge
4	1210.5	35.4	613	2	T15905	hypothetical prote
5	821	24.0	594	2	F84085	butyryl-CoA dehydr
6	815.5	23.8	594	2	C70021	butyryl-CoA dehydr
7	711	20.8	650	2	A70817	probable fadE10 pr
8	699	20.4	382	2	B87302	acyl-CoA dehydroge
9	691.5	20.2	384	2	B83443	probable acyl-CoA
10	690	20.2	379	2	G84124	acyl-CoA dehydroge
11	682	19.9	378	2	D69658	acyl-CoA dehydroge
12	682	19.9	381	2	AC3536	butyryl-CoA dehydr
13	678	19.8	381	2	B87472	acyl-CoA dehydroge
14	658	19.2	380	2	F84124	acyl-CoA dehydroge
15	652.5	19.1	379	1	S55421	acyl-CoA dehydroge
16	652	19.0	387	1	D75417	acyl-CoA dehydroge
17	648	18.9	379	2	T45286	butyryl-CoA dehydr
18	644	18.8	456	2	AF3637	butyryl-CoA dehydr
19	630	18.4	389	2	C70979	probable fadE25 pr
20	629.5	18.4	381	2	E75458	acyl-CoA dehydroge
21	626	18.3	380	2	F99299	probable acyl-CoA
22	626	18.3	380	2	A12983	acyl-CoA dehydroge
23	625.5	18.3	379	2	T47262	butyryl-CoA dehydr
24	625.5	18.3	379	2	F97233	butyryl-CoA dehydr
25	617.5	18.0	387	2	A83393	probable acyl-CoA
26	615	18.0	419	2	T15088	hypothetical prote
27	613	17.9	380	2	T44811	acyl-CoA dehydroge
28	611.5	17.9	402	2	D69530	probable acyl-CoA
29	610.5	17.8	381	2	B83791	butyryl-CoA dehydr
30	609	17.8	389	2	B87001	probable acyl-CoA
31	606	17.7	380	2	G69893	butyryl-CoA dehydr
32	604	17.6	432	1	A55680	acyl-CoA dehydroge
33	603.5	17.6	375	2	F83326	probable acyl-CoA
34	594.5	17.4	422	2	H75382	acyl-CoA dehydroge
35	593	17.3	397	2	B69378	probable acyl-CoA
36	588.5	17.2	398	2	B75411	acyl-CoA dehydroge
37	587.5	17.2	423	2	A37033	isovaleryl-CoA deh
38	586	17.1	397	2	H84225	acyl-CoA dehydroge
39	585.5	17.1	382	2	AE3492	isovaleryl-CoA deh
40	585.5	17.1	424	1	C34252	isovaleryl-CoA deh
41	583	17.0	412	2	A30605	acyl-CoA dehydroge
42	579	16.9	412	2	B30605	acyl-CoA dehydroge
43	579	16.9	412	2	T16568	hypothetical prote
44	576.5	16.8	421	2	AD2984	acyl-CoA dehydroge
45	576.5	16.8	421	2	C98299	probable acyl-CoA

ALIGNMENTS

```
RESULT 1
JC7892
acyl-CoA dehydrogenase (EC 1.3.99.3) - 9 - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C;Accession: JC7892
R;Zhang, J.; Zhang, W.; Zou, D.; Chen, G.; Wan, T.; Zhang, M.; Cao, X.
Biochem. Biophys. Res. Commun. 297, 1033-1042, 2002
A;Title: Cloning and functional characterization of ACAD-9, a novel member of human acyl-
-CoA dehydrogenase family.
A;Reference number: JC7892; MUID:22246103; PMID:12359260
A;Accession: JC7892
A;Molecule type: mRNA
A;Residues: 1-621 <ZHA>
A;Cross-references: UNIPROT:Q9H845; GB:AF327351
C;Experimental source: Dendritic cells
C;Comment: This enzyme, which belongs to a family of mitochondrial enzymes that catalyze
-long-chain acyl-CoA and has specific activity toward palmitoyl-CoA (C16:0).
C;Genetics:
A;Gene: acad-9
A;Map position: 3q26
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.:              5e-200            Length:          621
Score:                  3149.00           Matches:         620
Percent Similarity:     99.84%            Conservative:    0
Best Local Similarity:  99.84%            Mismatches:      1
Query Match:            92.00%            Indels:          0
DB:                     2                 Gaps:            0

US-09-945-326-3 (1-1863) x JC7892 (1-621)

Qy    1 ATGAGCGGCTGCGGGCTCTTCCTGCGGCCACCACGGCTGCGGCTGCCTGCCGGGGGTCTG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu   20

Qy   61 GTGGTCTCTACCGGCGAACCGGCGGCTACTGCGGCCACCAGCCCGCCGCCTGTACGAGCTTTCGCC  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Qy  1201 CTCGGGGGCTTGGCTACACAAGGGACTACGAGCGCATACTGCCTGACACCCGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 LeuGlyGlyLeuGlyLeuTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420

Qy  1261 ATCCCCTCCATCTTCGAGGAACCAATGAGATTCCCGGATGTACATCCTGACGGGT 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 IleLeuLeuIlePheGluGluProMetArgPheProAspValHisProAspGly 440

Qy  1321 CTGCAGCATGCGGCGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuGlnHisAlaAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460

Qy  1381 AGCACAGTCATGGATACCGTTGGCCGGAGCCTTCGGACTTCCTGGCCAACTGTGGAC 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 SerThrValMetAspThrValGlyArgSerLeuGlyArgAspThrValAsp 480

Qy  1441 CTGGGGGCTGACAGGCAACCATGGAGTTGTGCGCAGTGCTTGCGACAGTGCCAACAAG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGlyLeuThrArgGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500

Qy  1501 TTTGAGAGACACCTACTGCTTCCGGCCGGACAGGTGGAGACACTGCTGCTCCGGCTTTGGC 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 PheGluGluAsnThrTyrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520

Qy  1561 AAGACCATCATGGAGGAGCAGTGTACTGAAGCCGGTGGCCAACATCCTCATCAACCTG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 LysThrIleMetGluGluGlnCysThrGluLeuValLeuArgValAlaAsnIleLeuIleAsnLeu 540

Qy  1621 TATGGCATGACGGGCCGTGCTCCGGCGGCCGGCCGCTCCATCCGCATTGGGCTCCGCAAC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560

Qy  1681 CACGACCACGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTC 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy  1741 TTCAGCCTCTTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGlnGlnIleLysLys 600

Qy  1801 GTGTCCCAGCAGATCCTTGAGAGAGGCGAGCCTATATCTGTGCCCACCCTCTGACACAGACA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ValSerGlnGlnIleLeuGluGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620

Qy  1861 TGC 1863
         |||
Db   621 Cys 621
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RESULT 2
A54872
acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain-specific precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54872
R;Aoyama, T.; Ueno, I.; Kamijo, T.; Hashimoto, T.
J. Biol. Chem. 269, 19088-19094, 1994
A;Title: Rat very-long-chain acyl-CoA dehydrogenase, a novel mitochondrial acyl-CoA dehyc
ced amino acid sequence and distinct specificities of the cDNA-expressed protein.
A;Reference number: A54872; MUID:94308174; PMID:8034667
A;Accession: A54872
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-655 <AOY>
A;Cross-references: UNIPROT:P45953; GB:D30647; NID:g533356; PIDN:BAA06331.1; PID:d100689
C;Keywords: oxidoreductase
F;1-40/Domain: signal sequence #status predicted <SIG>

Alignment Scores:
Pred. No.:
Score: 1.18e-81   Length: 655
Percent Similarity: 63.36%   Matches: 295
Best Local Similarity: 46.38%   Conservative: 108
                                                     Mismatches: 192

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Db       21 ValValSerThrAlaArgArgLeuArgThrSerProProValArgAlaAlaPheAlaAla 40

Qy      121 AAAGAGGCTTTCCTAGGCAAATCAGAAGAAGAAGTTTCCCATTCCAGAAGTTAGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60

Qy      181 CAAGATGAACTTAATGAAATCAATCAGTTCTTCTGGGACCCGTGGAAAAATTCTTCACTGAA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GlnAspGluLeuAsnGluIleAsnGlnPhePheTrpAspProTrpLysAsnSerSerLeu 80

Qy      241 GAGGTGGACTCCCGAAAAAATTGACCAGGAAGGGAAAAATCCAGATGAAACTTTGGAGAAA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 GluValAspSerArgLysAsnEndGlnGluGlyLysIleProAspGluThrLeuGluLys 100

Qy      301 TTGAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGCCTGGGCTTC 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe 120

Qy      361 TCCAACACCATGTACTCCAAGACTACCAGGAGATCATCAGCATGATGGGTCCATCACTGTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleIleSerMetAspGlySerIleThrVal 140

Qy      421 ACCCTGGCAGCGCACCAGGCTATTGCTCCTCAAGGGGATCATCTTGGCTGCTGAGGAG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 ThrLeuAlaAlaHisGlnAlaIleAlaLeuGlyLeuLeuGlyTyrIleLeuLeuLeuAlaGlyLysThrGluGlu 160

Qy      481 CAGAAGCCAAATACTGCCTAAACTGGCCTCCGGGGCGGCCACATTGCAGCCTTCTGCCTC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleGlyAlaLeuAlaPheCysLeu 180

Qy      541 ACGGAGCCAGTGGGATGCAGCGCCTCAATCCGGAGCAGAGCCCACTAAGTGAA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ThrGluProValSerGlySerAspAlaAlaSerIleArgSerArgAlaAlaSerGluGlu 200

Qy      601 GACAAGAAGCACTACATCCTCAAGGTCTGATTACTAATGGCACTGGCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 AspLysLysHisTyrIleLeuLysAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy      661 AATATTTTACTGTGTTGCAAAGATCGAGGTCGTTGATTCTGATGGATCAGTGAAAGAC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 AsnIlePheThrValPheAlaLysIleGluValValAspSerAspGlySerValIleSerAsp 240

Qy      721 AAAATCACAGCATTCATAGTAGAAAGAGACTTGGTGAGTCACTAATGGGAAACCCGAA 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 LysIleThrAlaPheIleValGluArgAspLeuValSerHisLysArgLeuAsnGlyLysProGlu 260

Qy      781 GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAAACACCAAGATA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280

Qy      841 CCTGTGGAAAAACATCCTTGGAGAGGTCGGAGAGGAGTGGTTTAAGGTGGCCATGAACATCCTC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      281 ProValGluGluIleLeuGlyGluValGlyValGlyAspValPheLysLysValAlaAlaMetAsnIleLeu 300

Qy      901 AACAGCGGGCCCGTTCAGCATGGGCAGCGCCTCCGTGGCCTGCTCCAAGAGAGATTGATTGAA 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AsnSerGlyArgPheSerMetGlySerGlySerValValAlaGlyLysLeuLeuLysLysArgLeuIleGlu 320

Qy      961 ATGACTGCTAGTACGCCTGACAACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGGA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      321 MetThrAlaGluTyrAlaCysThrProAspAsnLysGluThrArgLysAsnLysArgLeuSerGluPheGly 340

Qy     1021 TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAGGGCTTACGCTCATGGGAGATGACC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      341 LeuLeuGlnGluLysPheAlaLeuMetAlaGlnArgLysLysGlyGlnIleGlnLysSerMetThr 360

Qy     1081 TACCTCACAGAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCC 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TyrLeuThrArgLeuGlyMetLeuAspGluAspProCysGlyProProSerIleGluGluAlaAla 380

Qy     1141 ATGGTGAAGGTGTTCAGCTCCGAGGCGCCGCCTGGCAGTGTGTGAGTGAGGCCGCTGCAGATC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      381 MetValLysValPheSerSerGluAlaAlaTrpProGlnCysValSerGluValValLeuGlnIle 400
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Query Match:    39.63%      Indels:   41
DB:             2           Gaps:     12
US-09-945-326-3 (1-1863) x A54872 (1-655)

Qy    25 CGACCACGGCTGCGGCTCGTGCCTCCGCGGGTCTGTGGTCTCTACCGGCAACCGGCGG   84
         |||  ||::||||  |||                      |||  :::  |||  ||
Db    32 ArgProThrSerAlaGlnArg---------------LeuTyrAlaSerGluAlaThrGlnAla   47

Qy    85 CTACTGCGC------------------------------ACCAGCCGCCTGTACGA  111
         ::|||||||                             ||:|||||| ||||| ||
Db    48 ValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAlaArg   67

Qy   112 GCT--------TTCGGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAGAGAAAGAAGTT  159
         |||        |||||  ::|:|||  |||||::  |||||  :::|:||||| |  ||
Db    68 AlaAlaGluSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnVal   87

Qy   160 TTCCCATTTCAGAGTTAGCCAAGATGAACTAATGAA------------ATCAAT  204
         |||||::||  ||  |||  |||  |  ||                  ::
Db    88 PheProTyrProSerVal------------LeuAsnGluGlyGlnThrGlnPheLeuLys  103

Qy   205 CAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGAC  264
         :::   ||||| |||  |||||||  |:||||| |||||||||  ||  |||||| |||
Db   104 GluLeuValGlyProValAlaArgPheGluGluValAlaArgPheGluAsnAspAlaLysAsnAsp  123

Qy   265 CAGGAAGGAAAATCCCAGATGAAACTTTGGAGAGAAAATTGAAGAGCCTAGGGCTTTTTGGG  324
         ||||  ::||| || :::||||| |||||  ||||| |||||||||  ||||  |||||||
Db   124 SerLeuGluLysValGluGluAspThrPheLeuGlnLeuGlyLeuGlyGluGlyLeuAlaPheGly  143

Qy   325 CTGCAAGTCCAGAGAAATATGTGCCTGGGCTTCTCCAACACCATGTACTCAGACTA  384
         ||| |||||||  :::||||||| |||||  || |||||||||  |:|| |||||
Db   144 LeuGlnValProSerGluGluGlyLeuGlyLeuLeuGlyLeuSerAsnThrGlnTyrAlaArgLeu  163

Qy   385 GGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGCAGCGCACCAGGCT  441
         |||||||||||||  |||   |||  :::::|||||  ||::|||||  ||||| ||||
Db   164 AlaGluIleValMetHisAspLeuGluValSerValThrLeuGlnArgThrArgLeuAlaHisGlnSer  183

Qy   442 ATTGGCCTCAAGGGGATCATCTTGGCTGCGGCACATTGAGGAGCAGAAAGCCAAATACTTGCCT  501
         ||| ||||| || |||||||  ||| ||   |||||  |||||||||||  ||||||||||||
Db   184 IleGlyPheLysGlyIleLeuLeuAlaArgGlyThrGlyValGlyAlaGlnIleLysLysGluLeuTyrLeuPro  203

Qy   502 AAACTGGGCTCCGGGAGCACATTGCGTTCTGCCTCACGGGAGCCCAGCCAGTCGGGAGC  561
         :::|||||:::   |||||||||  :::|||||||| ||||||||||||||||:::|||
Db   204 ArgValAlaSerGlyValGlnAlaLeuAlaLeuAlaAlaPheCysLeuThrGluGluSerGlySer  223

Qy   562 GATGCAGCCCAATCCGGAGCAGCAGCCACCAAGTGAAGACAAGAAGACTACTACCTC  621
         |||||| |||| |||||||||||||:::|||||  |||||||||||||  ||||||
Db   224 AspValAlaSerIleArgSerSerArgSerValProSerArgProCysGlyLysTyrTyrTyrLeu  243

Qy   622 AATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCCAATATTTTACTGTGTTTGCA  681
         |||||||||||| |||| | ||||||:::|||||||||||||||  :::|||| |||||
Db   244 AsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAlaAspValValIleAlaValPheAla  263

Qy   682 AAGACTGAGGTCGTTGAT---TCTGATGATCAGTGAAGAAGACAAAATCACAGCATTCATA  738
         |||||  :::|| |||  |||   |  |||| ||||  ::||||| |:::|  |||
Db   264 LysThrProIleLeuLysAspAlaAlaThrGlyAlaValLysAlaValLysGlyIleLeuThrAlaPheVal  283

Qy   739 GTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAAACCCGAAGATAAATTAGGCATTCCG  798
         ||| ||||| ||||:::|||||||  ||||||||  ||||| :::|||||||||||| ||
Db   284 ValGluArgSerPheGlyGlyValThrHisGlyValThrHisGlyMetGlyLeuGlyLysLysGlyIleLeuLys  303

Qy   799 GGCTCCAACTTGTGAAGTCCATTGAAATACCTGTGAAAAAACATCCTT  858
         |||||| |||||:::  |||||||  |||| ||||:::|||||||||
Db   304 AlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnValLeu  323

Qy   859 GGGAGGTCGGAGAGTGGGTTTAAGGTGCCATGGAGCATCTCAACACGCGCCGGTTCAGC  918
         |||||||||||||||||||:::|||||||||| ||||| |||||||||||||||||||
Db   324 GlyGluValGlyAlaGlyAspGlyPheLysValProTrpAlaIleLeuAsnAsnGlyArgPheGly  343

Qy   919 ATGGGAGCGGCTCGTCGTGCCGGCTCGGGCTGCTCAAGAGATTGATTGAAGACTGCTAGTACGCC  978
         |||  |||||||||  ||||| |||||  || |||||||||| |||| :::|| ||::||||||
Db   344 MetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleIleAlaLysAlaValAlaAspHisAla  363

Qy   979 TGCACAAGGAAACAGTTAACAGAGGCTCAGTGAATTGATTGATTCAGAGAAATTT 1038
         |||||||  :::|||||| |||||||||| ||||| |||||  ||::|| :::|:
Db   364 ThrAsnArgThrGlnPheGlyAspLysHisGlyIleHisAsnPheGlyValIleGlnGluLysLeu  383

Qy  1039 GCACTGATGGCTCAGAAGGCTTACGTCATGGAGGAGTATGACCTACCTCACAGCAGGATG 1098
         |||  |||  |||  |||||||  |||||||||||||||| || ||||||  ||  |||
Db   384 AlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerArgLeuAlaAsn  403

Qy  1099 CTGGACCAACCTGGCTTCCCGACGTGCTCCATCGAGGCAGCAGCCATGGTGAAGGTGTTCAGC 1158
         :::||||||||:::|  ||    |||||  |  ||||||| || ||||| ||||||||||||
Db   404 MetAspGln--GlyPheLysAspGlnIleIleGluAlaAlaIleSerLysLysPheGly  422

Qy  1159 TCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGCGCTCAGATCCTCGGGGGCCTTGGGCTAC 1218
         |||||||||||  |||  |||||  |||||| ||||||:::|| || |||| |||||||
Db   423 SerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetGlyPhe  442

Qy  1219 ACAAGGGACTACCGTACGAGCCGCCATACTGCGTCGACACCCCGACACCGGCCGCCGC 1278
         |||  ||  |||||  |||||  |||||||  ||||| || || ||||  ||||||||
Db   443 MetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGlu  462

Qy  1279 GGAACCAATGAGATTCCGGATGTACATCGCGCCCGACGGGTCTGCAGCATGCGGCCGCC 1338
         ||||||||||||||| || |||  |||||||||||| |  :::|||||||||  |||||
Db   463 GlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLys  482

Qy  1339 ATCCTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCACAGTCATG 1392
         |||||| ||||||||||||||||||| |||||      |||||||||||||||  ||||
Db   483 GluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLeuIle  502

Qy  1393 GATACCTGGCCGGAGGCTTCGGAGACCTCCCTGGGCCGAACTGTGGACCTGGGGCTGACA 1452
         ||||||||| ||||| ||:::|||  ||||  |||||| || |||||  ||:::||||
Db   503 GlyGluAlaSerLysGlnLeuLeuArgArgArgThrGlyIleGlySerGlyLeuSerLeuSer  522

Qy  1453 GGCAACCATGAGGTTGTGCACCCCAGTTCTGCGGACAGTGCCAACAAGTTTGAGGAGAAC 1512
         |||||||||||||||||||  ||| |||  |||  |||   || ||||| |||||||
Db   523 --------GlyIleValHisProGluLeuSerArgSerGlyGluAlaValValGlnAla  539

Qy  1513 ACCTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGCTTGGCAAGACCATCATG 1572
         |||||||||||||| || || ||||||||||||  ||||||:::||||||||||||
Db   540 LeuGluGlnPheAlaThrValGluAlaLysLeuMetLysHisLysGlyIleLeuVal  559

Qy  1573 GAGGAGCAGCGTGGTACTGAAGCGGTGGCCAACATCCTCATCAACCTGTATGGCATGACG 1632
         |||||||||||:::|| |||||||| || |||||||| |||||||||| |||||||||
Db   560 AsnGluGlnLeuGlnLeuGlnIleArgLeuGluLeuAlaAspGlyAlaIleLeuTyrAlaMetVal  579

Qy  1633 GCCGGTGTCGCGGGCAGCCGCTCCATCGGCCATTGGGCTCCGCAACCACCAGCAGCAG 1692
         |||||||||||  |||||||  ||||||  |||||| |||::||||||||  |||||
Db   580 ValValLeuSerArgAlaSerArgArgSerLeuSerArgArgGlyTyrProThrAlaGlnHisHisGlu  599

Qy  1693 GTTCTCTTGGCCACACCTTCTGCGTGGAAGCT------TACTTGCAGAATCTCTTC 1743
         :::|||||  ||||||||| |||||||||:::      |||||||||||||:::||
Db   600 LysMetLeuCysAspSerTrpCysIleLeuAspAlaAlaThrArgIleArgGluMetAla  619

Qy  1744 AGCCCTCTCCAGTCTGACAAGTATGCTCCAGAAAAACCTAGATGAGCAGATTAAGAAAGTG 1803
         ||||||||||||||  |||  |||||||||||||:::|| ||||||| :::||||||||
Db   620 SerLeuGlnSerAsnProGln------GlnGlnGlyLeuGluPheArgAsnPheArgSerIle  637

Qy  1804 TCCCAGACGTCCTTGAGAAGCGAGCGCTATATCTGTGCCCACCCTG 1851
         |||||  |||||||:::|||||||||||||||| |||||||||||
Db   638 SerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu  653
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A;Cross-references: UNIPROT:P49748; EMBL:X86556; NID:g790446; PID:g790447
C;Genetics:
A;Gene: GDB:ACADVL; VLCAD
A;Cross-references: GDB:1248185; OMIM:201475
A;Map position: 17p11.2-17p11.1
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.:   1.89e-78   Length: 655
Score: 1308.00   Matches: 276
Percent Similarity: 64.97%   Conservative: 106
Best Local Similarity: 46.94%   Mismatches: 194
Query Match: 38.21%   Indels: 12
DB: 2   Gaps: 8

US-09-945-326-3 (1-1863) x S54183 (1-655)

Qy 109 CGAGCTTCCCAAAGAGCTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTCCCATTT 168
            :::||||||||| ::|||::: ||||||| :::|||||||||||||||||
Db   71 LysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnValPheProTyr 90

Qy 169 CCAGAAGTTAGCCAAGATGAACTTAATGAA---ATCAATCAGTTCTTGGGACCCTGGAA 225
         ||| :::   ::: ||| ::: |||
Db   91 ProSerValLeuAsnGluGlnIleThrGlnPheLeuLysGlyLeuValGluProValSer 110

Qy 226 AAATTCTTCACTGAAGAGGTTGGACTCCCAGAAAAATTGACCAGGAAGGGAAAATCCCAGAT 285
         ::||||| ||| |||||||
Db 111 ArgPheGluGluValAlaAsnAspProAlaLeuAlaArgIleLeuMetValGluGlu 130

Qy 286 GAAACTTTGGACAAATTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATAT 345
            :: |||||| ||| ||| :::|||||||||||||
Db 131 ThrThrTrpGlnGlyLeuLysGlyLeuGlyAlaPheGlyLeuGlnValProSerGluLeu 150

Qy 346 GGTGGGCTGGGCTTCTCCAACACCATGACTACTCAAGACTAGGGAGATCATCAGCATG--- 402
         ||| :::||| ||| ||||||:::||| |||:::
Db 151 GlyGlyValGlyLeuCysAsnThrGlnThrLeuArgLeuIleValGlyIleValGlyMetHis 170

Qy 403 GATGGGTCCATCACTGTGACCCTGCAGCGCACCAGGCTATTGGCCTCAAGGGATCATC 462
         |||:::||| ::: |||
Db 171 AspLeuGlyValGlyIleThrLeuGlyAlaHisGlnSerIleGlyAlaHisGlnSerIleGlyLeu 190

Qy 463 TTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCTCCCGGGGAGCAC 522
         ||| |||||||::: ||| ||| ||| |||
Db 191 LeuPheGlyThrLysArgLysLeuAlaGlnThrLeuProLysLeuAlaSerGlyLeuGluThr 210

Qy 523 ATTGCAGCCTTCTGCTCACCGGAGCCCAGTGGAGCGATGCAGCCTCAATCCGGAGC 582
         :::||||::|| ||| :::|||||:::
Db 211 ValAlaAlaPheCysSerLeuThrGluProSerGlySerAspAlaAlaSerIleArgThr 230

Qy 583 AGAGGCCACAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATT 642
         :::||| ||| ||| ||||||:::||| :::|||||||
Db 231 SerAlaValProSerProCysGlyLysTyrTyrThrLeuAsnGlySerLysValTrpIle 250

Qy 643 ACTAATGAGGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGAT--- 699
         :::||||||||| ||| :::|||||||||:::
Db 251 SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrProValThrAspPro 270

Qy 700 TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAGAGACTTTCGTGTGGA 759
         ::: ||||||||||||||:::|||
Db 271 AlaThrGlyAlaMetHisIleLeuLeuAsnAsnGlyArgPheGlyMetAlaAlaLeuAlaGly 290

Qy 760 GTCACTAATGGGAAACCCGAAGAATAAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTC 819
         |||||||:::||| ||||||::::::||||||||
Db 291 IleThrHisGlyProProGluLysProGluLysMetGlyIleIleLysAlaSerAsnThrAlaGluVal 310

Qy 820 CATTTTGAAAACACCAAGATACCTGTGGGAAAACATCCTTGGAGAGATGGGTTT 879
         :::|||:::   :::||||||||||:::|||
Db 311 PhePheAspGlyValArgValProSerGluAsnValLeuGlyValGluValGlySerGlyPhe 330

Qy 880 AAGGTGGCCATGAACATCCTCCAACAGCGGCCGGTTCAGCATGGCAGCGTCGTGGCTGGG 939
         ||||||||||||:::||||||||:::|||
Db 331 LysValAlaMetAsnIleLeuLeuAsnGlyArgPheGlyMetAlaAlaLeuAlaGly 350

Qy 940 CTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAAC 999
            :::|||||:::||||| :::
Db 351 ThrMetArgGlyLysIleIleAlaLysHisAlaValAlaAspHisAlaThrAsnArgThrGlnPheGly 370

Qy 1000 AAGAGGCTCAGTGAATTTGGATTGAATTCAGGAGAAATTGCACTGATGGTCAGAAGGCT 1059
         |||:::|||||||||||||||||||||||:::
Db 371 GluLysIleHisAsnPheGlyLeuIleGluGlnLysLeuAlaLeuArgMetValMetLeuGln 390

Qy 1060 TACGTCATGGAGAGATGACCTACCTCACAGCAGGGATGCTGGACCAACCTGGCTTTCCC 1119
         |||||||||||||||:::   ::::::
Db 391 TyrValThrGlySerMetAlaTyrMetValSerAlaAsnMetAspGln---GlyAlaThr 409

Qy 1120 GACTGCTCCATCGAGCAGCAGCCATGGTGAAGTGTTCAGCTCGAGGCCGCCTGGCCAGTGT 1179
         |||:::|||||||||:::|||||||:::
Db 410 AspPheGlnIleLeuGluAlaLysIleAlaIleSerLysLysIlePheGlySerGluAlaAlaTrpLysLysVal 429

Qy 1180 GTGAGTGAGCGCTGCAGATCCTCCGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAG 1239
            :::   :::
Db 430 ThrAspGluCysIleGlnIleLeuMetGlyGlyMetGlyPheMetLysGluProGlyValGlu 449

Qy 1240 CGCATACTGCGTGACACCGGCATCCTCCCTCATCTTCGAGGGAACCAATGAGATTCTCCGG 1299
         :::||||||:::   :::|||||||||||
Db 450 ArgValLeuArgAspLeuArgIlePheGluGlyThrAsnAspIleLeuArg 469

Qy 1300 ATGTACATCGCCCTGACGCGGTCTCGCAGCATGCCCGCATCCTGACTACCAGGATCCAT 1359
         :::|||||||:::   :::||||||
Db 470 LeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysLeuLysGluSerGlyLeuGlySer 489

Qy 1360 GAGCTTAAACAG------GCCAAAGTGAGCACAGTCATGGATACCGTTGGCCGGAGGCTT 1413
         :::||| ||||||:::
Db 490 AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeu 509

Qy 1414 CGGGACTCCCTGGCCGAACTGTGACCCTGGGCTGCAACAGGCAACCATGAGTTGTGCAC 1473
         ||||:::||||||
Db 510 ArgArgArgAlaGlyLeuGlySerGlyLeuSerLeuSer-------GlyLeuValHis 526

Qy 1474 CCCAGTCTTGCGGACAGTGCCAACAAGTTGAGGAGAACACCTACTGCTTCGGCCGGACC 1533
         ||| :::|||||
Db 527 ProGluLeuSerArgSerGlyGluLeuLeuAlaValAlaArgGluLeuGlnPheAlaThrVal 546

Qy 1534 GTGGAGACACTGCTGCTCCGCTTTGCCAAGCACCATCATGGAGGAGCAGCTGGTACTGAAG 1593
         ||| :::|||||||
Db 547 ValGluAlaLysLeuLeuIleLysHisLysLysGlyIleValAsnGluGlnPheLeuLeuGln 566

Qy 1594 CGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACGGCCGTGCTGTCGCGGGCCAGC 1653
         ||||||:::|||
Db 567 ArgLeuAlaAspGlyAlaIleIleAspLeuProValTyrAlaMetValValLeuSerArgAlaSer 586

Qy 1654 CGCTCCATCCGCATTGGGCTCCGCAACCACGACGAGGTTTCTTGGCCAACACCTTC 1713
         ||||||:::
Db 587 ArgSerLeuSerGluGlyHisProThrAlaGlnHisProThrAlaGlnHisMetLeuCysAspThrTrp 606

Qy 1714 TGCGTGGAA------GCTTACTTGGAGAATCTTCAGCCTCCTCAGCTGGACAAGTAT 1767
         :::|||:::
Db 607 CysIleGluAlaAlaAlaArgIleArgIleGluGlyMetAlaAlaLeuAlaLeuGlnSerAspProTrp 626

Qy 1768 GCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGA 1827
         ||| :::|||
Db 627 GlnGlnGlu---LeuTyrArgAsnPheLysSerIleSerGlyAlaLeuValGluValArgGly 645

Qy 1828 GCCTATATCTGTGCCACCCTCTG 1851
             :::   :::|||||||
Db 646 GlyValValThrSerAsnProLeu 653

RESULT 4
T15905
hypothetical protein E04F6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15905
R;Pauley, A.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid E04F6.

A;Reference number: Z18427
A;Accession: T15905
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-613 <PAU>
A;Cross-references: UNIPROT:Q19057; EMBL:U28943; NID:g861333; PID:g861335; PIDN:AAA68357
C;Genetics:
A;Gene: CESP:E04F6.5
A;IntronB: 55/3; 90/2; 195/3; 233/3; 472/2; 518/1; 567/3

Alignment Scores:
Pred. No.:   Length: 613
Score: 1210.50   Matches: 272
Percent Similarity: 61.16%   Conservative: 109
Best Local Similarity: 43.66%   Mismatches: 205
Query Match: 35.36%   Indels: 37
Db: Gaps: 14

US-09-945-326-3 (1-1863) x T15905 (1-613)

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Qy   19  TTCCTGCGCACCACGGCTCGGGCTCGTGCCTGCGCGGGGTCTGGTCGTCTCTACCGCGAAC  78
         ||:||||| ||  ::::|||||  |||                    :::
Db   16  PheIleArgLeuSerHisSerAlaAlaAlaAlaLys----------AspAlaLysPro  31

Qy   79  CGGCGGCTACTGCGCACCAGCCCGCGTACGAGCTTTCGCCAAAGACTTTTCCTAGGC  138
         :::::||||||          ||||| ||||||||   :::
Db   32  LysLysValAlaAlaValAspSerPro--------SerPheValMetAsnLeuPheArgGly  49

Qy  139  AAAATCAAGAAGAAAGAAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA  198
         ||||:|||||||||||||:::|||
Db   50  LysAlaValThrAspGlnValPheProTyrProLeuAsnMetThrAspGluGlnLysGlu  69

Qy  199  --ATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAGGAGGTGGACTCCCGA  255
            :::  ||:::|||||||
Db   70  ThrLeuGlyMetValMetSerProLeuGluLysMetLeuValGluValAlaAsnAspValVal  89

Qy  256  AAAATTGACCAGGAGGAAGGAAAATCCAGATGAAACTTGGAGAAATTGAAGAGCCTAGGG  315
         ||||||            :::
Db   90  LysAsnAspAspLeuAlaThrSerAspIleProArgAlaValLeuAspGlnPheAlaGluLeuGly  109

Qy  316  CTTTTTGGGCTGCAAGTCCAGAAGAATATGTGGCCTGGCTTCTTCCAACCACATGTAC  375
         ||||||||             :::||||||||:::
Db  110  ThrPheGlyValLeuValProProGluGluGluGlySerGlyTyrPheAsnGlySerGlnMet  129

Qy  376  TCAAGACTAGGGGAGATCATC---AGCCATGGATGGTCCATCATCTGTGACCCTGGCCAGCG  432
         ||:::   :::|||||||
Db  130  AlaArgValAlaAlaIleLeuValGlyIleAlaTyrAspLeuGlyPheGlyValValMetGlyAla  149

Qy  433  CACCAGGCTATTGGGGCCTCAAGGGATCATCTTGGCTGGCACTGAGGAGAAAGCCAAA  492
         |||||||           |||||:::
Db  150  HisGlnSerIleGlyTyrLysGlyIleLeuLeuLeuGluGlyThrArgAlaGlnIleGlyGlnLys  169

Qy  493  TACTTGCCTAAACTGCGTCCGGGAGCCGTCCGCAGCCTTCTGCCTCACGGAGCCAGCC  552
         ||:::||||||            :::
Db  170  TyrLeuProAspLeuAlaThrGlyLysPheLysArgLysAlaAlaPheAlaAlaLeuThrGluProThr  189

Qy  553  AGTGGGAGGCCGATGCAGCCTCAATCCGGGAGCAGAGCCACCAAGTCAACAACAAGAAGCAC  612
         :::|||||||          :::|||||||:::
Db  190  ThrGlySerAspAlaSerValArgThrArgAlaGluLeuSerArgAlaAlaAspGlyLysHis  209

Qy  613  TACATCCTCAATGGCTCCAAGGTCTCCAAGGTCTCCAAGGTCTCCAATATTTTACT  672
         ||:::               :::
Db  210  TyrValLeuAsnAlaGlyLysLysIleValGlyLysIleTrpIleSerArgAsnGlyValAspPheThr  229

Qy  673  GTGTTGCAAAGACTGAGGTCGTTGATTCTGATGATGCAGAAAGACAAAAATCACAGCA  732
         ||||||||:::|||              ::::::
Db  230  ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysGlySerMetSerSerAla  249

Qy  733  TTCTTCAGCTGGACAAGACTATGTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCC  792
         ||||||||             |||||||:::
Db  250  PheIleValGluArgAlaPheGlyLeuGlyValAsnAlaPheGlyLeuGlyProGlnLysLysMetGly  269
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Qy  793  ATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAAAAC  852
         ||:::|||||             :::|||||||
Db  270  IleLysGlySerAsnThrThrGluValHisPheGluAsnLeuIleProValGluAsn  289

Qy  853  ATCCTTGAGAGGTCGGAGATGGTTAAGTGGCCATGAACATCCTCAACAGCGGCCGG  912
         :::||||||             :::|||
Db  290  LeuLeuGlyLysGlyGluGlyPheLysGlyPheAlaMetAsnLeuAsnGlyArgArg  309

Qy  913  TTCAGCATGGGCAGCGTCGTGGCTGGGCTGCTCAAGAGATTGATTGAAATGACTCTGAG  972
         |||  :::||:::|||
Db  310  PheGlyIleLeuProAlaAlaCysThrGlyIleAlaMetLysHisCysIleGlnLysThrValAsp  329

Qy  973  TACGCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGATTCAGGAG  1032
         :::|||||||            :::|||||||
Db  330  HisIleThrThrArgValGlnPheGlyLysLysGlyLysGlnIleGlnGlu  349

Qy 1033  AAAATTGCACTGATGGCTCAGAAGCTTACGTCATGGAGAGATGACCTACCTCACAGCA  1092
         ||              :::|||||||
Db  350  LysLeuValGluMetIleSerLysLeuTyrAlaThrGluSerIleValTyrMetLeuSer  369

Qy 1093  GGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCAGCCATGGTGAAGGTG  1152
         :::||||||             :::|||
Db  370  SerAsnMetAspArg---GlyIleLeuGluTyrGlnLeuGlnLeuGluAlaIleGlyLysLysVal  388

Qy 1153  TTCAGTCCGAGGCCGCCTGCAGTGTGTGAGTGAGCGGCTGCAGATCCTCCGGGGGCTTG  1212
         ||:::|||||||            :::|||
Db  389  LeuAlaSerGluIleAsnAlaTrpLeuVal CysAspAspValHisGlnValHisGlyGlyMet  408

Qy 1213  GGCTACAACAAGGGACTATCCGTACGAGCGCCATACCCGACACCCGGCCATCCTCCATC  1272
         :::|||||||             :::
Db  409  GlyPheMetArgGluThrGlyLeuGluValLeuArgValLeuArgAspLeuArgIlePheArgIle  428

Qy 1273  TTCGAGGGAACCAATGAGATTCCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCC  1332
         |||||||             :::|||||||
Db  429  PheGluGlyAlaAlaAsnAspValLeuGluArgLeuPheIleAlaLeuThrGlyAlaGlnHisHisAla  448

Qy 1333  GGCCGCATCCTGACTACCACCAGGATCCATGAGCTTAAACAGGCCAAGTGACCAGTCATG  1392
         :::|||||||             |||:::
Db  449  GlyLys----------HisLeuAlaGluHisLeuAla-----SerGlyValGlyGly  460

Qy 1393  GATACCCTTGGGCCGGAGGCTTCGGAACTGCTGACCTGGGACTGGGACTGACA  1452
         ||:::             :::||||||
Db  461  GlyLeuIleGlyLeuAlaValSerArgValThrGly----------GlyAsnThr  475

Qy 1453  GGC---AACCATGGA----GTTGTGCACCCCAGTCTTGGGACAGTGCCAACAAGTTTGAG  1506
         |||              :::|||||||
Db  476  GlySerAsnPheGlyGlnValValAspAspAlaSerLeuGlnAspSerAlaLysValLeuAsp  495

Qy 1507  GAGAACACCTACTGCTTCGGGCCGACCGTGAGAGACACTGCTGCTCCCGCTTGGCAAGACC  1566
         :::|||||||             |||:::
Db  496  GlnGlnIleAlaLeuPheGlyLysGlyInThrValGlnGlyLeuLeuMetLysHisLysLysGly  515

Qy 1567  ATCATGGAGGAGCAGTCTGAGCGGGTGGCCAACATCCTCATCAACCTGTATGGC  1626
         ||:::             :::|||||||
Db  516  IleIleAspArgIleTyrGluMetHisArgValAlaAlaAspAlaIleAlaIleTyrSer  535

Qy 1627  ATGACGCGGTGTCGTGCGCGGCAGCCTCCATCCGCCATTGGCTCCAACCACGAC  1686
         :::             :::|||||||:::
Db  536  SerAlaAlaValLeuSerArgAlaIleLysLysAsnSerSerSerAlaAsp  555

Qy 1687  CACGAGGTTCTCTTGCCAACACCTTCTGCGGTGGAAGCTTACTTGCAGAATCTCTTCAGC  1746
         ||              :::
Db  556  PheGluArgLysValAla---ThrTyrTyrValAspLysAlaMetLys--------Ser  571

Qy 1747  CTCTTCCAGCTGGACAAGTAGTCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCC  1806
         ||              :::|||
Db  572  SerAsnArgPheLeuLysAspAlaGlySerGlyValGluLeuuAsnAlaSerLysValAlaThr  591

Qy 1807  CAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC----------CAC  1845
         :::             :::|||
Db  592  IleGluSerLeuAlaLysGlu-----ValCysGlyAsnGlyLeuThrLeuGluHis  609

Qy 1846  CCTCTGGAC  1854
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Db   610 ProValGlu 612
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RESULT 5
F84085      828
butyryl-CoA dehydrogenase BH3486 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84085
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-594 <STO>
A;Cross-references: UNIPROT:Q9K784; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB072

C;Genetics:
A;Experimental source: strain C-125
A;Gene: BH3486

Alignment Scores:
Pred. No.:                          Length:          594
Score:               2.64e-46       Matches:         207
Percent Similarity:  821.00         Conservative:    105
Best Local Similarity: 50.00%       Mismatches:      210
Query Match:         33.17%         Indels:          102
DB:                  23.98%         Gaps:            13

US-09-945-326-3 (1-1863) x F84085 (1-594)
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Qy   133 CTAGGCAAAATCAAGAAGAAGAAGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAAACTT 192
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Db    16 LeuAspGluIleAspAlaAspLysValPhe----------ThrProGluAspPhe 30

Qy   193 AATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACT------------ 237
             |||    ::|||||    |||  ::  |||
Db    31 ThrGluGluHisGluMetIleGlyLysThrGlyLysThrGluGluPheValValAsnGluValVal 50

Qy   238 ----------GAAGAGGTGGACTCCCAGAAAATTGACCAGGAAGGGAAAATCCCAGATGAA 288
                      :||||||    |||    :::
Db    51 ProValLeuAspGluIleGluAspLysAsnHisGlnPheAsp----------IleSerArgArg 66

Qy   289 ACTTTGGAGAAATTGAAGAGCTAGGGCTTTGCGTCGCTGGCTCCCAGAAGAATATGGT 348
             |||      :::    |||||||||    ::||
Db    67 LeuLeuThrGlnAlaGlyLeuLeuGlyLeuAlaAspValProGluGluTyrGly 86

Qy   349 GGCCTTGGCGTTCTCCAACACCATGTACTAGGGGAGATCATCAGCAGGATGGGATGGG 408
             ||| |||||||||||||    ::: ||
Db    87 GlyLeuGlyLeuAspLysIleSerSerIleIleThrGluLysPheGluLysSerArgAlaAlaGly 106

Qy   409 TCCATCACTGACCCTGGCGCCACCAGCTATTGGCTCAAGGGGATCATCTTGGCT 468
             |||     :::||
Db   107 GlyPheSerLeuSerTyrGlyTyrAlaHisValGlyIleGluSerLeuProIleValPhePhe 126

Qy   469 GGCACTGAGGACGCAGAAAGCCAAATACTTGCCTAAACCTGGCGTCCGGGGCACATTGCA 528
             |||     :::||||     ||||||
Db   127 GlyAsnGluAspGlnLysLysTyrLeuProAspLeuAlaThrGlyAlaArgIleAla 146

Qy   529 GCCTTCTGCCTCACGGAGCCCAGTCGAGCCGATGCAGCCTCAATCCGAGCAGAGCC 588
             |||||||||    :::     ||||
Db   147 AlaTyrAlaLeuThrGluThrGlyHisLysAsnGlyTyrSerAspAlaLeuGlyAlaLysThrArgAla 166

Qy   589 ACACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAAT 648
             ||||||       :::
Db   167 ValLeuLysAsnGluAlaGlyThrHisTyrHisTyrValLeuAsnGlyLysGluLysGlnTrpIleThrAsn 186

Qy   649 GGAGGACTGGCCAATATTTTTACTGTGTTTGAATACTGCGTTGATTCTGATGGA 708
             ||||||       :::|||||
Db   187 SerAlaPheAlaAspValPheIleValTyrAlaLysIle----------AspGly 201

Qy   709 TCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAAT 768
             ||||||                :::
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Db   202 ----------GluHisPheSerAlaPheIleValGluLysAspPheGluGlyValSerThr 218
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Qy   769 GGGAAACCGGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAA 828

Qy   219 GlyProGluGlyLysMetGlyIleLysGlySerThrArgThrLeuIleLeuGlu 238
             |||    ::: |||    :::|||
Db   829 AACACCAAGATACCTGTGGAAAACATCCTTGAGAGGTCGGAGATGGGTTAAGGTGGCC 888

Db   239 AspAlaLeuVa1ProLysGluAsnLeuLeuGlyValGlyLysValGlyHisValIleAla 258
             :::    |||||||||||
Qy   889 ATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGGTCGTGGCTGGCTGCTCAAG 948

Qy   259 PheAsnIleLeuAsnValGlyArgTyrLysLeuGlyValGlyCysIleGlyGlySerLys 278
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Db   949 AGATTGATTGAAATGACTGCTGAGTACGCCTCCACAAGAAACAGTTTAACAAGAGAGGTC 1008

Db   279 ArgGlyIleGluLeuAlaAlaLysTyrAlaAsnGluArgLysGlnPheLysGlnProIle 298
             ||| :::  |||||||||
Qy  1009 AGTGAATTTGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCACGTCATG 1068

Db   299 AlaLysPheThrLeuIleGluGlnGluLysLeuLeuAlaAsnMetAlaValThrThrTyrAlaAla 318
             ||||||:::  :::
Qy  1069 GAGAGTATGACCTACCTCACAGCAGGAGGATGCTGGACCAA---------- 1107

Db   319 GluSerSerIleTyrArgThrGlyLeuPheGluAspArgLeuGlyGlyLeuSerGlu 338
             |||||     ::: |||||
Qy  1108 ----------CCTGGCTTCCCGACTGCTCCATCGAGGCA 1137

Db   339 GluGlnGlnLysAspGlyArgGluValAlaLysProGlyValValAlaIleAlaIleAlaGluGluCys 358
             :: :::|||||||
Qy  1138 GCCATGGTGAAGGTGTTCAGCTCCGAGGCCCGGCTGCAGTGTGAGTGAGGCGCTGCAG 1197

Qy   359 SerLeuAsnLysValValGlySerGluAlaLeuAsnAspPheValAlaLysAspGluAlaValGln 378
             ::::|||||     :::
Db  1198 ATCCTCCGGGGCTTGGCTACCACAGGGACTATCCGTACGAGCGCCATACTGCGTGACACC 1257

Db   379 IleHisGlyGlyTyrGlyPheMetAlaGluTyrGluValGluArgMetTyrArgAspSer 398
             |||||  :::|||||
Qy  1258 CGCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACCGCCCTGACG 1317

Qy   399 ArgIleAsnArgIlePheGluGlyThrAsnGluIleLeuAsnArgLeuLeuValProGlyThr 418
             ||||||    |||
Db  1318 GGTCTGCAGCATGC---------GGCCGCATC---CTGACTACCAGGATCCATGAGCTTAAA 1368

Db   419 IleLeuArgLysAlaMetLysGlyGluLeuProPheLeuLysAlaAlaThrAlaLeuGln 438
             :::    |||
Qy  1369 CAGGCCAAAGTGACAGAGAGCAGTCATGATACCGTGGCCGGAGGCTTCGGGACTCCCTGGGC 1428

Qy   439 GluGluLeuMetMetLeuMetProGlnGluValGly----------GluGly 450
             :::
Db  1429 CGAACTGTGGACCTGGGGCTGACAGGCAACCATGAGTTGTGCACCCAGTCTTGCGGAC 1488

Db   450 ---------- 450

Qy  1489 AGTGCCAACAGTTTGAGGAGAACAAGTTCTTGGCCGGCCGACCTGGAGGACACTGCTG 1548

Db   451 ---AspGluProLeuGlnGluLeuGlnLysTyrLeuLeuSerMetAlaLysValPheLeu 469
             :: :::|||||
Qy  1549 CTC----------CGCTTTGGCAAGACCATCATGAGGAGGAGCAGTCGTA 1587

Db   470 MetIleAlaGlyThrGlyAlaGlnThrTyrGlyValLysLeuGlnGlnGluLeu 489
             ::: |||||||
Qy  1588 CTGAAGCGGGTGGCCAACATCCTCATCAACCTGATAGGCATGACGGCGCCGTGTCCGCGG 1647

Db   490 LeuAlaAsnValAlaAspIleSerAspIlePheSerMetGluSerValIleLeuArg 509
             :::||||||
Qy  1648 GCCAGCCGCTCCATC---CGCATTGGGCTCGCAACCACGACGAGGTTCTTTGGCC 1704

Db   510 ThrGluLysAlaIleArgArgAsnGlyLeuGluGlnLysLeuAlaLeuGlnLysLeuGlnThr 529
             |||||     ||||||
Qy  1705 AACACCTTCTGCGTGGAAGCTTAC----------- 1728
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Db   109  SerLeuSerTyrGlyAlaHisValGlyIleGlySerLeuProIleValPhePheGlySer  128
Qy   475  GAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCACATTGCAGCCTTC  534
          |||||||||||||||| |||||   ||||||  ||||||||||||||
Db   129  GluGluGlnLysLysTyrLeuProGlyLeuAlaSerGlyValIleLeuIleAlaAlaTyr  148
Qy   535  TGCCTCACGGAGCCCAGTGGAGCGATGCAGTCCAATCCGGAGCAGAGCCACACTA       594
          :::  ||||||| ||||| ::::::::||::  |||||||| |||||
Db   149  AlaLeuThrGluProIleSerGlySerAspAlaGlyLyAlaLysThrArgIleValLeu   168
Qy   595  AGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGATTACTAATGGAGGA   654
          :::    ||||||||||  |||   :: |||||||||||||
Db   169  AsnGluAlaGlyThrHisTyrValLeuThrGlyGluLysGlnTrpIleThrAsnSerAla  188
Qy   655  CTGGCCCAATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATGATGATCAGTG     714
          |||||||||| ||| ||||||||||||
Db   189  PheAlaAspValPheValValTyrAlaLysVal--------AspGly------        201
Qy   715  AAAGACAAAATCACAGCATTCATAGTAGAAGAGACTTGGTGGAGTCACTAATGGGAAA   774
          :: |||    |||||||||:::::||  |||
Db   202  ---AspLysPheSerAlaPheIleValGluGluThrLeuValSerGlyValSerThrGlyPro  220
Qy   775  CCCGAAGATAAATTAGGCATTCGGGGTCCAACACTTGTGAAGTCCATTTGAAAACACC   834
          ||||| :::||||||||:::::|||||
Db   221  GluGluLysLysMetGlyIleLeuLysGlySerSerThrArgThrLeuLeuAspGlnAla  240
Qy   835  AAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAAC  894
          :::::|||    |||||||||:::|||   ||||||
Db   241  GluValProLysGluAsnLeuLeuGlyLleuGlyHisGlyHisValIleValIleAlaPheAsn  260
Qy   895  ATCCTCAACACGCGGCCGGTTCAGCATGGGCAGCGTCGGTGGCTGCTCAAGAGATTG   954
          |||:::   ||||||||||
Db   261  IleLeuAsnIleGlyArgTyrIleLysLeuAlaValGlyThrIleLeuAlaSerLysLysArgVal  280
Qy   955  ATTGAAATGACTGCTGAGTACGCCCTGAGCAACAGAAACAGTTAACAAGAGGCTCAGTGAA  1014
          |||||||||| :::::||||
Db   281  IleGluLeuSerAlaAlaTyrAlaAsnGlnAsnArgGlnPheLysThrProLeuAlaGly  300
Qy   1015 TTTGGATTGATTCAGGAGAAATTTCCACTGATGGCTTCAGAAGGCTTACGTCATGGAGAGT  1074
          ||| :::   :::  |||
Db   301  PheSerLeuThrGlnGluLeuGlyIleLysGlyThrMetAlaSerArgLeuTyrAlaMetGluSer  320
Qy   1075 ATGACCTACCTCACAGCAGGGATGCTGGACCAA----------------------       1107
          :::  :::
Db   321  SerValTyrArgThrValGlyLeuPheGluAspAsnMetSerGlnPheThrAlaGluAsp  340
Qy   1108 --------------CCTGGCTTCCCGACTGCTCCATCGAGGCCAGCCATG          1143
          :: ||||||||
Db   341  LeuLysAspGlyArgGlnIleAlaAlaGluSerIleAlaGluGlyTyrAlaIleGluCysSerLeu  360
Qy   1144 GTGAAGGTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGCCGTCGAGATCCTC  1203
          :::|| ||||||   |||
Db   361  AsnLysValPheGluSerGluTyrIleGlyThrValIleAlaAspGluGluValGlnIleHis  380
Qy   1204 GGGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCGTGACACCCGCATC  1263
          |||:::  :::   :::
Db   381  GlyGlyTyrGlyPheMetGlnLeuTyrGluValGlnValAlaTyrArgAspSerArgIle  400
Qy   1264 CTCCTCATCTTCGAGGGAACCAATGAATTCTCCAGGAAGATGAAACTTTG           1323
          :: |||||||||||
Db   401  AsnArgIlePheGluGlyThrAsnGluIleAsnArgLeuIleValProSerThrPheLeu  420
Qy   1324 CAGCATGCC------GGCCAGCATC---CTGACTACCAGGATCCATGAGCTTAAACAGGCC  1374
          :::   :::
Db   421  LysLysAlaLeuLeuGlyLeuGluLeuProLeuPheGlyGlyAlaGlnSerLeuGlnGluGlu  440
Qy   1375 AAAGTGAGCACAGTCATGATACCGGTTCGGGCCGGAGCCTTCGGGGACTTCCCTGGGCCGAACT  1434
          |||||| |||
Db   441  LeuMetMetProGluGluProGly----------------                     450
Qy   1435 GTTGGACCTGGGGCTGACAGGCAACCATGAGTTGTGCACCCAGTCTTGCGGACCAGTGCC  1494
          :: :::
Db   451  ------------SerGlyValLeu-----------                          454
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RESULT 6
C70021
butyryl-CoA dehydrogenase homolog yusJ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C70021
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berten
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C70021
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-594 <KUN>
A;Cross-references: UNIPROT:O32176; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15271.
A;Experimental source: strain 168
C;Genetics:
A;Gene: yusJ
```

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Alignment Scores:
Pred. No.:
Score:                  6.1e-46         Length:        594
Percent Similarity:     815.50          Matches:       201
Best Local Similarity:  49.58%          Conservative:  97
Query Match:            33.44%          Mismatches:    202
                        23.82%          Indels:        101
DB:                                     Gaps:          2
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US-09-945-326-3 (1-1863) x C70021 (1-594)

Qy   175  GTTAGCCAAGATGACTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAATTCTTC    234
          ::  |||||||  |||  ||   ||
Db   45   IleGluGlnAspValLeuProHisIle---------------------------      53
Qy   235  ACTGAAGAGGTGGACTCCCGAAAAATTGACCAGGAGGGAAAATCCCAGATGAAACTTTG  294
          ::::::::::::: :: ||| :: |||
Db   54   ---AspAspIleGluAsnHisGlnPheGluHisSerValArgLeu----------Leu  68
Qy   295  GAGAAATTGAAGAGCCTAGGGCGTTTTGGGCTGCCAGTCCAAGAGAATATGGTGGCCTG  354
          ::|||    |||||| || |||| |||||
Db   69   LysLysAlaLeuLeuGlyLeuLeuGlyLeuAlaAspValProGluGluTyrGlyLyLeu  88
Qy   355  GGCTTCTCCAACAACCATGTACTCAAGACTACTAGGGAGGAGTCATCAGCATGAGGTTCCATC  414
          |||   :: :::  ||::  |||||
Db   89   GlyLeuAspLysIleSerSerAlaLeuIleThrGluLysPheSerArgAlaGlySerPhe  108
Qy   415  ACTGTGACCCTGGCAGGCGCCACCCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACT  474
          |:::|  |||||  |||||
Db        --------------------SerGlyValLeu-----------                 454
```

```
Db   530  GlnValPheCysGlnGlnAlaPheAsnArgIleGluAlaHisAlaAlaLysGluSerLeuVal  549
Qy   1729 -------------------TTGCAGAATCTTCAGC---CCTCTCAGCTGGACAAG       1764
          :::   ||  ||  :::  |||   ||| |||||
Db   550  AlaMetGlnSerGlyAspThrArgMetThrSerIleLeuArgLysLeuThrArg          569
Qy   1765 TATGCTTCCGAAAACCTAGATGAGCAGATTAAGAAGTGTCCAGCAGATCCTTGAGAAG    1824
          :::  ||| ||||   ::::::::::||| :::||||||
Db   570  HisThrProIleAsnValIleLysAlaLysLysArgGluIleLeuAlaGlyArgIleLeuGluAla  589
Qy   1825 CGAGCCTATATC                                                 1836
          |||||||||||
Db   590  GluArgTyrVal                                                 593
```

```
Qy   232 TTCACTGAAGAGGTGGACTCCGAAAAATTGACCAGGAAGGCAAAATCCCAGATGAAACT 291
             :::   ||||||  ||::::  |||||    |:::::  ||||||
Db    68 Leu--AspThrValAspGlySerValIleGluArgGlnAlaAlaGlnIleProAspGluTyr 86

Qy   292 TTGGAGAAATTGAAAGCCTAGAGCCTTTTTGGGCTGCCAAGTCCAAGAAGATATGGTGGC 351
             ::::::  |||||||||  ||:::||  ||||||:||  |||||||
Db    87 ValLysGlyLeuLeuGlyCysPheGlyLeuLysIleProSerGluTyrGlyGly 106

Qy   352 CTGGGCTTCTCCAACACCATGTACTACCAAGA---CTAGGGAGATCATCAGCATGGATGGG 408
             |||    ||::::||||  ::  :::  |||
Db   107 LeuAsnMetSerGlnValAlaThrArgAsnArgValLeuMetMetValThrValHisSer 126

Qy   409 TCCATCACTGTGACCCTGGCAGCGCCACCAGGCTATTGGCCTC---AAGGGGATCATCTTG 465
             |||::||  ||  ::  ::  |::|  |||||  ::  :::  :::
Db   127 SerLeuGlyAlaLeuSerAlaHisGlnSerIleGlyValProGluLysLysLeu 146

Qy   466 GCTGGCACTGAGGAGGCAGAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCACATT 525
             ||::::  :::  |||||  ||::||||  ||:::|||||:::|||Ala---Ile
Db   147 AlaGlyThrAlaGluGlnLysArgAsnLeuProArgCysAlaAlaGlyAla--Ile 165

Qy   526 GCAGCCTTCTGCTGCCGAGCCAGCCAGTGGGAGGCGATGCAGCCTCAATCCGGAGCAGA 585
             :::|||  ||||  |||||  ||::::||  |||:::|  ::||
Db   166 SerAlaPheLeuLeuThrGluProAspValGlySerAspProAlaArgMetAlaSerThr 185

Qy   586 GCCACACTAAGTGAAGACAAGAAGCACTACATCCTCAAGTGCTGGATTACT 645
             ||::::  :::  |:::  ::::  |||||||
Db   186 AlaThrProIleAspAspAspGlyGlnAlaTyrGluLeuGlyValLysValLysTrpThrThr 205

Qy   646 AATGGAGGACTGGCCAATATTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATTCTGAT 705
             |||  :::  :::||||  ::  :||||||------ValProArgSerGlu
Db   206 AsnGlyValValAlaAlaCysAlaAsnLeuLeuValValMetAlaArg------ 223

Qy   706 GGATCAGTGAAAGACAAAATCACAGCATTCATAGTAGAAAAGAGACTTGGTGGAGTCACT 765
             |||    GlyHis---ArgGlyIleSerAlaPheValValGluAlaAspSerProGlyIleThr 242
Db   224 GlyHis---ArgGlyIleSerAlaPheValValGluAlaAspSerProGlyIleThr 242

Qy   766 AATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAGTCCATTT 825
             ::::::  ||||||  |||||  |||||||
Db   243 ValGluArgAsnLysPheMetGlyLeuArgGlyIleGluAsnGlyValThrArgLeu 262

Qy   826 GAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGAGATGGGTTTAAGGTG 885
             |||||||||::::  :::||||
Db   263 HisArgValArgValProLysAspAsnLeuIleGlyArgGluGlyLysLeuLysIle 282

Qy   886 GCCATGAACATCCTCAACACGCGCCGGTTCAGCATGGCAGCGTCGGCGTGGGCTGCTC 945
             :::  :::  |||||  |||::::::  ::::::
Db   283 AlaLeuThrThrLeuAsnAlaGlyArgLeuSerLeuProAlaIleAlaThrGlyValAla 302

Qy   946 AAGAGATTGATTGAAAATGCTGCTGAGTAGCGCCTGCACAAGGAAAACAGTTTAACAGAGG 1005
             |||  :::::  |||  ||||  :||  |||||  :::  |||
Db   303 LysGlnLeuLysIleAlaArgGluTrpSerValGluArgValGlnTrpGlyLysPro 322

Qy  1006 CTCAGTGAATTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTC 1065
             ::::  :::::  ||||||  |||  :||||
Db   323 ValGlyGlnHisGluAlaValAlaSerLysIleSerPheIleAlaAlaThrAsnTyrAla 342

Qy  1066 ATGGAGGATGACCTACCTCCACAGCAGGATGCTGGACCAACCTGGCTTTCCCACTGC 1125
             ::::::::::  |||||::::  :::::::  |:::||||:::---GlyArgAsnAspIle
Db   343 LeuAspAlaValGluLeuSerGlnMetAlaAspGlu--GlyArgAsnAspIle 361

Qy  1126 TCCATCGAGGCAGCCATGTGAAGGTGTTCAGCTGGAAGTTGGTGGCAGTGTGTGAGT 1185
             ||::::  |||||::::  :::||||  |||||
Db   362 ArgIleGluAlaAlaLeuAlaLysGluSerGluMetAlaCysLeuValGlyLeuValGlyAsp 381

Qy  1186 GAGGCGCTGCAGATCCTCGGGGGCTTGGGCTAC----- 1218
             ||||||||||||||  :::::|||||||||
Db   382 GluLeuLeuGlnIleLysArgGlyArgGlyTyrGluThrAlaGluSerLeuAlaAlaArg 401

Qy  1219 ---ACAAGGGACTATCCGTACGACGCCATACTGCGTGACACCCGTCCTCCATCTTC 1275
             ||||||||||  ||::::  |||||
Db   402 GlyGluArgAlaValProValGluGlnMetValArgAspLeuAsnArgIleAsnArgIlePhe 421

Qy  1276 GAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT------------CTG 1323
```

```
Qy  1495 AACAAGTTGAGGAGAACACTTACTGCTTCGGCGGCCGTGGAGACACTGCTGCTC--- 1551
             ||::::|  |||  :::  |||||  :::  |||::||||||
Db   455 -------GluGlnGluLysTyrIleValLysGlnAlaLysLeuAlaAlaLeuPheAla 471

Qy  1552 --------CGCTTGGCAAGACCATCATGGAAGCCATCATGGAGGAGCAGCTGGTACTGAAG 1593
             :::::::||||  ||||||||  :::::  :::|:::  |||||
Db   472 AlaGlyAlaLeuAlaAlaGlnIleLysArgGlyLysAlaIleAlaAspArgGlyIleGlnIleLeuLeuVal 491

Qy  1594 CGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACGCGCCGTGCTGTCCGGGCCAGC 1653
             :::  |||::::  |||||||  :::  :::  ::: :::
Db   492 AsnValAlaAspIleValSerAsnValTyrAlaMetGluSerAlaValLeuArgThrGlu 511

Qy  1654 CGCTCCATCCGCATT--GGGCTCCGCAACCAACGCACCACGAGGTTCTTGGCCAACACC 1710
             ||:::|  :::||||  ::  |||||  :::  :::  :::  ||||
Db   512 LysAlaIleAlaAlaGlnLysAlaLeuGlyAlaLeuAlaAlaGlnLysValIleGluThrGluIle 531

Qy  1711 TTCTGCGTGGAAGCTTACTTGCAG------- 1734
             ||:::  |||||  ::  :::
Db   532 PheValGlnGluAlaPheAsnGlnIleGluGluHisAlaHisAlaLysGluSerLeuIleAlaMet 551

Qy  1735 --------AATCTCTTCAGCCTCTCCAGCTGCGACAAGTATGCT 1770
             :::||||  :::||
Db   552 GluGluGlyAspSerLeuArgMetMetSerAlaLeuArgLeuAlaLeuArgLysLeuThrArgValThr 571

Qy  1771 CCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCCAGCAGATCCTTGAGAAGCGAGCC 1830
             :::  :::::  ::||  ::  ||:::|||
Db   572 ProLysAsnValIleGlnLysLysLysArgGluAlaAlaAlaIleAlaGlyIleIlePheGluGluAlaGluLys 591

Qy  1831 TAT 1833
             |||
Db   592 Tyr 592
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RESULT 7

A70817

probable fadE10 protein - Mycobacterium tuberculosis (strain H37RV)

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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
  sequence
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70817
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-650 <COL>
A;Cross-references: UNIPROT:Q10535; GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA1767
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: fadE10
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Alignment Scores:

Pred. No.:	4.98e-39	Length:	650
Score:	711.00	Matches:	194
Percent Similarity:	49.68%	Conservative:	113
Best Local Similarity:	31.39%	Mismatches:	223
Query Match:	20.77%	Indels:	88
DB:		Gaps:	16

US-09-945-326-3 (1-1863) x A70817 (1-650)

```
Qy   112 GCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAAGAAGTTTTCCATTTCCA 171
             :::||||||||||||||||||:::  ||||||||||:::  ||||||
Db    28 SerPheAlaLysGluLeuPheLeuGlyLysIleLysLysLysGluValPheHisProPhePro 47

Qy   172 GAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGACCCCGTGGAAAAATTC 231
             |||  :::||||||  :::||  :::::  |||||:::
Db    48 LysProSerAspAlaGluArgThrGluAlaPheLeuAlaPheLeuValLysLysValArgGluPhe 67
```

```
Db   187 GAACTTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTG 246
             :::|||      |||||:::|||||||||||::|||         |||       ||
Qy   422 GluGlySerSerGluIleMetArgLeuLeuIleAlaArgGluAlaValAlaAspAlaHisLeu 441

Db     4 AspLeuGluThrArgGluGlnLeuIleLeuAspThrValAlaAlaArgPheValAlaArgLeu 23

Qy  1324 CAGCATGCCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGC 1383
             :::|||||              :::     ||:|||::|||
Db   247 GAC------TCCCGAAAAATTGACCAGGAAGGAAAATCCCAGATGAAACTTTGGAGAAA 300

Qy   442 ThrAlaAlaGlyLeuAlaAsnProLysAla---AspLeuArgGlnLysAlaAlaAla 460

Db    24 ArgProIleGluAlaGlnLeuAlaLeuAlaLysAsnAspAlaValProAspValIleGluGlu 43

Qy  1384 ACAGTCATGGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGCCACTGTGGACCTG 1443
             :::||||||::|||||||::|||::||::::|||||||||||::::|||||||
Db   301 TTGAAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAAGAGAGATATGTGGCCTGGGCTTC 360

Qy   461 AlaAla-------------------------------------------------------- 462

Db    44 MetLysGlyLeuPheGlyLeuThrIleProGluGluProGluGluGlyLeuGly-- 62

Qy  1444 GGGCTGACAGGCAACCATGAGTTGTGCACCCCAGTCTTGCG-------------------- 1485
             |||::|||      :::           |||  :::
Db   361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGATGGGTCCATCACTGTG 420

Qy  1486 -----------------------------------------------GACAGT 1491
                                                            |||
Db    63 ------------------------------------------LeuThrMetGluGluGlyLeuVal 71

Db    72 AlaIleGluLeuGlyArgAlaSerProAlaPheArgSerValGlyThrAsnValGly 91
             :::|||
Qy   483 ProThrThrTyrArgGluPheGlyAlaLeuAlaThrHisLeuArgPheValGluArgSer 502
             ||||||
Db   421 ACCCTGCAGCGCACCAGGCT-------------------------------------- 441

Qy  1492 GCCAACAAGTTGAGGAGAACACTTACTGCTTCGGCCGACGTGGAGACACTGCTC 1551
             :::|||          |||||              :::
Db   442 ATTGGCCTCAAGGGGATCATCTTGGCTGGTACTGAAGCGGGTGGCCAACATCCTC 501

Qy   503 SerArgLysLeuAlaArgAsnThrPhe---TyrGly---------------MetAla 515

Db    92 IleGlySerGlnGlyLeuValMetPheGlyAsnAspGlnGlnLysAlaLysTrpLeuPro 111

Qy  1552 CGCTTGGCAAGACCATCATGGAGAGACAGCAGCCGGGTACTGAAGCGGGTGGCCAACATCCTC 1611
             |||:::         |||||||      :::|||||||
Db   502 AAACTGGCGTCCGGGACCACATTGCAGCTTCGGCTTCACGGAGCCAGTGGGAGC 561

Qy  1612 ATCAACCTGTATGGCATGACCGGCCGTCGTCGCGGGCCAGCGCCGTCCATCCGCATTGGG 1671
             ::::::      :::|||||||||
Db   112 GlyIleAlaSerGlyAlaValIleThrSerPheAlaLeuThrGluProGluAlaGlySer 131

Db   132 AspSerAlaAlaValAlaValGlnThrArgAlaThr------ArgAspGlyAlaAspTyrIleLeu 149

Qy  1672 CTCCGACCACCAGGTTCTCTGCCCAACACCTTCTGC-------------------------- 1716
             :::                          ||||||
Db   562 GATGCAGCCTCAATCCGGAGCAGAGCCACTAAGTGAAGACAAGAGAGCACTACATCCTC 621
             |||:::|||        :::|||::||||||
Qy   536 AlaGluLeuPheAlaIleSerAlaAlaCysValArgAlaAlaCysValAlaValAlaValAlaGlnThrArgAlaAsp 555

Db   150 AsnGlySerLysArgTyrIleThrAsnAlaGlyLysAlaSerLeuPheThrValMetAla 169

Qy  1717 ---GTGGAAGCTTACTTGCAGAATCTTCAGCCTGGTGACAAGTATGCTCCA 1773
             |||::::::|||||||
Db   622 AATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTTACTGTGTTTGCA 681

Qy   556 ProValGluGlyGluGlnAlaTyrGluLysAlaLeuAlaTyrGluAlaGlnLeuAlaPheCysPheGlnGlnAlaThrLeu 575

Db   170 ArgThrAsn---ProAspAlaLysGlyGlyAla------GlyValSerAlaPheLeuVal 186

Qy  1774 GAAAACCTAGATGAGGAGCAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGA 1827
             :::      :::||||||      ::::|||||||
Db   682 AAGACTGAGGTCGTTGATCGTTGATGGATGACGTCAGTGAAAGACAAAATCACCAGCATTCATAGTA 741

Qy   576 ArgValGluAlaLeuPheAspAlaLeuTrpSer-------------------- 586

Db   187 ProArgAspLeuProGlyLeuThrValGlyProGluLysProGluLysMetGlyMetGlyGlnGlnGly 206

Qy   742 GAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGC 801
             ::::::|||      :::||||||::::::
Db   802 TCCAACACTTGTGAAGTCCCATTTTGAAAAAACACCAAGATACCTGTGAAAAACATCCTTGGA 861

Qy   587 ---AsnThrAspSerIleAspValArgLeuLeuAsnAspValArgLeuLeuAsnAspValGluGlyArg 603

Db   207 AlaHisIleHisAspValThrPheAspAsnValArgValProAlaTrpAsnArgArgLeuGly 226

Qy   862 GAGGTCGGAGATGGGTTAAGGTGCCCATGAACATCTCAACAGCAGCGGTTCAGCATG 921
             |||:::|||||||||::::|||      ||||||
Db   227 AlaGluGlyGluGlyPheLysValAlaMetGlnValLeuAspArgGlyArgLeuHisIle 246

Qy   922 GGCAGCGTCGTTGGCTGGCTGCTCAAGATGGCTGAGTACGCCTGC 981
             :::|||      ::::::|||:::||||||
Db   247 AlaAlaValCysValGlyValAlaAlaGlyLeuIleAlaAspCysValAlaSer 266

Qy   982 ACAAGGAAAACAGTTAACAACAGAGGCTCAGTGAATTTGGATTGATTCAG--------- 1029
             ||||||          :::          :::
Db   267 GluArgLysGlnGlyGlnProIleAlaSerPheGlnLeuLeuGlnAlaMetIleAla 286

Qy  1030 ---GAGAAATTGCAGTGGTCTCATGGCTACAAGGCTTACGTCATGGAGAGTATGACCTACCTC 1086

Db   287 AspSerLysThrGluAlaLeuAlaAlaLysAlaLysValLeuGluThrAlaArgLysArg 306

Qy  1087 ACAGCAGGGATGCTGACCAACCTGCGTTTCCCGACTGTCATCGAGGCAGCCATGTGTG 1146
             |||:::      :::
Db   307 AspAlaGlyVal------------AsnValThrLeuGluAlaAlaAlaSerSer 319

Qy  1147 AAGGTGTTCAGCTCCGAGGCCGCCTGGCCAGTGTGTGAGTGAGGCGGCTGCAGATCCTCGGG 1206
             |||:::||||||||||
Db   320 LysLeuPheAlaSerGluMetValGlyValArgValAlaAspArgValAlaValGlnValPheGly 339
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RESULT 8

B87302

acyl-CoA dehydrogenase, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87302
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
  B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
  n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
  Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <STO>
A;Cross-references: UNIPROT:Q9AB07; GB:AE005673; NID:gi3421592; PIDN:AAK22414.1; GSPDB:C
C;Genetics:
A;Gene: CC0427
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:   2.64e-38   Length: 382
Score: 699.00   Matches: 155
Percent Similarity: 58.31%   Conservative: 80
Best Local Similarity: 38.46%   Mismatches: 124
Query Match: 20.42%   Indels: 44
                                    Gaps: 8

US-09-945-326-3 (1-1863) x B87302 (1-382)

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Qy  1207 GGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCCTGACACCCGCATCCTC 1266
         ||| :::::|||||   ||||||      |||||:   ||||| |||||
Db   340 GlyAlaGlyThrValAlaAspThrTyrGlyIleGluArgLeuTyrArgAspValArgIlePhe 359

Qy  1267 CTCATCTTCGAGGGAACCAATAGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAG 1326
         |||||||  :::::       :::::::   |||||:
Db   360 ArgIleTyrArgGluGlyThrSerGlnValGlnGlnLeuIleIleAlaArgGluThrLeuLys 379

Qy  1327 CATGCCGGC 1335
         ||||||
Db   380 ArgGlyGly 382

RESULT 9
B83443
probable acyl-CoA dehydrogenase PA1631 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83443
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <STO>
A;Cross-references: UNIPROT:Q9I391; GB:AE004590; GB:AE004091; NID:g9947587; PIDN:AAG0502
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1631
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:            8.27e-38        Length:        384
Score:               691.50          Matches:       147
Percent Similarity:  58.87%          Conservative:  82
Best Local Similarity: 37.79%        Mismatches:    121
Query Match:         20.20%          Indels:        39
DB:                  2               Gaps:          8

US-09-945-326-3 (1-1863) x B83443 (1-384)

Qy   199 ATCAATCAGTTCTTCGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTG-----GACTCC 252
         ::|||    :: ||||     ::|
Db     8 LeuAsnLeuLeuAspSerIleArgGlnPheValArgGluSerLeuValProHisGlu 27

Qy   253 CGAAAAATTGACCAGGAGGGAAATCCCAGTGAAACTTTGGAGAAATTGAAGAGCCTA 312
         :::::::   :::       :: ||||||||   |: :::
Db    28 GlnGluValAlaGluThrAspArgIleProGluAlaIleIleAlaArgMetArgGluMet 47

Qy   313 GGGCTTTTTGGGCTGCAAGTCCAGAAGAATAATGGTGGCCTTCCTGGGCTTCTCCAACACCATG 372
         ::||||:|||| ||::::        ::::::||
Db    48 GlyLeuPheGlyLeuSerIleProGluAlaTyrGlyLyGlyLeuGly--------------- 62

Qy   373 TACTCAAGACTAGGGAGGAGATCATCAGCATGATGGGTCCATCACTGTGACC---------- 423
         :::::|||||::: |: :::||::::
Db    63 -------------ValThrMetGluGluValSerIleAlaPheGluAlaLeu 75

Qy   424 ------------------------CTGGCAGCGCACCAGGCTATTGGCCTCAAG 453
         ||| :::
Db    76 GlyArgThrSerProAlaPheArgSerLeuLeuGlyThrAsnAsnGlyIleGlySerGln 95

Qy   454 GGGATCATCTTGGCTGGCACTGGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCC 513
         |||||: |:||| |||||||
Db    96 GlyIleValIleAspThrGlyThrGluGlnLysArgThrLeuProArgLeuAlaSer 115

Qy   514 GGGGAGGCACAATTGCAGCCTTCTGCCTCACCGGACGGCCGCCAGTGGACGATGCAGCCTCA 573
         ||||||||:::::: |||||||      |||||||
Db   116 GlyGluLeuLeuSerPheCysLeuThrGluProAspSerGlySerAspSerAlaAlaSer 135

Qy   574 ATCCGGAGCGAGCCACACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAG 633
```

Right column:

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Qy       :::::::: ||| ---ArgAspGlyGlyHisTyrValLeuAsnGlyThrLys 153
Db   136 LeuLysThrThrAlaVal------

Qy   634 GTCTCGGATTACTAATGGAGGACTGCCAATATTTTACTGTGTTTGCAAGACTGAGGTC 693
         :: |||||||    |||||||||::: :::
Db   154 ArgPheIleThrAsnAlaProGlnAlaGlyIleIleTyrThrValMetAlaArgThr----- 171

Qy   694 GTTGATTCTGATGGATCAGTGAAAGACAAA-------ATCACAGCATTCATAGTAGAAAAGA 747
         |||||||||      ||||||||||:::
Db   172 -------AspProAlaIleArgGlyAlaGlyIleGlyIleSerAlaPheValValGluArg 188

Qy   748 GACTTTGGTGGAGTCACTAATGGAGGAAACCCGAAGATAAAATTAGGCATTCGGGCTCCAAC 807
         ||::::::|||||       ::: ||||| :::||:
Db   189 GlyThrProGlyLeuSerLeuGlyLysProAspArgLysMetGlyGlnLysGlyAlaHis 208

Qy   808 ACTTGTGAAGTCCATTTGAAAACACCAGATACCTGTGGAAAACATCCTTGGAGAGGTC 867
         |||||||:::|||||   :::::   ::::: |||||
Db   209 ThrCysAspValIlePheAspAspCysArgValProAlaSerGlnLeuIleLeuGlyGlyVal 228

Qy   868 --GGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGC 924
         :::::::: |||||  ||||||| :::||||
Db   229 GlnGlyValGlyPheLysPheThrAlaMetLysMetLysValLeuAspLysProLysHisIleAla 248

Qy   925 AGGCTGCGTGCGTGGCCGTGCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTGCACA 984
         :::|||   :::||::::   :::|||::: ::::|||||
Db   249 AlaValCysValGlyValAlaGluArgMetLeuGluAspAspAlaLeuArgTyrAlaLeuGlu 268

Qy   985 AGGAAACAGTTTAACAAGAGGCTCAGTGAATTGGATGATTCAGAGAGAAATTTGCACTG 1044
         ||||||||||  :::::::||||       |||||||||
Db   269 ArgLysIleGlnPheGlyValGlnProIleAlaGluGluGlnIleAlaMetLeuAlaMetAlaAsp 288

Qy  1045 ATGGCTCAGAAGGCTTACGTCATGGAAGATGATGAGAGTATGATGAGCCACCACCAGCAGGGATGCTGGAC 1104
         ||||||||        :::::|||:::: :: ::::::|||||
Db   289 SerLysAlaGluAlaTyrAlaLAlaArgCysMetValIleAspAlaAlaArgGlnArgGlnArgAsp 308

Qy  1105 CAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCCATGGTGAAGGTGTTCAGCTCCGAG 1164
         ::: |||||:|: |||||:::|||::||||||
Db   309 GluGly-----ArgAspValGlyThrGluAlaGlyPheAlaLysLeuPheAlaSerGlu 326

Qy  1165 GCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCCGGGGGCTTGGGCTACACAAGG 1224
         ||||||| ::::::: :::|||      :::||||
Db   327 MetCysGlyArgValAlaAspArgAlaValGlnIlePheGlyValGlyIleTyrrIleGly 346

Qy  1225 GACTATCCGTACGAGCGCCATACTGCCTGACACCCGCATCCTCCATCTTCGAGGGAACC 1284
         ||||||       |:::||||||      |:::||:::: ||||| ||
Db   347 AspTyrGlyIleGluArgPheTyrArgAspValArgLeuPheArgIleTyrGluGlyThr 366

Qy  1285 AATGAGATTCTCCGGATGTACATCGCC 1311
         :::| |||||      ||::::
Db   367 ThrGlnIleGlnIleGlnLeuLeuIleAla 375
```

RESULT 10
G84124
acyl-CoA dehydrogenase mmgC [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G84124
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ÷
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G84124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:Q9K6D0; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB0751
A;Experimental source: strain C-125
C;Genetics:
A;Gene: mmgC
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:   1.04e-37   Length: 379

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Score:                    690.00         Matches:        147
Percent Similarity:       61.39%         Conservative:   74
Best Local Similarity:    40.83%         Mismatches:     125
Query Match:              20.16%         Indels:         14
DB:                                      Gaps:           6

US-09-945-326-3 (1-1863) x G84124 (1-379)

Qy   232  TTCACTGAAGAGGTGGACTCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACT   291
               |||  ||||||::::::::
Db    27  PheValGluGluMetGluThr--------AsnAspThrPheProMetHisIle         41

Qy   292  TTGGAAAATTGAAGAGCTAGGGCTTTTGGGCTGCAAGTCCAGAAGAATATGGTGGC      351
          :: ||||::::||| ||||||
Db    42  ValLysGluMetGlyGluLeuGlyLeuMetGlyIleProIleProGluAlaTyrGlyGly   61

Qy   352  CTGGGCTTCTCCAACACCATGTAC---TCAAGATAGGGAGGATCATCAGCATGGATGGG   408
          ||||| :::  ||||::     :::
Db    62  AlaGluMetAspPheThrSerTyrIleIleAlaIleHisGluSerLysValSerAla     81

Qy   409  TCCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCT   468
          :||||  ||||| :::
Db    82  ThrValGlyValIleIleLeuSerValHisThrSerValGlyThrAsnProIleLeuPhePhe  101

Qy   469  GGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAGCACATTGCA   528
          |||||||||  :::::::
Db   102  GlyThrGluGluGlnLysSerArgPheIleLeuProLysLeuAlaLysGlyGluTyrLeuGly  121

Qy   529  GCCTTCTGCCTCACGGAGCCAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCC   588
          |||||||
Db   122  AlaPheGlyLeuThrGluProSerAlaGlySerAspAlaAlaAsnLeuLysThrThrAla    141

Qy   589  ACACTAAGTGAAGACAAGAGAGCCACTACATCCTCAATGGCTCCAAGGTCTGATTACTAAT  648
          |||:||:   ||||||||::||||||
Db   142  LeuLysGlnGlyAsp------HisTyrArgLeuAsnGlySerLysValPheIleThrAsn    159

Qy   649  GGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACTGAGGTCCGTTGAATTCTGATGGA  708
          |||||| ||| :::  ::: ::
Db   160  GlyGlyAlaAlaAspThrTyrValValPheAlaSerThr---------AsnProSer       175

Qy   709  TCAGTGAAAGACAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAAT    768
          |||||||| :::   :::
Db   176  AlaGlyArgLysGlyIleSerArgAlaPheIleValGluValGlyLysGlyTyrLysIleAla 195

Qy   769  GGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAA   828
          ||||| :::  ::: ||||||
Db   196  GlyLysLysGluLysLysMetGlyLeuHisGlyLeuSerAsnThrThrGluIlePheGlu    215

Qy   829  AACACCAAGATACCTGTGGAAAACATCCTTGGAGATGGGTCGGAGATGGGTTTAAGGTGGCC  888
          :::  ||:||| :::::
Db   216  AspAlaLeuLeuValProLysGluLeuValGlyLysGluGlyAspGlyTyrLysIleAla    235

Qy   889  ATGAACATCCTCAACACGGCCGGGTTCAGCATGGGCAGCCGTGTCGTGGCTGCTCAAG    948
          ||| :::  :::
Db   236  MetAlaAsnLeuGluAlaGlyIleGlyIleAlaAlaAlaGlnSerLeuGlyIleAlaGlu    255

Qy   949  AGATTGATTGAAATGAAATGCCTGAGTACGCCTGACTGCTCCAACACAGTTAACAAGAGGCTC 1008
          :::||| :::
Db   256  AlaAlaLeuGluAlaLeuThrSerTyrAlaLysGluLysTyrAlaArgGlyLysGlnPheGlnSerIle 275

Qy  1009  AGTGAATTCGATTGATTCAGGAGAAATTTGCCACTGAGATGGCTCAGAAGGCTTACGTCATG 1068
          ||| :::  :::
Db   276  GlyGlnGlnGlnIleAlaIleAlaPheLysLysAspLeuAlaAlaThrGlnLysValGluAlaAla 295

Qy  1069  GAGAGTATGAACCTACCTCACACAGCAGGATGCTGACCAACCTGGCTTTCCCGACTGCTCC 1128
          |||||||  :::
Db   296  LysLeuLeuThrTyr---ArgAlaAlaGlnLeuLysGlyGlnGlyIle---SerCysAla   313

Qy  1129  ATCGAGGCAGCCATGGTGAAGGTGTTCAGCTCCGAGGTGCTGCCAGTGTGTGAGTGAG    1188
          ||||||:: :::  :::
Db   314  LysGluSerSerMetAlaLysLysThrAlaMetLysAlaAlaIleAlaIleGlu        333

Qy  1189  GCGGCTGCAGATCCTCCGGGGCTTGGGCTACACAAGGGACTATCCGTACGACGCCCATACTG 1248
```

```
Db   334  AlaValGlnIleProPheGlyGlyTyrGlyTyrThrLysProValGlnArgTyrPhe       353
               ||::::||||||||   ||||||||||::::||||||
Qy  1249  CGTGACACCCGACATCCTCCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATC    1308
          ||::||
Db   354  ArgAspAlaLysValCysGluIleTyrGluGlyThrSerGluIleGluIleGlnArgIleIleValIle 373
```

RESULT 11
D69658
acyl-CoA dehydrogenase mmgC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69658
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel,
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69658
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-378 <KUN>
A;Cross-references: UNIPROT:P45857; GB:299116; GB:AL009126; NID:g2634723; PIDN:CAB14346.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: mmgC
C;Superfamily: acyl-CoA dehydrogenase

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Alignment Scores:
Pred. No.:              3.49e-37         Length:         378
Score:                  682.00          Matches:        157
Percent Similarity:     56.33%          Conservative:   70
Best Local Similarity:  38.96%          Mismatches:     130
Query Match:            19.92%          Indels:         46
DB:                     2               Gaps:           8

US-09-945-326-3 (1-1863) x D69658 (1-378)

Qy   106  GTACAGGCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAGAAGAAGAAGTTTCCCA   165
               ||| ||:::||||| :::||||
Db    14  ValArgAspPheAla--------------ArgLysGluIleAlaPro                 24

Qy   166  TTTCCAGAAGTTAGCCAAGATGAACTTAATGAAATCAATCAGTTCTTGGACCCGTGGAA   225
          |||::
Db    25  AlaAlaGluIle--------                                            28

Qy   226  AAATTCTTCACTGAAGAGGTGGACTCCGACAAGAAGGGAAAAATTGACCAGGAAGGGAAAATCCCAGAT 285
               :::::: :::
Db    29  --------MetGluLysThrArgAspGluPheProPhe                          37

Qy   286  GAAACTTTGGAGAAATTGAAGAGCTCAGGGGCTTTTGGGCTGCAAGTCCCAGAAGAATAT   345
          :::  :::
Db    38  GlnLeuLeuLysGlyMetGlyLysHisGlyLeuMetGlyIleProValProGluGlnTyr   57

Qy   346  GGTGGCTGGGCTTCTCCAACACCATGTAC---TCAAGACTAGGGGAGGATCATCAGCATG  402
          ||||| :::
Db    58  GlyGlyAlaGlyAlaAspValValSerTyrIleLeuAlaIleHisGluIleSerArgIle   77

Qy   403  GATGGGTCCATCACTGTGACCCTGGCAGCCACCGTCATTGGCCTATTGGCCTCAAGGGGATCATC 462
          :::::  ||||||  :::
Db    78  SerAlaAlaValGlyValIleLeuSerValHisThrSerValGlyThrAsnProIleLeu   97

Qy  1189  GCGGCTGCAGATCCTCCGGGGCTTGGGCTACACAAGGGACTATCCGTACGACGCCCATACTG 1248
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A;Molecule type: DNA
A;Residues: 1-381 <KUR>
A;Cross-references: UNIPROT:Q8YDG3; GB:AE008918; PIDN:AAL53454.1; PID:gi17984354; GSPDB:GN
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0213
A;Map position: II
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.:                          Length:         381
Score:              3.5e-37         Matches:        151
Percent Similarity: 682.00          Conservative:    73
Best Local Similarity: 60.70%       Mismatches:     131
Query Match:        40.92%          Indels:          14
DB:                 19.92%          Gaps:             7
                    2
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US-09-945-326-3 (1-1863) x AC3536 (1-381)

Qy   220 GTGGAAAAATTCTTCACTGAGAGAGTG--------GACTCCGAAAAATTGACCAGGAA 270
             :::  ||||                 ||||||||||||
Db    16 ValArgArgPheValArgGluArgLeuValProAlaGluSerArg--ValGluGluThr 34

Qy   271 GGGAAAATCCCAGATGAAACTTGGAGAATTGAAGAGCCTAGGCGTTTTGGGCTGCAA 330
             :::||:::::    ||||||:::  :::|||||||||
Db    35 AsnArgIleProAspAspIleIleIleGluGlyMetArgAlaMetGlyLeuPheLeuSer 54

Qy   331 GTCCCAGAAGAAATATGGTGGCCTGGCCTTCTCCAACACCATGTACTCAAGACTAGGG--- 387
             :::||||||||||||||||  :::|||||||
Db    55 IleProGluGluTyrGlyGlyLeuThrMetGluGluGlyValArgValGlyPhe 74

Qy   388 GAGATCATCACGATGGTCCATCACTGTGAAGTCCAT 447
             |||||    :::  ||
Db    75 GluLeuGlyTyrThrSerProAlaPheArgSerValIleGlyThrAsnAsnGlyIleGly 94

Qy   448 CTCAAGGGGATCATCTTGGCTGGCACTGAGGAGGTCGGAGAGGCTTAAG 507
             ||||||  :::||||||||||::::::|||
Db    95 SerGlnGlyIleIleIleAlaAlaAspGlyThrArgAspArgAspArgPheLeuProArgLeu 114

Qy   508 GCGTCCGGGGAGACCATTGAGCCTTCGCCGAGCCAGTGGAGCGGATGCA 567
             |||||||||||:::||||||||||||||
Db   115 AlaSerGlyLysGlyIleIleAlaSerPheAlaLeuThrGluProAspValGlySerAspAla 134

Qy   568 GCCTCAATCCGGACAGCAGCAGCTCAAGTGAAGACAAGAGCACTACATCCTCAATGGC 627
             |||||||                 :::|||
Db   135 GlyAlaValArgThr------ThrAlaGluArgGlyAspGlyAspSerTyrIleIleAsnGly 152

Qy   628 TCCAAGGTCTGGATTACTAATGGAGGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACT 687
             ||||||:::||||||||||||||||
Db   153 ThrLysAspPheIleIleThrAsnAlaAlaProValAlaGlyValPheThrLeuMetAlaArg--- 171

Qy   688 GAGGTCGTTGATTCTGATGGATCAGTGAAGACAAAATCACAGCATTCATAGTAGAAAGA 747
             :::  ||||||||||||||||  :::  :::||
Db   172 ------MetGlyGlySerGlyProSerGlyIleSerGluAlaPheLeuAlaGluArg 187

Qy   748 GACTTTGGTGGAGTCACTAATGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAC 807
             ::::
Db   188 AspLeuProGlyLeuThrValGlyLeuThrProAspHisLysMetGlyGlnArgGlyThrGln 207

Qy   808 ACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGAAAAACATCCTTGGAGAGGTC 867
             :::||:::||:::
Db   208 ThrCysAspValTyrLeuGluAsnValArgValProAlaThrSerIleIleGlyValGlyVal 227

Qy   868 ---GGAGATGGTTAAGTGGCCATGAAACATCCTCAACAGCGGCCGGTTCAGCATGGGC 924
             ::::||||||||||||||
Db   228 GlyGlyArgGlyPheLysThrAlaMetLysValLeuAsnArgGlyArgLeuHisIleSer 247

Qy   925 AGCGTCTGCGTCGGCTGCTCAAGATTGAAATGAAATGACTGCTGAGTACGCCTGCACA 984
             ||||||||||||  :::  ::::::|||
Db   248 SerValCysAlaGlyThrAlaGluArgProIleGluSerValGlyPheAlaGlySer 267

Qy   985 AGGAAACAGTTTAACAAGAGGCTCAGTGATTGATTCAGGAGAGAATTTGCACTG 1044
```

```
Qy   463 TTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCTGGTCCGGGGAGCAC 522
             ||||||          |||||||::::::||
Db    98 TyrPheGlyAsnGluGluGlnLysMetLysTyrIleProAsnLeuAlaSerGlyAspHis 117

Qy   523 ATTGCAGCCTTCTGCCTCACGGAGCCAGCCAGTGGAGGCCATGCAACCTTCAATCCGGAGC 582
             :::  |||||||||
Db   118 LeuGlyAlaPheAlaLeuThrGluProHisSerGlySerAspAlaGlySerLeuArgThr 137

Qy   583 AGAGCCACTCAAGTGAAGACAAGAGCACTACATCCTCAATGGCTGTCTGGATT 642
             ||||||          ||||||
Db   138 ThrAlaIleLysLysAsnGlyLys------TyrLeuLeuAsnGlySerLysPheIle 155

Qy   643 ACTAATGGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACTGAGGTCGTTGATTCT 702
             ||||||          :::    ::::::
Db   156 ThrAsnGlyGlyAlaAspSerIleThrIleTyrIleTyrIleThrPheAlaLeuThr--------Ala 171

Qy   703 GATGGATCAGTGAAGACAAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTC 762
             :::||||||||||
Db   172 ProAspGlnGlyArgHisGlyArgIleSerGluAlaPheIleGluLysAsnThrProGlyPhe 191

Qy   763 ACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAACACCTGTGAAGTCCAT 822
             ::::||||||||||||||
Db   192 ThrValGlyLysGluArgLysGlyLeuGlyLeuTyrGlyLeuGlySerAsnThrArgThrGluLeuIle 211

Qy   823 TTTGAAAACACCAAGATACCTGTGAAAAACATCCTTGGAGAGGTCGGAGAGGCTTTAAG 882
             |||  ::::::|||||||
Db   212 PheGluAsnAlaLysGluLeuProGluAlaAsnIleAsnLeuLeuGlyLysGlyAspGlyPheHis 231

Qy   883 GTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGCATGGGCAGCGTCGGCGTG 942
             :::  :::||||||||||
Db   232 IleAlaMetAlaAsnLeuAsnValGlyArgIleGlyIleAlaAlaGlnAlaLeuGlyIle 251

Qy   943 CTCAAGGATTGATTGAAATGAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAAG 1002
             :::  ||        :::  ::::::||
Db   252 AlaGluAlaLeuGluHisAlaLeuValAspTyrAlaLysTyrArgAlaLysGlnAsnPheGlyArgArg 271

Qy  1003 AGGCTCAGTGAATTTGGATTGCATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTAC 1062
             |||                ||||||::::::
Db   272 ProIleAlaAlaAsnGlnGlyIleSerPheLeuLysLeuLeuGlyGluArgProIleArgLeuGlu 291

Qy  1063 GTCATGAGAGTATGACCTCACCTCAGCAGGATGGGCCGTTCTTTCCCGAC 1122
             |||||||
Db   292 AlaAlaArgHisLeuValTyrHisAlaAlaAsp------LeuHisAsnArgGlyLeu--Asn 309

Qy  1123 TGCTCCATCGAGGCCATGGTGAAGGTGTTCAGCTCCGAGGGCCGCTCCGTGTG 1182
             |||||::::::|||
Db   310 CysGlyLysGluAlaSerMetAlaLysGlnPheAlaLeuSerProAlaAlaValLysAlaLeu 329

Qy  1183 AGTGAGGCGCTGCAGATCCTCGGGGCTTGGCTACACAAGGAACTATCCGTACGAGCGCC 1242
             ::::::||||||||
Db   330 ---AspAlaValGlnIleLeuTyrGlyTyrGlyTyrMetLysAspTyrProValGluArg 348

Qy  1243 ATACTGCGTGACACCGCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATG 1302
             |||::::::  :::
Db   349 LeuLeuArgAspAlaLysValThrGlnIleIleTyrGluGlyThrAsnGluIleArgLeu 368

Qy  1303 TACATCGCC 1311
             ::: |||
Db   369 IleIleSerSer 371
```

```
RESULT 12
AC3536
butyryl-CoA dehydrogenase (EC 1.3.99.2) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3536
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
  .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3536
A;Status: preliminary
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Db   |||          ||||||||         ::||||||
     268 ArgValGlnPheGlyLysArgIleAlaGluHisGlnMetIleGlnAlaMetLeuAlaAsp 287

Qy   1045 ATGGCTCAGAAGGCTTACGTCATGAGAGTATGACCTACCTCACAGCAGGGATGCTGAC 1104
Db   288 MetSerThrGlyAlaTyrAlaGlyArgCysMetValLeuAspAlaAlaArgAlaArgGlu 307

Qy   1105 CAACCTGGCTTTCCCGACTGCTCCATCGAGCAGCAGCCATGGTGAAGGTGTTCAGCTCCGAG 1164
Db   308 GluSerAsnVal---AspIleIleArgLysAlaAlaSerCysLysLysPheCysSerGlu 326

Qy   1165 GCCGCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCCGGGGGCTTGGGCTACAAAGG 1224
Db   327 MetValGlyArgValAlaAlaAspAsnAlaValGlnIleIleHisGlyGlySerGlyTyrMetGln 346

Qy   1225 GACTATCCGTACGAGCGCATACTGCGTGACCACCCGCCATCCTCCTCATCTTCGAGGGAACC 1284
Db   347 AsnTyrProValGluHisPheTyrArgAspValArgLeuPheArgLeuTyrGluGlyThr 366

Qy   1285 AATGAGATTCTCCGGATGTACATCGCC 1311
Db   367 SerGlnIleGlnArgIleIleIleAla 375
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RESULT 13

B87472
B87472 acyl-CoA dehydrogenase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87472
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <STO>
A;Cross-references: UNIPROT:Q9A7C6; GB:AE005673; NID:g13423230; PIDN:AAK23774.1; GSPDB:C
C;Genetics:
A;Gene: CC1798
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:   6.43e-37   Length: 381
Score: 678.00   Matches: 149
Percent Similarity: 59.13%   Conservative: 81
Best Local Similarity: 38.30%   Mismatches: 135
Query Match: 19.81%   Indels: 24
DB: Gaps: 7

US-09-945-326-3 (1-1863) x B87472 (1-381)

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Qy   199 ATCAATCAGTTCTTGGGACCCGTCGAAAAATTCTTCACTGAAGAGGTGACTCCCGAAAA 258
Db   7   LeuSerAlaLeuIleAspValIleAspAlaIleArgPheValAlaGlnArgGluArgProIleGlu 26

Qy   259 -----ATTGACCAGAAGGAGAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTA 312
Db   27  GlyLeuValSerGluThrGluGluGlnValProGlySerIleGluGluMetLysGlnLeu 46

Qy   313 GGGCTGTTTTGGGCTGCGCAGTCGCAGAAGAATAATGTGGCCTGGCTTCCAACACCATG 372
Db   47  GlyLeuPheGlyLeuSerIleGluProGluSerTyrGlyLeuGlyLeuSerLeuGluGlu 66

Qy   373 TACTTCAAGACTAGGGGGAGATCATCAGCATG-------GATGGGTCCATCACTGTGACC 423
Db   67  GluAlaArgVal----IleValAlaPheCysHisThrAlaProAlaPheArgSerThr 84

Qy   424 CTGGCAGCCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAG 483
Db   85  PheGlyThrAsnValGlyIleGlySerGlnGlyLeuLeuMetPheGlyAspGluAlaGln 104
```

```
Qy   484 AAAGCCAAATACTTGCTAAACTGGGCTCGGGAGGAGCAGATTGCAGCCTTCTGCCTCACG 543
Db   105 LysAlaLysArgTrpLeuProSerIleAlaSerGlyGluThrArgIleThrAlaPheAlaLeuThr 124

Qy   544 GAGCCCAGCCAGTGGAGGAGGCTCAGCTGCATCCGGAGCAGCAGCCACTAAGTGAAGAC 603
Db   125 GluAlaGluAlaGlySerAlaSerValGlnThrArgAlaVal------ArgAsp 142

Qy   604 AAGAAGCACTACATCCTCAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAAT 663
Db   143 GlyAspHisTyrValLeuAsnGlyValLysArgTyrIleThrAsnAlaGlyArgAlaAsn 162

Qy   664 ATTTTACTGTGTTGCAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGACAAA 723
Db   163 LeuPheThrValMetAlaArgThrArgProAsnThrLysGlyVal GlyAla--------- Gly 179

Qy   724 ATCACAGCATTCATAGTAGAAAGAGACTTTGTGGAGTCACTAATGGAAACCGGAGAT 783
Db   180 ValSerAlaPheLeuValProAlaAspLeuProGlyLeuSerValGlyLysProGluLys 199

Qy   784 AAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAAACACCAAGATACCT 843
Db   200 LysMetGlyGlnGlnGlyLysAlaHisIleHisAspValPheGluHisAspValArgValPro 219

Qy   844 GTGGAAAACATCCTTGGAGATGGTTTAAGGTGCCATGAAACATCCCAAC 903
Db   220 ValGluAsnArgLeuGlyAlaGluGlyGluGlyPheThrValAlaMetArgValLeuAsp 239

Qy   904 AGCGGCGGTTCAGCATGGGCAGGCGTCGTGGCCATGAGGATTGATTGAAATG 963
Db   240 ArgGlyArgValHisIleSerAlaValCysValGlyValAlaGluArgLeuIleAlaAsp 259

Qy   964 ACTGCTGGAGCACGCCTGCACAAGGAGAAACAGTTAACAAGAGGCTCAGTGAATTGGATTG 1023
Db   260 CysValAlaTyrAlaSerGluArgLysGlnPheGlyGlnProIleLeuSerPheGlnLeu 279

Qy   1024 ATTCAG---------------GAGAAATTGCACTGATGGCTCAGAGGCTTACGTCATG 1068
Db   280 IleGlnAlaMetIleAlaAspSerLysThrGluAlaLeuAlaLeuAlaLysAlaLeuVaPhe 299

Qy   1069 GAGAGTATGACCTACCTCACAGCAGGGATGCTGGCAACCTGGCTTTCCCGACTGCTCC 1128
Db   300 AspThrArgAlaLysArgAspAlaGly 312

Qy   1129 ATCGAGCAGCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCGCCGGCCTGGCAGTGTGAGTGAG 1188
Db   313 LeuGluAlaAlaAlaThrLysLysPheAlaSerGluMetValGlyArgValAlaAspArg 332

Qy   1189 GCGCTGCAGATCCTCCGGGGCTTGGGCTTGGGCTTACCAACAGGGGACTATCCGTACGAGCGCATACTG 1248
Db   333 AlaValGlnValPheGlyGlyAlaGlyTyrValAlaAlaAspTyrGlyTyrIleGluArgLeuTyr 352

Qy   1249 CGTGACCACCCGCCATCCTCCTCATCTTCGAGGAGAACCAATGAGATTCTCCGGATGTACATC 1308
Db   353 ArgAspValArgIlePheArgLeuTyrGluGlyIleAlaSerGlnIleGlnIleLeuIleIle 372

Qy   1309 GCCCTGACGGGTCTCGCAGCATGCCGGC 1335
Db   373 AlaAlaArgGluThrLeuLysArgGlyGly 381
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RESULT 14

F84124
F84124 acyl-CoA dehydrogenase acdA [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84124
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84124
A;Status: preliminary

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Qy  1003 AGGCTTCAGTGAATTGGATTGATTCAGGAGAAAATTTGCACTGATGGCTCAGAAGGCTTAC 1062
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Db   274 ProIleGlyGlnGlnGlnGlyIleAlaPheLysLeuLeuAlaAspMetAlaThrLysValGlu 293

Qy  1063 GTCATGGAGAGTATGACCTACCTACCAGCAGCAGGATGCTGGACCAACCTGGCTTCCCGAC 1122
              |||||||                                              :: |||
Db   294 AlaSerArgLeuLeuThrTyr---GlnAlaAlaTrpArgGluSerGluGlyLeu---Ser 311

Qy  1123 TGCTCCATGGAGCAGCCATGGTGAAGGTGTTCAGCTCAGAGGTGTTCAGCCCTGGCAGTGTG 1182
              |||||||||||         |||::::  :::  :::  |||||||
Db   312 TyrGlyLysGluSerAlaMetSerLysPheAlaGlyAspThrAlaMetAspValThr 331

Qy  1183 AGTGAGGCGCTGCAGATCCTCGGGGCTTGGCTACCACCAAGGGACTATCCGTACGAGCGC 1242
              :::::::::|||||||::::|::|||||||||||||||||::::
Db   332 ValGluAlaValGlnValPheGlyValPheGlyTyrTyrThrLysGluTyrProValGluArg 351

Qy  1243 ATACTGCGTGACACCCGCATCCTCCTCGAGGAGACCAATGAGAATTCCCGGATG 1302
              ::|||||||   ::|||                    |||||||||
Db   352 TyrMetArgAspAlaLysIleThrGlnIleTyrGluGlyThrAsnGluIleGlnArgLeu 371

Qy  1303 TACATCGCC 1311
              |||:::
Db   372 ValIleSer 374
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RESULT 15

S55421

acyl-CoA dehydrogenase (EC 1.3.99.3) acdA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S55421; B69581
R;Glaser, P.; Danchin, A.
A;Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3:
A;Reference number: S55414
A;Accession: S55421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <GLA>
A;Cross-references: UNIPROT:P45867; EMBL:Z49782; NID:g853752; PIDN:CAA89868.1; PID:g8537(
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
C.; Bron, S.; Brouillet, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69581
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-379 <KUN>
A;Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15745.1; PID:g2636254
A;Experimental source: strain 168
C;Genetics:
A;Gene: acdA
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.:   379
Score: 3.1e-35   Matches: 155
Percent Similarity: 58.42%   Conservative: 60
Best Local Similarity: 42.12%   Mismatches: 140
Query Match: 19.06%   Indels: 13

A;Molecule type: DNA
A;Residues: 1-380 <STO>
A;Cross-references: UNIPROT:Q9K6D1; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB075
C;Genetics:
A;Gene: acdA
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.:   380
Score: 1.34e-35   Matches: 156
Percent Similarity: 57.96%   Conservative: 66
Best Local Similarity: 40.73%   Mismatches: 139
Query Match: 19.22%   Indels: 22
DB: Gaps: 8

US-09-945-326-3 (1-1863) x F84124 (1-380)

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Qy   184 GATGAACTTAATGAAATCAATCAGTTCTTCGGGACCCCTGGAAAAATTCTTCACTGAAGAG 243
             ||||||           |||                   :::
Db     7 AspGluGlnGlnMetIleLysLysMet--------ValArgAspPheAlaGluAsnGlu 23

Qy   244 GTG------GACTCCCGAAAAATTGACCAGGAGGGAAATCCCAGATGAAACTTTGGAG 297
             :::       ::  |||||||  ::| |||                  ::
Db    24 ValAlaProThrAlaGluArgAspGluGluGluArgPheAspArgGluIlePheAsp 43

Qy   298 AAATTGAAGAGCCTAGGGCGTTTTGGGCTGCAAGTCCCAGAGAATATGTGGCTGGCTGGC 357
             :::::::|||||||||||:::|       ||||||||||||||:::::
Db    44 GlnMetAlaGluLeuGlyLeuThrGlyLeuProIleProGlyGluTyrGlyLysGlyGly 63

Qy   358 TTCTCCAACACCATGTAC--TCAAGACTAGGGGAGATCATCAGCATGATGGGTCCATC 414
             |||                :::  ||||||||||||||||||||||
Db    64 AlaAspTyrValSerTyrValIleAlaValGluLeuSerArgValCysAlaSerThr 83

Qy   415 ACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTAACAGGGGATCATCTTGGCTGGCACT 474
             :::                |||||||||||||||:::  :::  ::
Db    84 GlyValThrLeuSerAlaHisLeuSerArgLeuAlaSerTrpProValTyrLysPheGlyThr 103

Qy   475 GAGGAGCAGAAGCCAAATACTTGCCTAAACTGGCTCCGGGAGCACATTGCAGCCTTC 534
             ||||||||||               :::||||||:::::
Db   104 GluGluGlnLysGlnLnPheLeuAsnArgProMetAlaGluGlyLyLysIleGlyAlaTyr 123

Qy   535 TGCCTCACGGAGCCCAGTGCGGACGATGCAGCCGAGCAGAGCCACACTA 594
             :::  |||||||||||||||||||||||||||||||||||:::
Db   124 GlyLeuThrGluProGlySerGlySerAspAlaAlaAsnMetLysThrAlaValLeu 143

Qy   595 AGTGAAGACAAGAAGCACTACATCTCCAATGGCTCCAAGTCTGATTACTAATGGAGGA 654
             |||||||||||||||||||||||||::  |||||||||||||||||||
Db   144 GluGlyAsp------AspTyrIleLeuAsnGlySerLysIlePheIleThrAsnGlyGly 161

Qy   655 CTGCCCAATATTTTTACTGTGTTGCAAGACTGAGGTCGTTGATTCTGATGGATCAGTG 714
             :::||:::  ::  :::|||                ||||||
Db   162 IleAlaAspIleTyrIleValPheAlaValThrGlu-------------------- 173

Qy   715 AAAGACAAA--------ATCACAGCATTCATAGTAGAAAGAGACTTTGGTCGGAGTC 762
             :::||||            ||| ||                   |||  |||
Db   174 ProGluLysArgHisLysGlyValSerArgAlaPheIleGluAlaAspThrProGlyPhe 193

Qy   763 ACTAATGGGAAACCCGAAGAGTAAATTAGGCATTCGGGGTCCAACACTTGTGAAGTCCAT 822
             :::                     :::|||||||||||::::::
Db   194 SerValGlyLyLysGluLysGlyIleLeuArgSerProThrThrGluIleIle 213

Qy   823 TTTGAAAACACCAAGATACCTGTGAAAAACATCCTTGGAGAGGTCGGAGATGGGTTTAAG 882
             |||:::        :::||||||||||||||||::::::
Db   214 PheGluAspCysArgValProLysGluAsnLeuGluGlyLysGluGlyLysAspGlyPheLys 233

Qy   883 CTGGCCATGAACATCCTCAACACAGCGGCCGTTCAGCATGGGCAGCGTCGTGGCTGGCTG 942
             :::  :::        |||||||||||||||||||
Db   234 IleAlaMetMetThrLeuAspGlyLyArgAsnGlyIleGluAlaGlnAlaValGlyIle 253

Qy   943 CTCAAGAGATTGATTGAAATGAACTACCGCCTGACAGAACAAGGAAACAGTTTAACAAG 1002
             :::||:::       ::::     :::    ||||||
Db   254 AlaGlnGlyAlaLeuAspAlaAlaAlaValAlaTyrAlaAlaAsnArgGluLysPheGlyLys 273
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DB:                    1              Gaps:        7

US-09-945-326-3 (1-1863) x S55421 (1-379)

Qy    220 GTGGAAAAATTCTTCACTGAGAGAGTG------GACTCCGAAAAATTGACCAGGAAGGG 273
          |||||                 ||||||   :::   |||||:::::
Db     16 ValArgAspPheAlaLysHisGluValAlaProThrAlaGluArgAspGluGlnGlu 35

Qy    274 AAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAAGTC 333
          :::        |||     :::::: :::|||||||||
Db     36 ArgPheAspArgGluLeuPheAlaGluLysMetAlaAsnLeuGlyLeuThrGlyIleProTrp 55

Qy    334 CCAGAAGAATATGGTGGCCTGGGCTTCTCCAACACCATGTAC---TCAAGACTAGGGGAG 390
          |||||:::||||:::                :: |||
Db     56 ProGluAspTyrGlyGlyLeuGlySerAspTyrLeuAlaTyrValIleAlaValGluGlu 75

Qy    391 ATCATCAGCCATGATGGGTCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCCTC 450
          :::    |||||||||||||||    ::|||||    :::::::
Db     76 LeuSerLysValCysAlaSerThrGlyValThrLeuSerAlaHisIleSerLeuCysSer 95

Qy    451 AAGGGGATCATCTTGCTGGCACTGAGGAGGAGAAAGCCAAATACTGCCTAAACTGGCG 510
          :::          ||||||||||         ::|||||   :::|||||
Db     96 TrpProLeuPheAlaPheGlyThrGluGluGlnLysThrGlyTyrLeuThrGlnLeuLeuAla 115

Qy    511 TCCGGGGAGCCACATGCAGCCTTCTGCCTCCACGGAGCCAGTGGGAGCGGATGCAGCC 570
          |||||            :::|||||||     |||||||
Db    116 LeuGlyGluLysIleGlyIleAlaPheAlaLeuThrGluAlaGlySerGlySerAspAlaGly 135

Qy    571 TCAATCCGGAGCAGAGCCACACTAAGTGAAGCAAGAAGCACTACATCCTCAATGGCTCC 630
          |||                 :::|||||       :::|||||
Db    136 SerMetLysThrThrAlaGluArgIleGlyAsp------AspTyrValLeuAsnGlySer 153

Qy    631 AAGGTCTGGATTACTAATGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACTGAG 690
          ||||::||||||||||||||||||||::|||||||       ||||||
Db    154 LysValPheIleThrAsnGlyGlyValAlaAspIlePheTyrIleValPheAlaValThr--- 172

Qy    691 GTCGTTGATTCTGATGGATCAGTGAAAGACAAA---ATCACAGCATTCATAGTAGAAAGA 747
          |||    |||              |||||||:::
Db    173 -------AspProGluLysLysLysLysGlyValThrAlaPheIleLeuThrAlaGluLeuLys 188

Qy    748 GACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAC 807
          ||||| ||   :::|||||||||   |||||||:::     |||
Db    189 AspPheGluGlyPhePheThrGlyPheGlyLysLeuGluLysGlyLeuIleArgGlySerSerPro 208

Qy    808 ACTTGTGAAGTCCATTTGAAAACCAAGATACTCTGTGAAAACATCCTTGGAGAGGTC 867
          |||      |||||||  ::|||||     |||||||
Db    209 ThrThrGluIleMetPheGluMetAspCysValValProAlaSerValProGlyGluGlyGlu 228

Qy    868 GGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGCCGGTTCAGCATGGGCAGC 927
          ||:::||||||||||||::||||||   |||    :::
Db    229 GlyLeuGlyPheLysValAlaMetThrThrLeuAspAspLysArgAspGlyIleAlaAla 248

Qy    928 GTCGTGGCCTGGGCTGCTCAAGAGATTGATTGAAATGAACTGCTGAGTACGGCCTGCACAAGG 987
          |||||:::       ::|||||||||    ||:::
Db    249 GlnAlaValGlyIleAlaGluAspGlnLeuAlaLeuAspAspAlaAlaLeuGlnTyrAlaLysGluArg 268

Qy    988 AAACAGTTTAACAGAGGGCCTCAGTGAATTTGGATTGATTCAGGAGAAATTGCACTGATG 1047
          |||||||||  ::::::|||       |||  ||||:::
Db    269 LysGlnPheGlyLysSerIleAlaGluGlnGlnGlnLeuGlyIleAlaPheLysLeuAlaAspMet 288

Qy   1048 GCTCAGAAGGCTTACGTCATGGAGTATGACCTACCTCACAGCAGGGGATGCTGACCAA 1107
          |||      ::||||||     :::
Db    289 AlaThrMetIleGluAlaSerArgLeuThrTyr---GlnAlaAlaTrpLeuGluSer 307

Qy   1108 CCTGGCTTTCCCGACTGCTCCATCGAGCGACCATGGAAGGTGTTCAGCTCCGAGGCC 1167
          |||      :::|||||||:::||||||       :::
Db    308 SerGlyLeuPro---TyrGlyLysAlaSerAlaMetSerLysLeuMetAlaGlyAspThr 326

Qy   1168 GCCTGCGCAGTGTGTGGCGTCGTGAGGGGCGCTTGGGCTACACAGGGAC 1227
          |||      :::|||||||||||::|||
Db    327 AlaMetLysValThrThrGluAlaValGlnIleIlePheGlyGlyTyrGlyTyrThrLysAsp 346

Qy   1228 TATCCGTACGAGCGGCATACTGCGTGACACCCGCATCCTCCTCATCTTCGAGGGAACCAAT 1287
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Db    347 TyrProValGluArgTyrMetArgAspAlaLysAlaLysIleThrGlnIleIleTyrGluGlyThrGln 366
          |||||           |||||        :::|||||      :::|||             ||:::|||||||

Qy   1288 GAGATTCTCCGGATGTACATCGCC 1311
          ||||||                   ||:::

Db    367 GluIleGlnArgLeuValIleSer 374
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Job time : 99.2291 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on:   May  2, 2005, 13:13:41 ; Search time 303.736 Seconds
                                   (without alignments)
                                   6281.796 Million cell updates/sec

Title:            US-09-945-326-3
Perfect score:    3423
Sequence:   1 atgagcggtcgcgggctctt.........acccctggacaggacatgc 1863

Scoring table:  BLOSUM62
          Xgapop 10.0 , Xgapext  0.5
          Ygapop 10.0 , Ygapext  0.5
          Fgapop  6.0 , Fgapext  7.0
          Delop   6.0 , Delext   7.0

Searched:   1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:   3224756

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09945326/runat_02052005_135410_22353/app_query.fasta_1.4686
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=-1 -END=-1 -MATRIX=blosum62 -TRANS=human62.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN_1_1_861 @runat 02052005_135410_22353 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03:*
        1:   uniProt_sprot:*
        2:   uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	3153	92.1	621	1	ACD9_HUMAN	Q9H845	homo sapien
2	2704	79.0	625	1	ACD9_MOUSE	Q8jzn5	mus musculu
3	2526	73.8	498	2	Q9H9W4	Q9h9w4	homo sapien
4	2374.5	69.4	622	2	Q6DDF2	Q6ddf2	xenopus lae
5	1739	50.8	343	2	Q9BUX5	Q9bux5	homo sapien
6	1360.5	39.7	659	2	Q7T2C2	Q7t2c2	brachydanio
7	1360	39.7	656	1	ACDV_MOUSE	P50544	mus musculu
8	1356.5	39.6	655	1	ACDV_RAT	P45953	rattus norv
9	1345	39.3	655	1	ACDV_BOVIN	P48818	bos taurus
10	1318	38.5	655	1	ACDV_MACFA	Q8hxy7	macaca fasc
11	1308	38.2	655	1	ACDV_HUMAN	P49748	homo sapien
12	1295.5	37.8	655	2	Q9V8T1	Q9v8t1	drosophila
13	1288	37.6	639	2	Q7Q868	Q7q868	anopheles g
14	1273.5	37.2	604	2	Q7Q870	Q7q870	anopheles g
15	1210.5	35.4	613	2	Q19057	Q19057	caenorhabdi
16	897.5	26.2	408	2	Q6AHQ5	Q6ahq5	caenorhabdi
17	895	26.1	589	2	Q67K07	Q67K07	symbiobacte
18	888.5	26.0	577	2	Q72KB1	Q72kb1	thermus the
19	845.5	24.7	594	2	Q631W4	Q631w4	bacillus ce
20	845.5	24.7	594	2	Q72Y79	Q72y79	bacillus ce
21	845.5	24.7	594	2	Q81XJ1	Q81xj1	bacillus an
22	845.5	24.7	594	2	Q6HBP9	Q6bbp9	bacillus th
23	845.5	24.7	600	2	Q815X2	Q815x2	bacillus ce
24	842.5	24.6	594	2	Q65F73	Q65f73	bacillus li
25	821	24.0	594	2	Q9K784	Q9k784	bacillus ha
26	815.5	23.8	594	2	O32176	O32176	bacillus su
27	789.5	23.1	594	2	Q8ENT4	Q8ent4	oceanobacil
28	751.5	22.0	569	2	Q738L4	Q738l4	bacillus ce
29	750.5	21.9	569	2	Q81DR7	Q81dr7	bacillus ce
30	749	21.9	569	2	Q6HJ21	Q6hj21	bacillus th
31	745.5	21.8	569	2	Q63BL2	Q63bl2	bacillus ce
32	742	21.7	569	2	Q81QR7	Q81qr7	bacillus an
33	737.5	21.5	571	2	Q65IW9	Q65iw9	bacillus li
34	734	21.4	169	2	Q9CZC5	Q9czc5	mus musculu
35	728	21.3	642	2	Q742M4	Q742m4	mycobacteri
36	719.5	21.0	382	2	Q8EM49	Q8em49	oceanobacil
37	713	20.8	386	2	Q7P5M8	Q7p5m8	fusobacteri
38	711	20.8	650	1	Y873_MYCTU	P63429	mycobacteri
39	711	20.8	650	1	Y897_MYCBO	P63430	mycobacteri
40	710	20.7	376	2	Q81JV7	Q81jv7	bacillus an
41	709.5	20.7	381	2	Q8R674	Q8r674	fusobacteri
42	709	20.7	158	2	Q7TSP3	Q7tsp3	rattus norv
43	705	20.6	376	2	Q72XA5	Q72xa5	bacillus ce
44	705	20.6	381	2	Q814S8	Q814s8	bacillus ce
45	704	20.6	376	2	Q6HAU1	Q6haul	bacillus th

ALIGNMENTS

```
RESULT 1
ACD9_HUMAN
ID   ACD9_HUMAN     STANDARD;       PRT;   621 AA.
AC   Q9H845; Q8WXX3;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
DE   (EC 1.3.99.-) (ACAD-9).
GN   Name=ACAD9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Dendritic cell;
RX   MEDLINE=22246103; PubMed=12359260; DOI=10.1016/S0006-291X(02)02336-7;
RA   Zhang J., Zhang W., Zou D., Chen G., Wan T., Zhang M., Cao X.;
RT   "Cloning and functional characterization of ACAD-9, a novel member of
RT   human acyl-CoA dehydrogenase family.";
RL   Biochem. Biophys. Res. Commun. 297:1033-1042(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura J., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
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RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung, and Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Has a dehydrogenase activity on palmitoyl-CoA (C16:0)
CC   and stearoyl-CoA (C18:0). It is three times more active on
CC   palmitoyl-CoA then on stearoyl-CoA. Has little activity on
CC   octanoyl-CoA (C8:0), butyryl-CoA (C4:0) or isovaleryl-CoA (5:0).
CC   -!- COFACTOR: FAD (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed in most normal human
CC   tissues and cancer cell lines with high level of expression in
CC   heart, skeletal muscles, brain, kidney and liver.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF127351; AAL56011.1; -.
DR   EMBL; AK024012; BAB14775.1; -.
DR   EMBL; BC013354; AAH13354.1; -.
DR   EMBL; BC007970; AAH07970.1; -.
DR   PIR; JC7892; JC7892.
DR   HSSP; P15651; 1JQI.
DR   Genew; HGNC:21497; ACAD9.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.

DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Mitochondrion; Oxidoreductase; Transit peptide.
FT   TRANSIT   ?   ?   Mitochondrion (Potential).
FT   CHAIN   ?   621   Acyl-CoA dehydrogenase family member 9.
FT   ACT_SITE   426   426   Proton acceptor (By similarity).
FT   CONFLICT   397   397   A -> V (in Ref. 1).
SQ   SEQUENCE   621 AA;   68760 MW;   064BCE0378877F54 CRC64;

                                     Length: 621
                                     Matches: 621
                                     Conservative: 0
                                     Mismatches: 0
                                     Indels: 0
                                     Gaps: 0

Alignment Scores:
Pred. No.:   2.08e-204
Score: 3153.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 92.11%
DB:

US-09-945-326-3 (1-1863) x ACD9_HUMAN (1-621)

Qy   1 ATGAGCGGCTCGGGCTTCTGCGGCCACCACGGCTGCGGCTGCCTGCGGGTCTG   60
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Db   1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu   20

Qy   61 GTGGTCTCTACCGGCAACCGGCGGCTACTGCGCAAGAAGAAGAGTTTCTCGCC   120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla   40

Qy 121 AAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAGAAGAGTTTCCCATTTCCAGAAGTTAGC   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 LysGluLeuPheLeuGlyLysIleLysLysLysLysGluValPheProPheProGluValSer   60

Qy 181 CAAGATGAACTAATGAAATCAATCAGTCTGGGACCGGTGGAAAATTCTTCACTGAA   240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GlnAspGluLeuAsnGluIleLeuAsnGlnLeuGlyProValGlyLeuGlyGlyGluLysLys   80

Qy 241 GAGGTGGACTCCGAAAATTGACCAGGAGGAAAATCCCAGATGAAACTTTGGAGAAA   300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GluValAspSerGluArgGlyIleAspGlnGluGluIleProArgGluAspProGluGluGluGlyLys   100

Qy 301 TTGAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGCCTGGGCTTC   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnHisLeuProGluGlyTyrGlyGlyLeuGlyLeuGlyPhe   120

Qy 361 TCCAACACCATGTACTCCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCACTGTG   420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SerAsnThrMetTyrSerArgLeuGlyLeuGlyIleIleIleSerMetAspGlySerIleThrVal   140

Qy 421 ACCCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAG   480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGluGlu   160

Qy 481 CAGAAAGCCAAATACTGCCTAAACTGGCGTCCGGGAGCACATTGCAGCGCCTTCTGCCTC   540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheAlaCysSerLeu   180

Qy 541 ACGGAGCCAGCCAGTGGGAGCCGATGGCAGCCACCAGCCTCAATCCGAGCAGAGCCACTAAGTGAA   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ThrGluProGlyAlaSerGlySerAspAlaAlaSerIleAlaGluArgSerArgAlaThrLeuSerGlu   200

Qy 601 GACAAGAAGCACTACATCCTCAATGGCTCTGGATTACTAATGGAGGACTGGCC   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 AspLysGlyHisTyrIleLeuAsnGlySerLysTrpIleThrAsnGlyGlyLeuAla   220

Qy 661 AATATTTTTACTGTGTTGCAAAGACTGAGGTCGTTGAATTCGATGGATCAGTGAAAGAC   720
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Db 221 AsnIlePheThrValPheAlaLysThrGluValAspAspSerAspSerValLysAsp   240

Qy 721 AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGAGTCAATGGAAACCCGAA   780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAspGlyValGlyLysLysProGlu   260

```
                                                             |||
Db                                  621 Cys 621

RESULT 2
ACD9_MOUSE
ID   ACD9_MOUSE    STANDARD;    PRT;   625 AA.
AC   Q8JZN5; Q8BK76; Q8C0B5;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
DE   (EC 1.3.99.-) (ACAD-9).
GN   Name=Acad9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
```

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Qy    781  GATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCATTTTGAAAACACCAAGATA  840
Db    261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle  280

Qy    841  CCTGTGGAAAACATCCTTGAGAGTTCGGAGATGGGTTAAGGTGGCCATGAACATCCTC  900
Db    281  ProValGluAsnIleLeuGluSerSerGluMetGlyTrpLysValAlaMetAsnIleLeu  300

Qy    901  AACAGCGGCCGGTTCAGCATGGGCAGCGTCGTGGCTGGCTGGCTCAAGAGATTGATTGAA  960
Db    301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu  320

Qy    961  ATGACTGCTGAGTACGCCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAATTTGGA  1020
Db    321  MetThrAlaGluTyrAlaCysThrLysAlaArgLysGlnPheAsnLysArgLeuSerGluPheGly  340

Qy   1021  TTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGAGAGTATGACC  1080
Db    341  LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr  360

Qy   1081  TACCTCACAGCAGGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCGCAGCC  1140
Db    361  TyrLeuThrAlaGlyMetLeuAspGlnProGlyPhePheAspCysSerIleGluAlaAla  380

Qy   1141  ATGTGGAAGGTGTTCAGCTGCCAGGCCGGCTGGCAGTGTGTGAGTGAGGCGCTGCAGATC  1200
Db    381  MetValLysValPheSerSerGlnAlaAlaLeuAlaTrpGlnCysValSerGluAlaLeuGlnIle  400

Qy   1201  TCCGGGGGCTTGGGCTACGACAAGGGACTATCCTACGAGGCGCATACTGCCTGACACCCGC  1260
Db    401  LeuGlyLeuGlyTyrAspLysGlyLeuSerTyrGluAlaHisThrAlaLeuThrProArg  420

Qy   1261  ATCTCCTCATCTTCGAGGGAACCAATGAGATTCCCGGATGTACATCGCCCTGACGGGT  1320
Db    421  IleLeuLeuIlePheGluGlyThrAsnGluIleProAspValHisArgProAspArgGly  440

Qy   1321  CTGCAGCAATGCCGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTG  1380
Db    441  LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal  460

Qy   1381  AGCACAGTCATGATGACCGTTGGCCCGGAGGCTTCCGGACTTCCCGGCCCCAACTGTGGAC  1440
Db    461  SerThrValMetAspThrValGlyArgArgLeuArgLeuGlyArgThrValAspAsp  480

Qy   1441  CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGACAGTGCCAACAAG  1500
Db    481  LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys  500

Qy   1501  TTTGAGGAGGAACAACACTACTGCTTCGGCGGACACTGTGCTGCTCCGCTTGGC  1560
Db    501  PheGluGluGlnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly  520

Qy   1561  AAGACCATCATGGAGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTG  1620
Db    521  LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu  540

Qy   1621  TATGGCATGACGACGCCGTGCTGTCGCGGGGGCCAGCCGCTCATCCGGATTGGGCTCCGCAAC  1680
Db    541  TyrGlyMetThrThrProValLeuSerArgArgSerArgSerIleArgIleGlyLeuArgAsn  560

Qy   1681  CACGACCACGAGGTTCTCTTGGCCAACAACACCTTCTGCGGTGGAAGCTTACTTGCCAGAATCTC  1740
Db    561  HisAspHisGluValLeuLeuAlaAsnThrPheCysGlyValGluAlaTyrLeuGlnAsnLeu  580

Qy   1741  TTCAGCCTCTTCAGCTGACCAAGTCATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAA  1800
Db    581  PheSerLeuSerGlnLeuAspLysSerTyrAlaProGluAsnLeuAspGlnIleLysLys  600

Qy   1801  GTGTCCCAGAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTGGACAGGACA  1860
Db    601  ValSerGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgArgThr  620

Qy   1861  TGC  1863
```

```
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Has a dehydrogenase activity on palmitoyl-CoA (C16:0)
CC       and stearoyl-CoA (C18:0). It is three times more active on
CC       palmitoyl-CoA then on stearoyl-CoA. Has little activity on
CC       octanoyl-CoA (C8:0), butyryl-CoA (C4:0) or isovaleryl-CoA (5:0)
CC       (By similarity).
CC   -!- COFACTOR: FAD (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AK031820; BAC27565.1; -.
DR   EMBL; AK075984; BAC36096.1; -.
DR   EMBL; BC031137; AAH31137.1; -.
DR   EMBL; BC032213; AAH32213.1; -.
DR   EMBL; BC033277; AAH33277.1; -.
DR   PIR; PT0697; PT0697.
DR   PIR; PT0721; PT0721.
DR   HSSP; P15651; 1JQI.
DR   MGD; MGI:1914272; Acad9.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Mitochondrion; Oxidoreductase; Transit peptide.
FT   TRANSIT       1      ?       Mitochondrion (Potential).
FT   CHAIN         ?     625      Acyl-CoA dehydrogenase family member 9.
FT   ACT_SITE    430     430      Proton acceptor (By similarity).
FT   CONFLICT     15      15      A -> G (in Ref. 1; BAC27565).
FT   CONFLICT     53      53      K -> E (in Ref. 1).
FT   CONFLICT    163     163      D -> E (in Ref. 1).
FT   CONFLICT    540     540      I -> V (in Ref. 1; BAC27565).
SQ   SEQUENCE   625 AA;  68707 MW;  4F06FFBFBD82F022 CRC64;
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Alignment Scores:

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Pred. No.:                                      Length:         625
Score:              4.69e-174                    Matches:        534
Percent Similarity: 91.81%                       Conservative:    38
Best Local Similarity: 85.71%                    Mismatches:      47
Query Match:        79.00%                        Indels:          4
DB:                 1                             Gaps:            1
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US-09-945-326-3 (1-1863) x ACD9_MOUSE (1-625)

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Qy      1 ATGAGCGGCTGGCGGCTCTTCCTGCGC---------------ACCACGGCTGCGGCTCGTGCC     48
          |||||||||||||||||      |||            |||||||||||||||||||||||
Db      1 MetSerGlyCysValLeuLeuSerArgGlyValAlaThrAlaAlaAlaAlaAlaAlaArgAla     20

Qy     49 TGCCGGGGTCGGTGGTCTTACCGGACCGGCGGCTACTGCCGCCACCAGCCCGCCCTGTA    108
          |||     ||||||||||     ||||||  |||||||
Db     21 SerArgValLeuArgGluPheThrAlaArgArgProLeuHisThrSerLeuGlnSer       40

Qy    109 CGAGCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAGAAGAAAGAGAGTTTTCCCATTT    168
          |||||||||||||||||||||||||||                 :::||||||||||||||
Db     41 CysSerPheAlaLysGluLeuPheLeuGlyLysIleLysArgArgLysArgValPheProPhe     60

Qy    169 CCAGAAGTTAGCCAAGATGAAACTAATGAAATCAATCAGTTCTTGGGACCCGTGGAAAAA    228
          |||||||||||||||||||||   :::|||||||||||||  :::|||||||||||||||
Db     61 ProGluValSerGlnHisGlyLeuSerGluLeuAsnGlnPheValGlyProLeuGluLys     80
```

```
Qy    229 TTCTTCACTGAAGAGAGTGGACTCCCGAAAAATTGACCAGGAAGGAAAATCCCAGATGAA    288
          |||||||||||||||||||||||||||||      :::  ::||||||||  ::
Db     81 PhePhePheThrGluGluValAspSerArgLysIleAspGlnGluGlyLysIleProValAsp    100

Qy    289 ACTTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGGCTCAAGTCCCAGAGAAATATGGT    348
          |||||||||||||||||||||||||||||     |||||||||||||||||||||||
Db    101 ThrLeuGluLysLeuLysSerLeuGlyLeuLeuPheGlyLeuGlnValProGluGluTyrGly    120

Qy    349 GGCCTGGGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGACTCATCAGCATGGATGGG    408
          |||||||||||||||||||||||||||||||||||||||  :::||
Db    121 GlyLeuGlyLeuSerAsnThrMetTyrAlaArgLeuGlyGluIleIleSerLeuAspAlaAla    140

Qy    409 TCCATCACTGTGACCCTGCAGCGCACCAGCTATTGGCTCAAGGGGATCATCTTGGCT    468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 SerIleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuVal    160

Qy    469 GGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCTGCCGGGGAGCCAATTGCA    528
          :::||||||||           :::|||||||||||||||||||||||||||||||
Db    161 GlyAsnAspGlnGlnLysAlaLysTyrLeuProLysSerGlyLysValGluHisIleAla    180

Qy    529 GCCTTCTGCCTCACGGAGCCAGTGGGACGGATGCAGCCTCAATCCGGAGCAGAGCC    588
          |||||||||||||||||||||||||||||  |||||||||||||:::|||||||||
Db    181 AlaPheCysLeuThrGluProAlaSerGlyGlySerAspAlaAlaSerIleGlnThrArgAla    200

Qy    589 ACACTAAGTGAAGACAAGAAGCACTACATCCTCAATGGCTCCAAGTCTGATTACTAAT    648
          :::||||||||||||||||||||||||||||||||||||||||||||||||::||||
Db    201 ThrLeuSerGluAspLysLysTyrPheIleLeuAsnGlySerLysValTrpIleThrAsn    220

Qy    649 GGAGGACTGGCCAAATATTTTACTGTGTTGCAAGACTGAGGTCGTTGATTCTGATGGA    708
          ||||||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db    221 GlyGlyLeuAlaAsnIleAsnValLeuGlyValGlyGlyPheLysValAspSerAspGly    240

Qy    709 TCAGTGAAAGACAAAATCACAGCATTCATAGTAGGAAAGACTTGGTGGAGTCACTAAT    768
          |||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db    241 SerLysThrAspLysMetThrAlaPheIleValGluArgAspPheGlyLyleIleThrAsn    260

Qy    769 GGGAAACCCGAAGATAAAATAGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAA    828
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GlyLysProGluAspLysIleLeuGlyIleArgGlySerAsnThrCysGluValHisPheGlu    280

Qy    829 AACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGATGGGGTTTAAGGTGGCC    888
          |||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db    281 AsnThrArgValProValGluAsnValLeuGlyValGlyGlyPheLysValAla    300

Qy    889 ATGAACATCCTCAACAGCGCCGGTTCAGCATGGCAGCGTCGTGGCTGGCGTCGTGCTCAAG    948
          ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db    301 MetAsnIleLeuAsnSerGlyArgPheSerMetGlySerAlaValAlaGlyMetLeuLys    320

Qy    949 AGATTGATTGAAAATGACTGCTGAGTACGCCTGACCAAGGAGAAAACAGTTAACAAGAGGCTC   1008
          :::|||||||||||     ||||||||||||:::||||||||||||   ::: ||||||||
Db    321 LysLeuIleGluLeuThrAlaGluTyrAlaCysThrArgLysGlnPheAsnArgAsnLeu    340

Qy   1009 AGTGAATTGGATTGATTCAGGAGAAATTGCACTGATGCTTCAGAAGGCTTACCTCATG    1068
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 SerGluPheGlyLeuIleGlnGluGluLysProAlaLeuMetAlaGlnIleLysAlaTyrValMet    360

Qy   1069 GAGAGTATGACCTACCTCACAGAGGGATGCTGACCAACCTGCTTCCCGACTGCTCC   1128
          :::||||||||||||||||||||||||||||||||:::||||||||||||||||
Db    361 GluSerMetAlaTyrLeuThrSerGlyMetLeuAspGlnProGlyPheProAspCysSer    380

Qy   1129 ATCCAGGCAGCCATGGTGAAGGTGTTCAGCTCCGCCAGTGTGTGAGTGAG    1188
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 IleGluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGlu    400

Qy   1189 GCGCTGCAGATCCTCGGGGCTTGGGCTACAAAGGGACTATCCGTACGAGCGCATACTG   1248
          |||||||||||||||||||||||||||                 :::|||||||||
Db    401 AlaLeuGlnIleLeuGlyGlySerGlyTyrMetLysAspTyrProTyrGluArgMetLeu    420

Qy   1249 CGTGACACCCGCCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATC   1308
          :::||||||||||||||||||||     ||||||||||||||  :::|||||||||||
Db    421 ArgAspAlaArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgLeuPheIle    440
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```
Qy   1309 GCCCTGACGGGTCTGCAGCATGCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAA 1368
               ||||:||:||||||||||:||||||||||||||::|||:
Db    441 AlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrSerArgIleLysGluLeuLys 460

Qy   1369 CAGGGCAAAGTGAGCACAGTCATGGACACCGTTGGCCGGAGGCTTCGGGACTCCTGGGC 1428
               ||||:::|:||:|||||:|||||||||||||||:||||||||||||||||||||||
Db    461 SerGlyAsnValThrThrValMetGluThrIleGlyArgIleArgAspSerLeuGly 480

Qy   1429 CGAACTGTGACCTGGGGTGACAGGCAACCATGGAGTTGTGCACCCAGTCTTCGCGAC 1488
               |||||||||||||||||||||:::
Db    481 ArgThrValAspLeuGlyLeuThrGlyLeuTrpGlyAspLysValValHisProSerLeuGlyAsp 500

Qy   1489 AGTGCCAACAGTTTGAGAGACAACCTACTGCTTCGGCCGGACCGTGGAGACACTGCTG 1548
               :::
Db    501 SerAlaAsnLeuLysLeuGluValHisTyrPheGlyArgThrValGluThrLeuLeu 520

Qy   1549 CTCCCGCTTTCGGCAAGACCCATCATGGAGAGGAGTACTGGTACGGCGGGTGGCCAACATC 1608
               ||||||||||||   ||||::||||||||||||||||||||||||||||||||||
Db    521 LeuArgPheGlyLysAsnIleValGluGlyGlnLeuLeuValLeuLysArgValAlaAsnIle 540

Qy   1609 CTCATCAACCTGTATGGCATGACGCGCCGTCGTCGTGCGGGCCAGCCGCCTTCATCCGCATT 1668
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 LeuIleAsnLeuTyrGlyMetThrArgAlaValAlaValLeuSerArgAlaSerArgSerIleArgIle 560

Qy   1669 GGGCTCCGCAACCACGACGAGTTCTTCCTTGGCCAACACCTTCTGCGTGGAAGCTTAC 1728
               |||||||||||||||||||||||||||||||||||||||
Db    561 GlyLeuArgAsnHisAspHisGluPheLeuLeuAlaAsnMetPheCysValGluAlaTyr 580

Qy   1729 TTGCAGAATCTCTTCAGCCTCTCTGACAACAGTATGCTCCAGAAAACCTAGGATGAG 1788
               |||||||||||||||||||||||||||||||||||||||||||||
Db    581 PheGlnAsnLeuPheSerLeuSerAspAsnSerGlnLeuAspLysAsnAlaProGluAsnLeuAspGlu 600

Qy   1789 CAGATTAAGAAAGTGTCCCAGCAGATCCTTGAGAGCGAGCCTATATCTGTGCCACCCT 1848
               |||||||||||:::|
Db    601 GlnIleLysLysValSerArgArgGlnIleLeuGluLysArgAlaTyrIleCysAlaHisPro 620

Qy   1849 CTGGACAGG 1857
               ||||||
Db    621 LeuAspArg 623
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RESULT 3

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Qy    370 ATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTGACCCTGCA 429
              1 MetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrValThrLeuAla 20

Qy    430 GCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGGAGCAGAAAGCC 489
             21 AlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGluGlnLysLysAla 40

Qy    490 AAATACTTGCCTAAACTGGCTCCGGGAGCACATTGCAGCTCCTGCCTCACGGAGCCA 549
             41 LysTyrTyrLeuProLysLeuAlaSerGlyAlaHisHisAlaPheCysLeuThrGluPro 60

Qy    550 GCCAGTGGGAGCCGATGGCAGCCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAAG 609
             61 AlaSerGlyAsnAspAlaAlaSerIleAsnGlyIleIleLeuLeuSerGlyArgAlaThrLeuSerGlyLysLysGlyLysLysAla 80

Qy    610 CACTACATCCTCAATGGCTCCAAGGTGCTGATTAATAACTGGCCAATATTTTT 669
             81 HisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyValLeuLeuAlaAsnIlePhe 100

Qy    670 ACTGTGTTGCAAAGACTGAGCTCGTTGATTCTGATGGATCAGTGAAAGACAAAATCACA 729
            101 ThrValPheAlaLysThrGluValValAspAsnGlySerValValAspLysAspLysLysThr 120

Qy    730 GCATTCATAGTAGAAAGAGACTTTGGTGGAGTCAGAAATGGGAAACCCGAAGATAAATTA 789
            121 AlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGluAspLysLeu 140
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Right column:

```
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki K.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa R.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; AK022568; BAB14104.1; -.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR005829; Sug_transporter.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
DR   PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE  498 AA;  55083 MW; A57B7121B8FB1310 CRC64;
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Alignment Scores:
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Pred. No.:                     4.64e-162
Score:                         2526.00
Percent Similarity:            100.00%
Best Local Similarity:         100.00%
Query Match:                   73.79%
DB:

                               Length:        498
                               Matches:       498
                               Conservative:    0
                               Mismatches:      0
                               Indels:          0
                               Gaps:            0
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US-09-945-326-3 (1-1863) x Q9H9W4 (1-498)

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Q6DDF2
ID   Q6DDF2          PRELIMINARY;      PRT;   622 AA.
AC   Q6DDF2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Acad9-prov protein.
GN   Name=acad9-prov;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocytes;
RX   MEDLINE=22341112; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocytes;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocytes;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; BC077618; AAH77618.1; -.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh_1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE 622 AA; 68429 MW; 1BA5F489FF08A9C9 CRC64;
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Qy    790  GGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAGATACCTGTGGAA    849
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Db    141  GlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrlysIleProValGlu  160

Qy    850  AACATCCTTGAGAGGTCGGAGGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGC    909
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161  AsnIleLeuGluGlyValGlyValGlyTyrAspGlyPheLysValAlaMetAsnIleLeuAsnSerGly  180

Qy    910  CGGTTCAGACATGGGCAGCGCTGCTGGCCTGCTCAAGAGATTGATTGAAATGACTGCT    969
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGluMetThrAla  200

Qy    970  GAGTACGGCCTGCACAAGGAAACAGTTTAACAGAGGCTCAGTGAATTGGATTGATTCAG    1029
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201  GluTyrAlaCysThrArgLysThrArgLysGlnPheAsnLysSerGluGluLeuIleGln  220

Qy   1030  GAGAAATTTGACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTCACA    1089
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221  GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrTyrLeuThr  240

Qy   1090  GCAGGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCCATGTGAAG    1149
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAlaMetValLys  260

Qy   1150  GTGTTCAGCTCCGAGGCCGCCTGCCAGTGTGTGAGTGAGGCGCTGCAGATCCTCCGGGGC    1209
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261  ValPheSerSerGluAlaAlaCysGlnCysValSerGluAlaLeuGlnIleLeuGlyGly  280

Qy   1210  TTGGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCGTGACACCCGCATCCTCTC    1269
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281  LeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArgIleLeuLeu  300

Qy   1270  ATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTCTCAGCAT    1329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  IlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyLeuGlnHis  320

Qy   1330  GCCCGGCCGCATCCTGACTACCCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTC    1389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321  AlaGlyArgIleLeuThrThrArgIleHisGluHisArgIleLysGlnAlaLysValSerThrVal  340

Qy   1390  ATGGATACCGTGGCCGGAGGCTTCGGACTCCCTGGGCCGAACTGTGACCTGGGGCTG    1449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341  MetAspThrValGlyArgArgLeuArgLeuProGlyProAsnCysAspLeuGlyLeu  360

Qy   1450  ACAGGCAACCATGAGAGTTGTGCACCCAGTCTTCGGACACGAGCAGTTGAGGAG    1509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ThrGlyAsnHisGluValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu  380

Qy   1510  AACACCTACTGCTTCGGCGACCGTGAGACCACTGCTCCGCTTTGGCAAGACCATC    1569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381  AsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGlyLysThrIle  400

Qy   1570  ATGGAGGAGCAGCTGGTACTGGAAGCGGGTGCCAACATCCTCATCAACCTGTATGGCATG    1629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401  MetGluGluGlnLeuValLeuGluAlaGlyValAlaAsnIleLeuIleAsnLeuTyrGlyMet  420

Qy   1630  ACGGGCCGTGTCGTCGCGGGCCAGCCGCTCCATCCGCCATTGGGCTTCCGCAACCACGACCAC    1689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  ThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgLeuArgAsnHisAspHis  440

Qy   1690  GAGGTTCTCTTGGCCAACACCTCTGCGGGAAGCTTACTTGCAGAATCTCTTCAGCCTC    1749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441  GluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeuPheSerLeu  460

Qy   1750  TCTCAGCTGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCCCAG    1809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461  SerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLysValSerGln  480

Qy   1810  CAGATCCCTGAGAGCGAGCCTATATCGTGCCCACCCCTCTGGACAGGACATG    1863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GlnIleLeuLeuGlyLysArgAlaTyrIleCysAlaHisProLeuAspArgArgAsnThrCys  498
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RESULT 4
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Alignment Scores:

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Pred. No.:                          Length:        622
Score:        8.8e-152              Matches:       453
              2374.50
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Percent Similarity:     85.41%          Conservative:  74
Best Local Similarity:  73.42%          Mismatches:    87
Query Similarity:       69.37%          Indels:         3
DB:                                     Gaps:           1

US-09-945-326-3 (1-1863) x Q6DF2 (1-622)
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Qy   10 TGCGGGCTCTTCCTCGCCACCAGGGCTGCGCCTCGCCTGGCCTTCTGCCGGGGTCGTGGTCTCT   69
        ||||||        |||          ||  :::    |||
Db    8 CysGly--------ArgAlaAlaSerLeuThrArgValTrpAlaGlyProAlaGlyPro       24

Qy   70 ACCGGCAACCGGCTACTGCCGCACCAGCCGCCTGTACGAGCTTTCGCCAAAGAGCTT       129
        ||||                    ||||||
Db   25 GluLeuProArgSerProThrCysSerProHisArgLeuAlaTyrArgLeuAlaLysGluLeuVal  44

Qy  130 TTCCTAGGCAAAATCAAGAGAAAGAAGTTTCCCATTTCCAGAAGTTAGCCAAGATGAA       189
        ||||     :::||||   |||||:::||||
Db   45 PheLeuGlySerIleLysArgLysLysPheProIlePheProGluValPheAlaLysMetLysGluGlu 64

Qy  190 CTTAATGAAATCAATCAGTTCTTGGACCCCTGGAAAAATTCTTCACTGAGAGGTGGAC       249
        ||::        ||||||||         |||||||   ||| :::
Db   65 LeuGluGluIleAsnGlnPheLeuAspProTrpLysAsnSerSerLeuArgGlyGlyValAsp       84

Qy  250 TCCCGAAAAATTGACCAGGAAGGGAAAAATCCAGATGAAACTTTGGAGAAAATTGAAGAGC    309
        ||::||   ||||||   ||||||||       ||   :::
Db   85 SerLysLeuIleAspGlnThrAlaLysIleLysProGluThrLeuAspLysLeuGluLysAsn      104

Qy  310 CTAGGGCTTTTGGGCTGCAAGTCCCAGAGAATAGTGGTGCCGCTTCTCCAACACC         369
        |||||||||:::|||   |||||   ||||:::
Db  105 LeuGlyLeuPheGlyMetGlnIleProGluTyrGlyLeuGlyLeuSerSerAsnThr         124

Qy  370 ATGTACTCAGACTAGGGAGGAGATCATCAGCATGGGTCCATCACTGTGACCCTGGCA      429
        ||||||||||||||            ||||||
Db  125 MetTyrAlaArgLeuGlyGluIleIleSerLeuAspGlyAlaIleAlaValThrLeuAla     144

Qy  430 GCGCACCAGGCTATTGGCTCCAAGGGGATCATCTTGGCTGCGCACTGAGGAGCAGAAAGCC    489
        ||||||||||||||       :::|||
Db  145 AlaHisGlnAlaIleGlyLeuLysGlyLeuIleLeuAlaGlyAsnAspGluGlyGlnLysAla    164

Qy  490 AAATACTTGCCTAAACTGGCTCCGGGGAGCCACATTGCAGCCTTCGCCTGCCCTGGAGCCA    549
        ||||||||||||||||   |||||||||||
Db  165 LysTyrLeuProLysLeuAlaSerGlyGluGlyGlyGluHisIleAlaAlaPheCysLeuProPro  184

Qy  550 GCCAGTGGGAGGCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGACAAGAAG    609
        |||||||||||||||      :::|||
Db  185 GlySerGlySerAspProAlaAlaSerGlnIleSerArgAlaThrLeuThrProAspGlyLys     204

Qy  610 CACTACATCCTCAAATGGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTT    669
        |||||||||||     :::||||   |||||||
Db  205 HisPheLeuLeuAsnGlySerLysSerTrpIleThrAsnGlyGlyLeuAlaAspIlePhe      224

Qy  670 ACTGTGTTTGCAAAGACTGAGGTCGTTGATTCTGATGGATCAGTGAAAGACAAAATCACA    729
        |||||:::   ||||||||||||||||||
Db  225 ThrValPheAlaArgThrGluValValAspSerAspGlySerValLysThrLysAspLysIleSer   244

Qy  730 GCATTCATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAAACCCGAAGATAAATTA    789
        ||||   :::|||
Db  245 AlaPheIleValGluArgAspAlaPheGlyGluSerLeuMetGlyLysProGluAspLysLeu      264

Qy  790 GGGCATTCGGGCTCCAACACTTGTGAAGTCCATTTTGAAAACACCAAGATACCTGTGGAA    849
        |||||   ||||||:::|||||
Db  265 GlyIleArgGlySerAsnThrCysGluHisPheGluAsnThrLysLysValProValGlu       284

Qy  850 AACATCCTTGGAGAGGTCGGAGATGGGTTAAGTGGCCATGAACATCCTCAACGCGGC      909
        :::||||   |||||||||||||||||||
Db  285 AsnValIleLeuGlyGluValGlyAspGlyLeuGlyGlyPheLysValAlaAlaMetLeuAsnSerGly 304

Qy  910 CGGTTCAGCATGGGCAGCCGTCGTGCTGGCGTGCTCAAGAGATTGATTGAAATGACTGCT    969
        ||||||:::|||   |||||||||
Db  305 ArgPheSerMetGlySerAlaSerArgAlaGlyIleLeuLysArgLeuIleGluMetThrAla      324

Qy  970 GAGTACGCCTGCACAAGGAAACAGTTTAACAGAGGCTCAGTGATTTGGATTGATTCAG   1029
        |||||||||||:::|||
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Db  325 GluTyrAlaCysThrArgLysGlnPheAsnLysLysLeuSerAspPheGlnLeuIleGln       344
        |||||||||||||||||||||||:::
Qy 1030 GAGAAATTGCACTGATGGCTCAGAGGCTTACGTCATGGAGAGTATGACCTACCTCACA      1089
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  345 GluLysPheAlaLeuMetAlaGlnLysAlaPheValMetGluSerMetAlaTyrLeuThr      364

Qy 1090 GCAGGGATGGTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCCATGGTGAAG   1149
        ||||||||||||||||||||||||||||||||
Db  365 AlaGlyMetMetAspArgProGlyLeuProAspCysSerValGluAlaAlaMetValLys      384

Qy 1150 GTGTTCAGCTCCGAGGCGCCTGGCAGTGTGGAGTGAGGCGGCTGCAGAATCCTCGGGGC   1209
        |||||||||||||||||||||||||||||
Db  385 ValPheSerSerGluGluLysGlnLeuSerValSerGluValSerGluGlnIleLeuGlyLeuGlyGly 404

Qy 1210 TTGGGGCTACACAGGGACTATCGTACGAGCGGCATACTGGCGTGACACCCGCATCCTCCTC  1269
        |||||||||||||||:::|||||
Db  405 LeuGlyTyrMetLysAspTyrProTyrGluArgHisTyrLeuArgTyrAspSerArgIleLeuLeu    424

Qy 1270 ATCTTCGAGGAGCAACCATGAGATTCTCCGGATGTACATCGGCCTGACGGGGTCTGCAGCAT 1329
        ||||||:::|||||   |||||||||||:::|||||||||
Db  425 IlePheGluGluGlnThrArgAsnGluIleLeuLeuArgMetTyrIleAlaLeuThrGlyMetGlnHis 444

Qy 1330 GCCGGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTC 1389
        ||||||   |||||   :::|||
Db  445 AlaGlyLysIleLeuThrGlyIleLeuGlyMetLysLysGlyAsnValGlyValAla        464

Qy 1390 ATGGATACCGTTGGCCGGAGGCTTCGGGACTTCCCTGGGCCGGACCTGTGGACCTGGCGTG  1449
        |||:::|||||||||||
Db  465 MetGluPhePheLysLeuArgAspAspSerMetGlyArgAsnValAsnLeuGlyLeu       484

Qy 1450 ACAGGCAACCATGAGTTGTGCACCCCAGTTCTGCGACAGTGCCAACAAGTTTGAGGAG   1509
        |||||||||||||||:::|||||||||||
Db  485 ThrGlyAsnGluGlyValValHisProSerLeuGluSerAlaLysLysLeuGluGlu        504

Qy 1510 AACACCTACTGCTTCCGGCGACCGTGGAGACACTGCTGTCCGCTTTGGCAAGACCATC   1569
        |||||||:::|||||
Db  505 AsnValTyrTyrProGlyThrThrValGluSerLeuLeuTyrArgPheGlyLysThrIle      524

Qy 1570 ATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCAAATCCTCATCATGTATGGCATG    1629
        |||:::|||   ||||||||||||||
Db  525 ValGluGluGlnLeuGlnLeuAlaLeuLysArgValAlaAspValIleIleAsnLeuTyrAlaMet    544

Qy 1630 ACGGCCGTGCTGTCCGGGGCTGTCGCCGGCCCAGCCGCCTCCATCCGCATTGGGCTCCGCAACCGACCAC 1689
        |||||||||||||||:::|||||||||
Db  545 ThrAlaValIleIleSerArgArgSerIleSerSerArgGlyIleTyrLeuProArgAsnHisAspPhe  564

Qy 1690 GAGGTTCTTGGCCAACACCTTCTGCGTGAAGCTTACTGCGAGAATCTCTTCAGCCTC   1749
        |||||:::|||   |||||||
Db  565 AspValLeuLeuAsnMetPheCysSerGluValTyrPheLysAsnAsnTyrThrLeu      584

Qy 1750 TCTCAGCTGACAAGTGATGCTCCAGAAAACCTAGAGCAGATTAAGAAAGTGTCCCAG   1809
        |||||||||:::|||
Db  585 AlaGlnLeuGlyLysHisSerProGluGlnAsnGlnAspAspSerIleArgLysIleAlaGly       604

Qy 1810 CAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCTCTGGACACGGACA     1860
        |||||||||||||||||||||||
Db  605 HisIleLeuGluLysArgGlyTyrTyrThrCysSerHisProLeuAspLeuAspArgThr       621
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RESULT 5
Q9BUX5
ID   Q9BUX5          PRELIMINARY;       PRT;   343 AA.
AC   Q9BUX5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ACAD9 protein (Fragment).
GN   Name=ACAD9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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Db   101  AlaAlaMetValLysValPheSerGluAlaTrpGlnCysValSerGluAlaLeu  120
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Qy  1195  CAGATCCTCGGGGCTTGGCTACACAAGGGACTATCCGTACGAGCGCCATACTGCCTGAC 1254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GlnIleLeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAsp  140
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Qy  1255  ACCCGACCATCCTCCATCTTCGAGGGAACCAATGAGATTCCCGGATGTACATCGCCCTG 1314
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Db   141  ThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeu  160
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Qy  1315  ACGGGTCTGCGAGCATGCCGGCCGCATCCTACCAGGATCCATGAGCTTAAACAGGCC 1374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161  ThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAla  180
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Qy  1375  AAAGTGAGCACAGTCATGGATACCGTTGGCGAGCTTCCGGACTCCCTGGCCGAACT 1434
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Db   181  LysValSerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThr  200
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Qy  1435  GTGGACCTGGGGCTGACAGGCAACCAGAGTGTGCACCCCAGTCTTGCGGACAGTGCC 1494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201  ValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAla  220
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Qy  1495  AACAAGTTTGAGGAGAACACCTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGC 1554
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Db   221  AsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArg  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1555  TTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGAAGCCGGTGCCAACATCCTCATC 1614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PheGlyLysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIle  260
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Qy  1615  AACCTGTATGGCATGACGGGCCGTGCTGTCGGCGGCCAGCCGCTCATCCGCATTGGGCTC 1674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261  AsnLeuTyrGlyMetThrAlaValLeuSerArgArgSerIleArgIleGlyLeu  280
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Qy  1675  CGCAACCACCACGAGGTTCTCTGGCCAACACCTTCCGTGGAGAGCTTACTTGCAG 1734
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Db   281  ArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGln  300
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Qy  1735  AATCTCTTCAGCCTCTTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATT 1794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIle  320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1795  AAGAAAGTGTCCCAGCAGATCCTTGAGAGCAGCGAGCCTATATCTGTGCCCACCCCTGGAC 1854
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Db   321  LysLysValSerGlnGlnIleLeuGluSerSerGluProIleSerValProThrProAsp  340
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Qy  1855  AGGACATGC 1863
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Db   341  ArgThrCys  343
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RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC001817; AAH01817.2; -.
DR   HSSP; P15651; 1JQI.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR005829; Sug_transporter.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
DR   PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
FT   NON_TER   1   1
SQ   SEQUENCE   343 AA; 38569 MW; 10E1781937745C00 CRC64;

Alignment Scores:
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Pred. No.:                    1
Score:                    6.39e-109      Length:             343
Percent Similarity:       1739.00        Matches:            343
Best Local Similarity:    100.00%        Conservative:         0
Query Match:              100.00%        Mismatches:           0
DB.:                      50.80%         Indels:               0
                          2              Gaps:                 0
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US-09-945-326-3 (1-1863) x Q9BUX5 (1-343)

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Qy   835  AAGATACCTGTGGAAAACATCCTTGGAGAGGTCCGAGATGGGTTTAAGGTGGCCATGAAC 894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  LysIleProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsn 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   895  ATCCTCAAACAGCGCGCCGGTTCAGCATGGGCAGCGTCGTGCTGCTCAAGAGAGATTG 954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21  IleLeuLysGlnArgAlaGlyPheSerMetGlySerValValAlaValAlaLeuLysArgLeu 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   955  ATTGAAAATGACTGCTGAGTACGCCTGCACAAGGAAACAGTTTAACAAGAGGCTCAGTGAA 1014
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41  IleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1015  TTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGACT 1074
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  PheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSer 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1075  ATGACTACCTCACAGCAGGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAG 1134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81  MetThrThrTyrLeuThrAsnLeuAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGlu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1135  GCAGCCATGGTGATGAGGGTTCAGCTCCGAGGCCGCCTGCGAGTGTGTGAGTGAGGGCGCTG 1194
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; BC054606; AAH54606.1; -.
DR   HSSP; Q06319; 1BUC.
DR   ZFIN; ZDB-GENE-030131-899; zgc:64067.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh;1.
DR   Pfam; PF02770; Acyl-CoA_dh_M;1.
DR   Pfam; PF02771; Acyl-CoA_dh_N;1.
DR   PROSITE; PS00072; ACYL_COA_DH_1;1.
DR   PROSITE; PS00073; ACYL_COA_DH_2;1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE   659 AA;  71111 MW;  C12D31F27C92F71F CRC64;

Alignment Scores:
Pred. No.:
Score:                  3.16e-83
                        1360.50
Percent Similarity:     63.62%
Best Local Similarity:  46.49%
Query Match:            39.75%
DB:                     2

Length:        659
Matches:       285
Conservative:  105
Mismatches:    204
Indels:        19
Gaps:          8

US-09-945-326-3 (1-1863) x Q7T2C2 (1-659)

Qy   28 ACCAGGGCTGCGGGCTCGTCGTGCTGGGGTCTCTACCGGGGACCCGGGCCTA          87
            |||||||||||||||||||||||||||||||
Db

Qy   59 CTGCGCCACCAGCCCGCCTGTACGAGCTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAG  147
            |||||||||||||||    :::::::|||  |||||
Db   76 -----------------------LysSerPheAlaValAlaAsnMetPheLysGlnIleSer  88

Qy  148 AAGAAGAAGTTTCCCATTTCCAGAAGAAGTTAGCCAAGATGAACTTAATGAA---ATCAAT  204
            ::|||||||||||:::||  :::::  ||||
Db   89 ThrSerGlnValPhePrOTyrProSerValLeuAsnGluGlnSerGlnPheLeuArg     108

Qy  205 CAGTTCTTGGACACCCTGGGAAAAATTCTTCACTGAAGAGTGAGACTCCCGAAAAATTGAC  264
            :::   |||:::  |||  ||||
Db  109 GluLeuValGlyProCysSerLeuSerPheAlaAsnAspProMetLysAsnAsp        128

Qy  265 CAGGAAGGAGAAATCCCAGATGAAAATCCCAGAGAAATTGGAGAAAATTGGAAAGACA     324
            ||||||||||||  :::  |||||||||||:::||
Db  129 AlaLeuGluLysValGluGluHisThrLeuGlnHisGlyLeuLysGluGlyMetGlyAlaPheGly  148

Qy  325 CTGCAAGTCCCAGAAGAATATGTGGCCTGGCCTCTCGGGCTTCTCCAACACCATGTACTCAAGACTA 384
            :::  :||||||||     ||||||  :::
Db
```

The remaining alignment block (right side):

```
Db  149 LeuGlnIleValProAlaAlaSerpLeuGlyLeuGlyIleGlyLeuValGlyLeuThrAsnThrGlnTyrAlaArgLeu  168
            ||||||||||  :::                    ::  |||||||||
Qy  385 GGGAGATCATCAGCATG---GATGGTCATCACTGTGACCCTGGCAGCGACCACAGGCT  441
            |||||||||||||||
Db  169 ValGluIleValGlyMetHisAspLysHisValAlaGlyLyvAlGlyIleThrLeuGlyIleAlaHisGlnSer  188
            ||||||||||||  |||:::||| |||
Qy  442 ATTGGCCTCAAGGGGATCATCTTGGCTCCACTTGGGAGGAGACAAAGCCAAATACTGCCT  501
            ||| |||  |||||:::|||
Db  189 IleGlyPheLeuLeuLeuPheGlyIleIleLeuLeuPheGlyAsnProGlnGlnLysGluLysTyrLeuPro  208
            :||||||||||  ||:::||
Qy  502 AAACTGGGCTCCGGGAGCACATTGCAGCCTTCGCCTCACGGAGCCAGCCAGTGGGAGC  561
            |||||||:::|||:::||||
Db  209 LysLeuAlaThrGlyGluThrGlyGluThrCysLeuThrGluPheGluProAlaSerGlySer  228
            :||||||||||||  ||||||  ::::::
Qy  562 GATGAGCGCTCAATCCGGAGCAGAGCCACACTAAGTGAACAACAAGAGCACTACATCCTC  621
            ||| |||||||||||||||
Db  229 AspAlaAlaSerIleLeysThrThrAlaValArgSerProCysGlyGlnTyrTyrThrMet  248
            |||||||||||:::||||| |||||||
Qy  622 AATGGCTCCAAGGTCTGGATTACTAATGGACGACTGGCCAATATTTTACTGTGTTGCA  681
            |||||||||||||  |||:::|||
Db  249 AsnGlySerLysIleTrpIleSerAsnGlyGlyThrAlaGlyIleLeuPheThrValPheAla  268
            ||||||||||||||:::|||
Qy  682 AAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATA  738
            ||||||||||||||  :::|||
Db  269 LysThrProValLysAspGluLysThrGlyMetLysAspLysAspValThrAlaPheIle  288
            :||||||||||||||:::|||
Qy  739 GTAGAAAGAGACTTTGGTGAGTCACTAATGGAAACCCGAAGATAAAATTAGGCATTCGG  798
            ||||||||||:::||||||
Db  289 ValGluArgPheGlyValSerSerSerGlyValProProGluLysValLysMetGlyIleLys  308
            :::|||||||||||:::||
Qy  799 GGCTCCAACACTGTGAAGTCCATTTGAAAACCCAAGATACCGTGGAAAACATCCTT  858
            |||||||||  ||||  ::::::
Db  309 AlaSerAsnThrAlaGluValTyrPheGluSerValArgValProAlaAsnValArgAspCysValLeu  328
            ||||||||||||||:::|||
Qy  859 GGAGAGGTCCGAGATGGGTTTAAGGTGGCCATGAACAATCCTCAACAGCGGCCGTTCAGC  918
            |||||||||||||  :::|||
Db  329 GlyGluValGlyGlyGlyLyoPheLysValPheLysLysAlaAlaLeuAsnAsnGlyArgPheGly  348
            ||||||||||:::|||
Qy  919 ATGGGCAGCGTCGTGCTGGCTGCTCGTCAAGAGATTGATTGAAATGACTGCTGAGTACGCC  978
            |||  :::||||||||
Db  349 MetAlaAlaAlaLeuSerGlyThrMetLysGlyValIleThrLysLysGlyValIleThrLysLysGlyValIleLysAlaValAlaAspHisAla  368
            |||||||||||:::|||
Qy  979 TGCAAGAGAAACAGTTAACAAGAGCTCCAGTGAATTGCAGGAGAAATTT 1038
            ||||||  :::|||||||
Db  369 AlaAlaAsnArgThrGlnPheGlyAsnLysIleHisAsnTyrGlyAlaIleGlyGlnValGluSerMet  388
            |||  :::|||||||
Qy 1039 GCACTGATGGCTCAGAGAGCTTACGTCATGAGAGTATGACTACCTCACAGCGAGGGATG 1098
            |||  :::|||||||
Db  389 AlaArgMetAlaMetAlaLeuGlnTyrValThrGlyMetAlaTyrMetValSerGlyLyvAsn  408
            ||||||||||||  :::|||
Qy 1099 CTGGACCAACCTGGCTTCCCGACTGCTCCATCAGGAGCAGCCATGTGAAGGTGTTCAGC 1158
            |||||||||||||||  :::
Db  409 MetAspSer---GlyAlaThrGluPheGlnIleGluGlnAlaIleLeuAlaIleSerLysLysPheAla  427
            |||:::
Qy 1159 TCCGAGGCCCCTGCCAGTGTGTGAGTGAGGCGCTGCAGATCCTGGGGCTTGGGCTAC 1218
            ||||||||  :::::
Db  428 SerGluAlaAlaTrpLeuValThrAspAspGlyCysIleGlnValMetGlyIleMetGlyPhe  447
            :::|||||||||||
Qy 1219 ACAAGGGACTATCCGTACGAGCGCATACTGGTGACACCCGCATCTCCTCATCTTCGAG 1278
            :::|||||||:::|||
Db  448 MetLysAspAlaGlyValValLeuArgGlyValLeuArgArgIlePheGluGlu  467
            |||:::
Qy 1279 GGAACCAATGAGATTCTCCGACGGTGTACATCGCCCCTCGACGGGTCTGCAGCATGCCGGCC 1338
            |||||||
Db  468 GlyThrAlaAsnProIleLeuLeuArgLeuValAlaLeuAsnGlyTyrPheGlnAsnAlaGlyAsnAsp  487
            |||||:::|||
Qy 1339 ATCCTGATACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCCAGAGTCATG 1392
            :::|||||||:::|||
Db  488 GlnLeuLysSerLeuGlnLysAlaLeuLysAsnProLeuGlyAsnAlaGlyMetLeuAla  507
            ||||||:::
Qy 1393 GATACCGTTGCCGGAGGCTTCGGGAGGACTCCCTGGGGACTGTGACA 1452
            ::: :::||||||
Db
```

```
Db   508 GlyGluIleThrLysArgAlaAlaLysArgArgAlaGly-----LeuGlySerGlyLeuThr 525
             |||||||
Qy  1453 GGCAACCATGAGTTGTGCACCCAGTCTTGCGGACAGTGCCAACCAAGTTGAGGAGAAC 1512

Db   526 ---LeuGlnGlyThrValHisProGluLeuAsnHisSerGlyGluLeuThrValLysAla 544
              |||||
Qy  1513 ACCTACTGCTTCGGCCGACCGTGGAGACACTGCTTCCGCTTTGGCAAGACCATCATG 1572

Db   545 IleGluGlnPheGlyAlaValIleGluGluLeuLeuLeuLysHisGlyLysLysIleIle 564
              :::|||
Qy  1573 GAGGAGCAGTCGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACG 1632

Db   565 AspGluGlnPheValLeuLysProGluLeuLysArgValAlaAspCysAlaIleAspLeuTyrAlaMetVal 584
              ||| :|
Qy  1633 GCCGTGCTGTCGCGGGCCAGCCGCCCATCCGCATTGGGCTCCGCAACCACGACCACCAG 1692

Db   585 ValValLeuSerArgAlaSerLeuAsnGlnGlyHisSerSerAlaGlnHisGlyGlu 604
              :::
Qy  1693 GTTCTTCTTGGCCAACACCTTCTGCGTGGAAGCTTACTTGCAGAATCTCTTCAGCCTCTCT 1752

Db   605 LysMetLeuCysGluThrTrpCysThrGluAlaHisGluArgValMetGlnAspIleLys 624
              :::
Qy  1753 CAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTCCCAGCAG 1812

Db   625 PheLeuArgSerGlyThrSerLysGlnThrPheLysAsnLeuArgAlaIleSerAlaAla 644
              :::
Qy  1813 ATCCTTGAGAAGGGAGCCTATATCTGTGCCCACCCTCTG 1851

Db   645 ValValGluAsnGlyGlyValValAlaProHisProLeu 657
              :::::|||
Qy       ValValGluAsnGlyGlyValValAlaProHisProLeu 657
```

RESULT 7
ACDV_MOUSE

```
ID   ACDV_MOUSE     STANDARD;      PRT;   656 AA.
AC   P50544; O35289; O55133;
DT   01-OCT-1996 (Rel. 34, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD) (MVLCAD).
GN   Name=Acadvl; Synonyms=Vlcad;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Blood;
RA   Andresen B.S., Lund H., Bross P., Gregersen N.;
RT   "Mouse very-long-chain acyl-CoA dehydrogenase (VLCAD) gene.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RA   Andresen B., Lund H., Bross P., Corydon M., Gregersen N.;
RT   "Cloning and characterization of mouse very-long-chain acyl-CoA
RT   dehydrogenase.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 84-656 FROM N.A.
RC   STRAIN=ICR; TISSUE=Liver;
RX   MEDLINE=98345418; PubMed=9680378;
RA   Cox K.B., Johnson K.R., Wood P.A.;
RT   "Chromosomal locations of the mouse fatty acid oxidation genes Cpt1a,
RT   Cpt1b, Cpt2, Acadvl, and metabolically related Crat gene.";
RL   Mamm. Genome 9:608-610(1998).
RN   [5]
RP   SEQUENCE OF 339-656 FROM N.A.
RA   Rao G., Krimer D., Krasikov T., Austin C., Skoultchi A.I.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y11770; CAA72435.1; -.
DR   EMBL; Z71189; CAA94919.2; -.
DR   EMBL; BC026559; AAH26559.1; -.
DR   EMBL; AF017176; AAC31642.1; -.
DR   EMBL; U41497; AAA85185.1; -.
DR   HSSP; Q06319; 1BUC.
DR   SWISS-2DPAGE; P50544; MOUSE.
DR   MGD; MGI:895149; Acadvl.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW   Oxidoreductase; Transit peptide.
FT   TRANSIT       1     41       Mitochondrion (By similarity).
FT   CHAIN        42    656       Acyl-CoA dehydrogenase, very-long-chain
FT                                specific.
FT   DOMAIN       42    483       Catalytic.
FT   CONFLICT    339    339       NNG -> GTR (in Ref. 5).
FT   CONFLICT    423    423       C -> W (in Ref. 5).
FT   CONFLICT    427    427       A -> G (in Ref. 5).
FT   CONFLICT    441    441       M -> I (in Ref. 5).
FT   CONFLICT    507    507       G -> A (in Ref. 5).
FT   CONFLICT    532    532       R -> P (in Ref. 5).
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FT   CONFLICT      567  567  Q -> K (in Ref. 5).
FT   CONFLICT      570  571  AD -> GG (in Ref. 5).
FT   CONFLICT      573  573  A -> P (in Ref. 5).
FT   CONFLICT      593  593  G -> A (in Ref. 5).
FT   CONFLICT      596  596  T -> A (in Ref. 5).
FT   CONFLICT      612  612  A -> P (in Ref. 5).
FT   CONFLICT      628  628  H -> Q (in Ref. 4).
SQ   SEQUENCE      656 AA;  70875 MW;  A0110CASC6CF4F89 CRC64;

Alignment Scores:
Pred. No.:          1
Score:              3.41e-83           Length:        656
                    1360.00            Matches:       287
Percent Similarity: 66.05%             Conservative:  106
Best Local Similarity: 48.24%          Mismatches:    184
Query Match:        39.73%             Indels:        18
DB:                                    Gaps:          9
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US-09-945-326-3 (1-1863) x ACDV_MOUSE (1-656)

```
Qy   103  CCTGTACGAGCT--------------TTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAG  150
              ||||||                   ||||||   ::||||   ||||||||
Db    66  ProAlaArgAlaGluSerLysPheAlaValGlyMetPheLysPheGlnLeuThrIle    85

Qy   151  AAAGAAGTTTCCCATTTCCAGAAGTT---AGCCAAGATGAACTTAATGAAATCAATCAG  207
             :::||||||||::||:|        ||||||||||       :::    :::
Db    86  AspGlnValPheProTyrProSerValLeuSerGluGluGlnAlaGlnPheLeuLysGlu  105

Qy   208  TTCTTGGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGACTCCCGAAAAATTGACCAG  267
              ::||||||        ||:||||||||||        :||    |||
Db   106  LeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaLysAsnAspAla  125

Qy   268  GAAGGGAAAATCCCAGATGAAACTTTGGAGAATGAAGAGCCTAGGGCTTTTGGGCTG  327
              ||||||        :::    ||||||||    ||||||    ||||||
Db   126  LeuGluLysValGluAspAspProThrLeuGlnLeuGluLeuGluLeuGlyAlaPheGlyLeu  145

Qy   328  CAAGTCCCAGAGAATATGTGGCCTGGGCTTCTCCAACACCATGTACTCAAGACTAGGG  387
             ||||||||||||        ||||||||||||        ||||||||
Db   146  GlnValProSerGluAsnGlyLeuGlyLeuLeuGlyLeuGlyLeuSerAsnThrGlnTyrGlnAlaArgLeuAla  165

Qy   388  GAGATCATCAGCATG---GATGGGTCCATCACTGTGACCCTGGCAGCCGACCAGGCTATT  444
             ||||:::    |||    |||        :::||||||||||||:||||||
Db   166  GluIleValGlyMetHisAspLeuGlyValSerValThrLeuAlaAlaHisGlnSerIle  185

Qy   445  GGCCTCAAGGGGATCATCTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAA  504
             |||||||        ||||||||||        ||||||||||||||||||
Db   186  GlyPheLysGlyIleLeuLeuLeuTyrGlyThrLysAlaGlnIleArgGluLysTyrLeuProArg  205

Qy   505  CTGGGCTCCGGGAGCAGCAATGCCAGCCTTCTGCCTCACGGAGGCCAGTGGGAGCGAT  564
             :::||||||||::    |||        ||||||||||||||||||||||
Db   206  ValAlaSerGlyGlnAsnAlaLeuAlaLeuAlaPheCysLeuThrGluProSerSerGlySerAsp  225

Qy   565  GCAGCCTCAATCCCGAGCAGCAGCCACCACTAAGTGAAGACAAGAAGCACTACCATCCTCAAT  624
             |||||||::    |||        ||||||||||||::||||||
Db   226  ValAlaSerIleArgSerSerAlaIleProSerProCysGlyLysTyrLysThrLeuAsn  245

Qy   625  GGCTCCAAGGTCTGGATTACTAATGGAGGACTGGCCAATATTTTTACTGTGTTTGCAAAG  684
             |||||||||::::||||        ||||||||        :::    |||||
Db   246  GlySerLysTrpIleArgSerAsnGlyGlyValGlyLeuValLeuProGlyLeuPheThrValPheAlaLys  265

Qy   685  ACTGAGGTCGTTGAT---TCTGATGCAGTGAAAGACAAAATCACCAGCATTCATAGTA  741
             |||    :::    |||        ||||||||::|||::||||||
Db   266  ThrProIleLeuLysAspAlaAlaThrGlyAlaValLysAlaIleLysGluLysGlyAspValValThrPheValVal  285

Qy   742  GAAAAGAGACTTTGGTGAGTGAGGAAATGGACTAATGGAAACCCGAAGATAAATTAGGCATTCGGGGGC  801
             |||||||||:::||||        |||||||        :::    |||||
Db   286  GluLysArgSerPheGlyValThrHisIleArgGlyGlyAspLysGlyValLysValProSerGluAlaIleLeuLysAla  305

Qy   802  TCCAACACTTGTGAGTCCATTTGAAAACACCAAGATACCTGTGAAAAACATCCTTGGA  861
             ||||||||        :::||||||        ||||||::||||||
Db   306  SerAsnThrSerGluValTyrPheAspGlyValLysValProSerGluAsnValLeuGly  325

Qy   862  GAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGACGGCCGGTTCAGCATG  921
             ||||||||||||        |||||||::||||||
Db                                                                  325
```

```
Db   326  GluValGlyAspGlyPheLysValAlaAlaValAlaAsnIleLeuAsnAsnGlyArgPheGlyMet  345
                     :::||||||      ||||||      :::
Qy   922  GGCAGCGTCGTGCGTGGCTGGGCTGCTCAAGAGATTGATTGAAATGACTGTGAGTACGGCCTGC  981
             ||||::||||||      :::
Db   346  AlaAlaThrLeuAlaGlyThrMetLysPheSerLeuIleAlaLeuAlaValAspHisAlaThr  365
             ||||||||||      ||||||||||
Qy   982  ACAAGAAACAGTTTAACAAGAGGCTTCAGTGAATTGATTCAGGAGAAATTTGCA  1041
             :::||||||||      ||||||
Db   366  AsnArgThrGlnPheGlyAspLysHisAsnPheGlyValIleGluGlnLysLeuAla  385
             |||||||||||||      ||||::    :::
Qy  1042  CTGATGGCTCAGAAGGCTTACGTCATGGAGAGTAGTGACCTACCTCACCTACCTG  1101
             :::||||||      ||||||
Db   386  ArgMetAlaIleLeuGlnInTyrValThrArgSerMetAlaTyrMetLeuSerAlaAsnMet  405
             ||||||||||||||      ::
Qy  1102  GACCAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCAGCCATGTGAAGGTGTTCAGCTCC  1161
             ||||||||||      |||||||::
Db   406  AspGln---GlyPheLysAspPheGlnIleGluGluAlaAlaIleSerLysLysPheCysSer  424
             |||||||||||||      ||||::
Qy  1162  GAGGCCGCCTGCAGTGTGAGTGAGGCGTGCAGAATCCTCGGGGCTGGGCTGCTACACA  1221
             ||||||||::||||||      ||||||
Db   425  GluAlaAlaTrpLysValAlaAspGluCysIleGlnIleMetGlyGlyMetGlyPheMet  444
             ||||::    ::    :::
Qy  1222  AGGGACTATCCGTACGAGCGCCATACTGCGTGACACCGCCATCCTCCTCATCTTCGAGGGA  1281
             |||||||||||      :::
Db   445  LysGluLeuProGlyValGluArgValLeuArgAspIleArgIlePheGluGluArgIlePheGluGly  464
             ::||||||||      :::
Qy  1282  ACCAATGAGATTCTCCGGATGTACATCGCCCCTGACGGGTCTCGCAGCATGCCGGCCGCATC  1341
             ||||||      ||||||
Db   465  AlaAsnAspIleLeuArgLeuPheValAlaLeuAspGlyCysMetAspLysLysGlyLysGlyLysGlu  484
             |||||||||||      :::
Qy  1342  CTGACTACCAGGATCCATGAGCTTAAACAG------GCCAAAGTGAGCACCAGTCATGAT  1395
             :::||||||      :::
Db   485  LeuThrLysArgLeuAsnAlaLeuLysAsnProHisGlyLeuAsnValGlyLeuLeuMetGly  504
             ||||::    |||
Qy  1396  ACCGGTTGCGCCGGAGGCTTCGGGACTGTGGACCTGGGCTCCAAGACCATCATGGAGCAGGC  1455
             :::||||||      :::
Db   505  GluAlaGlyLysGlnLeuLeuArgArgThrGlyIleGlySerGlyLeuSerLeu---  523
             ||||||      :::
Qy  1456  AACCATGGAGTTGTCACCCCAGTCTTGCGGACAGTGCCAACAAGTTGAGGAGAACACC  1515
             :::    :::
Db   524  ------GlyIleValHisProGluLeuSerArgSerGlyLeuGluLeuAlaValGlnAlaLeu  541
             |||||||||||      :::
Qy  1516  TACTGCTTCGGCCGGAGGCTTGGAGACACTGCTGCTCCGCTTTGGCAAGACCATCATGAG  1575
             ||||||      |||
Db   542  AspGlnPheAlaThrValAlaGluAlaLysLysLeuValLysLeuAlaHisLysLysGlyIleIleValAsn  561
             ||||||      |||
Qy  1576  GAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATGGACGGCGCC  1635
             :::||||||      |||
Db   562  GluGlnPheLeuLeuGlnArgLeuValAlaAspGlyAlaIleAlaAspProLeuTyrAlaAlaMetValVal  581
             |||||||||||      :::
Qy  1636  GTGCTGTCGCGGGCGAGCCAGCCGCTCCATCCGAGCAGCGAAGAAGCACCAGCAGGTT  1695
             ||||||      |||
Db   582  ValLeuSerArgAlaSerArgSerLeuSerGlyProThrAlaGlnHisGluLysLys  601
             :::    -------TACTTGCAGAATCCTCTTCAGC  1746
Qy  1696  CTCTTGCCCAACACCTTCTCGCGTGGGAAGCT-------
             ::||||||      :::
Db   602  MetLeuCysAspSerTrpCysSerIleGluAlaIleAlaThrArgIleArgGluAsnMetAlaSer  621
             ||||||      ::
Qy  1747  CTTCTCCAGCTGGACAGTATGCTCCAGAAAATCTAGATGAGCAGATTAAGAAAGTGTCC  1806
             ||||||      ::
Db   622  LeuGlnLeuSerProGlnHis------GlnGluLeuPheArgAsnPheArgSerIleSer  639
             ||||||      ||||::
Qy  1807  CAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCCACCCCTG  1851
             :::||||||      :::
Db   640  LysAlaMetValGluAsnGlyLyGlyLeuValThrGlyValAsnProLeu  654
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RESULT 8
ACDV_RAT
ID   ACDV_RAT       STANDARD;      PRT;    655 AA.
AC   P45953;
DT   01-NOV-1995  (Rel. 32, Created)
DT   01-NOV-1995  (Rel. 32, Last sequence update)
DT   05-JUL-2004  (Rel. 44, Last annotation update)
```

```
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD).
GN   Name=Acadvl; Synonyms=Vlcad;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=94308174; PubMed=8034667;
RA   Aoyama T., Ueno I., Kamijo T., Hashimoto T.;
RT   "Rat very-long-chain acyl-CoA dehydrogenase, a novel mitochondrial
RT   acyl-CoA dehydrogenase gene product, is a rate-limiting enzyme in
RT   long-chain fatty acid beta-oxidation system: cDNA and deduced amino
RT   acid sequence and distinct specificities of the cDNA-expressed
RT   protein.";
RL   J. Biol. Chem. 269:19088-19094(1994).
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC       ---------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC       or send an email to license@isb-sib.ch).
CC       ---------------------------------------------------------
DR   EMBL; D30647; BAA06331.1; -.
DR   PIR; A54872; A54872.
DR   HSSP; Q06319; 1BUC.
DR   RGD; 2014; Acadvl.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh_1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   Mitochondrion; Oxidoreductase; FAD; Fatty acid metabolism; Flavoprotein;
KW   Mitochondrion; Transit peptide.
FT   TRANSIT       1     40       Mitochondrion.
FT   CHAIN        41    655       Acyl-CoA dehydrogenase, very-long-chain
FT                                specific.
FT   DOMAIN       41    482       Catalytic.
SQ   SEQUENCE   655 AA;  70749 MW;  E808EDEB0E4595D7 CRC64;
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Alignment Scores:

Pred. No.:	5.87e-83	Length:	655
Score:	1356.50	Matches:	295
Percent Similarity:	63.36%	Conservative:	108
Best Local Similarity:	46.38%	Mismatches:	192
Query Match:	39.63%	Indels:	41
DB:	1	Gaps:	12

US-09-945-326-3 (1-1863) x ACDV_RAT (1-655)

```
Qy    25  CGCACCACGGCTGCGGCTCGTGCTCGCGGGGTCTCGTGGTCTCTACCGGCGAACCGGCGG   84
              |||   ||||::|||   |||
Db    32  ArgProThrSerAlaGlnArg------------------LeuTyrAlaSerGluAlaThrGlnAla   47

Qy    85  CTACTGGCGC------------------------------------ACCAGCCCGCCTGTACGA  111
          ::|||
Db    48  ValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAlaArg   67

Qy   112  GCT------------TTCGCCAAAGAGCTTTCCAGGCAAAATCAAGAAGAAGAAGAGTT  159
          |||                    :::|||         ::|||
Db    68  AlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnInVal   87

Qy   160  TTCCATTCCAGAAGTAGCCAAGATGAACTTAATGAA------------ATCAAT  204
          ||||||::|||  ||              |||||||
Db    88  PheProTyrProSerVal------------LeuAsnGluGlyGlnThrGlnPheLeuLys  103

Qy   205  CAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAAATTGAC  264
          :::            ::|||
Db   104  GluLeuValGlyProValAlaArgPheGluGluValAlaAsnAspProAlaLysAsnAsp  123

Qy   265  CAGGAAGGGAAAATCCCAGATGAAACTTGGAGAAATTGAGAGCCTAGGGCTTTTGGG  324
              ||||         |||||::|||      |||
Db   124  SerLeuGluLysValGluGluLysGlnLeuGlnLeuGlyLeuGlyLeuGlyAlaPheGly  143

Qy   325  CTGCAAGTCCCAGAAGAATATGGTGGCCTGGCTTCTCCAACACCATGTACTCAAGACTA  384
          :::                   :::|||
Db   144  LeuGlnIleValProSerGluLeuGlyLeuGlyLeuLeuSerAsnThrGlnTyrAlaArgLeu  163

Qy   385  GGGGAGATCATCAGCATG--GATGGTCATCACTGTGACCCTGCAGCCGCACCAGGCT  441
          ||||||||||||            |||||::|||||||
Db   164  AlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSer  183

Qy   442  ATTGGCCTCAAGGGGATCATCTGGCTGGCACTGGAGGAGAAAGCCAAATACTTGCCT  501
          ||||||||||:::||||||
Db   184  IleGlyPheLysGlyIleIleLeuLeuTyrGlyThrLysGluLysGluLysTyrLeuPro  203

Qy   502  AAACTGGCTCCGGGGAGCACATTGCAGCCTTCGCCTCACGGGAGCCAGTGGGAGC  561
          :::|||||||||||:::||||::|||
Db   204  ArgValAlaSerGlyAsnGlnAlaLeuAlaAlaPheCysLeuThrGluProSerSerGlySer  223

Qy   562  GATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGAAGCAGAAGCACTACATCCTC  621
          ||||||||||
Db   224  AspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyrTyrThrLeu  243

Qy   622  AATGGCTCCAAGGTCTGGATTACTAATGAGGACGACTGGCCAATATTTTACGTGTTTTGCA  681
          ||||||||||:::||||||
Db   244  AsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPheAla  263

Qy   682  AAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAAATCACAGCATTCATA  738
          ||||||                  :::|||||||||
Db   264  LysThrProIleLysAspAlaAlaThrGlyAlaValLysGlyLysValIleThrAlaPheVal  283

Qy   739  GTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGGAGATAAATAGGCATTCGG  798
          ||||||||||
Db   284  ValGluArgGlyPheGlyGlyValThrHisGlyLeuProGluLysGlyMetGlyIleLeuLys  303

Qy   799  GGCTCCAACCTGTGAAGCCCCATTTGAAAACACCAAGAAGTGGAAAACATCCTT  858
          |||||||||||:::|||
Db   304  AlaSerAsnThrSerGluValTyrProAlaGlyValLysValProAlaGluValAsnValLeu  323

Qy   859  GGAGAGGTCGGAGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGGCCGGTTCAGC  918
          ||||||||||:::|||
Db   324  GlyGluValGlyAspGlyPheLysValAlaValAlaAsnIleLeuAsnAsnGlyArgPheGly  343

Qy   919  ATGGGAGCGTCGTGGCTGGCTGCTCAAGGATTGATTGAAATGACTGGTGAGTACGCC  978
          ||||||:::|||
Db   344  MetAlaAlaThrLeuAlaGlyThrMetLysMetLysAlaIleAlaValAlaValAspHisAla  363

Qy   979  TGCACAAGGAAACAGTTTAACAAGAGGCTTCCAGTGAATTGGATTCAGGAGAAATTT  1038
          ||||||:::||||||
Db   364  ThrAsnArgThrGlnPheGlyAspLysProIleHisAsnPheGlyValIleGluGlnLysLeu  383

Qy  1039  GCACTGATGGCTGCTCAGAAGGCTTACGTGTCATGGAGAGTGATGACTTACCTCCACAGCAGGGATG  1098
```

RA Zhang X., Liu W., Zhu H., Sun X.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC   fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC   ETF.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC   step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC   of different substrate specificities are present in mammalian
CC   tissues.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC --
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CC --
DR EMBL; U30817; AAA74051.1; -.
DR HSSP; Q06319; 1BUC.
DR InterPro; IPR006089; Acyl-CoA_dh.
DR InterPro; IPR006090; Acyl-CoA_dh_C.
DR InterPro; IPR006091; Acyl-CoA_dh_M.
DR InterPro; IPR006092; Acyl-CoA_dh_N.
DR InterPro; IPR009100; AcylCoA_dehyd_NM.
DR InterPro; IPR009075; AcylCoADH_C_like.
DR Pfam; PF00441; Acyl-CoA_dh; 1.
DR Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW Oxidoreductase; Transit peptide.
FT TRANSIT   1   40   Mitochondrion (By similarity).
FT CHAIN   41   655   Acyl-CoA dehydrogenase, very-long-chain
FT   specific.
FT DOMAIN   41   482   Catalytic.
SQ SEQUENCE   655 AA; 70520 MW; F9DC06285023CFC0 CRC64;

Alignment Scores:
Pred. No.:
Score: 3.52e-82   Length: 655
Percent Similarity: 1345.00   Matches: 285
Best Local Similarity: 65.51%   Conservative: 110
Query Match: 47.26%   Mismatches: 194
DB: 39.29%   Indels: 14
                                            Gaps: 9

US-09-945-326-3 (1-1863) x ACDV_BOVIN (1-655)

Qy   67 TCTACCGCGAACCGGCCGGCTACCTGCCGACCAGCCCGTACGAGCTTTCCGCCCAAAGAG 126
                 ||||| || || || || || :: || |||||| :::||::||||
Db   57 SerGluAlaSerThrArgGluLysArgAlaAlaAsnValSerLysSerPheAlaValGly   76

Qy   127 CTTTTCCTAGGCAAAATCAACAAGAAGAAAGAAGTTTCCATTTCCGAAGAGTT--AGCCA 183
                 ||||| :::::::   ::||||||||| ::: ||||| :: |||
Db   77 ThrPheLysGlyGlnLeuThrThrAspGlnValPheProValLeuAsnGlu--- 96

Qy   184 GATGAACTTAATGAAATCAATCAATCAGTTCTTGGACACCGGTGGAAAAATTCTTCACTGAGAG 243
                 || ||| ::: ::: :::||||||: ::||||||||| :::||||||
Db   97 AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPheGluGluVal 116

Qy   244 GTGGACTCCCGAAAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTTGGAGAAATTG 303
                 || :::: ||::: ::::   ::   :::: ::   ::: || :::||||||
Db   117 AsnAspAlaAlaLysAsnAspMetLeuGlnArgValGluThrThrMetGlnPheLeu 136

Qy   304 AAGAGCCTAGGGCTTTTTGGGCTGCAAGTCCCAGAAGAATATGTGGCCTGGCTTCTCC 363
                 || ||||| ||||||||||||||||| ||| |||| :::|||

```
Db  137 LysGluLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyLeuGlyValGlyLeuCys 156

Qy  364 AACACCATGTACTCAAGACTAGGGGAGATCATCAGCCATG---GATGGGTCCATCACTGTG 420
            ||||||||::||::|||||||||   ::           ::
Db  157 AsnThrGlnTyrAlaArgLeuValGluIleValGlyMetTyrAspLeuGlyIleGlyIle 176

Qy  421 ACCTGGCAGCGCACCAGGCTATTGGCCTCAAGGGGATCATCTTGGCTGCTGGCACTGAGGAG 480
            ||||||||:::|||||:||  ||||||||||:::|||| |||||||||:::
Db  177 ValLeuGlyAlaHisGlnSerIleIleLeuSerGlyIleLeuLeuPheGlyThrLysAla 196

Qy  481 CAGAAAGCCAAATACTTGCCTAAACTGGCCTCCGGGAGCACATTGCAGCCTTCTGCCTC 540
            ||||||      |||   ||||||  ||||
Db  197 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluThrIleAlaAlaPheCysLeu 216

Qy  541 ACGGAGCCAGTGGGAGCGATCGCAGCCTCCAATCCGGACAGCAGCCACACTAAGTGAA 600
            |||||||:::||||||||:::|||||||||||||||:||||||||
Db  217 ThrGluProSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro 236

Qy  601 GACAAGAAGCACTACATCCTCAAGGTCTGGATTACTAATGAGGAGGACTGGCC 660
            ||::|||   ||||||||:::|||||||||||||||||::|||||||||||||
Db  237 CysGlyLysTyrTyrThrLeuAsnGlySerLysIleTrpIleSerArgAsnGlyLeuAla 256

Qy  661 AATATTTTTACTGTGTTTGCAAAGACTGAGGTCGTTGAT---TCTGATCAGTGAAA 717
            |||||||   ||||||||:::   |||||  ::  ::||   |||::|||
Db  257 AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys 276

Qy  718 GACAAAATCACAGCATTCATAGTAGAAAAGACTTTGGTGGAGTCACTAATGGGAAACCC 777
            :::|||||||||||||::|||:::|||||||:::||||||||||||:::|||||||||
Db  277 GluLysIleThrAlaPheValAlaValGluArgSerPheGlyGlyValThrHisGlyProPro 296

Qy  778 GAAGATAAATTAGGCATTCGGGGCTCCAACACTTGTGAAGTCATTTGAAAAACACCAAG 837
            |||   ||||:::||||:::|||||||||||||||||||:::||||||:::|||
Db  297 GluLysLysMetGlyIleLeuLysSerAlaSerAsnThrAlaGluValIleTyrPheAspValArg 316

Qy  838 ATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATC 897
            |||||||||||||||||:::||||||||:::|||||||||   ||||:::||||||:||
Db  317 ValProAlaGluAsnValLeuGlyGluValGlyLysGlyIleGlyPheLysGlyValAlaMetHisIle 336

Qy  898 CTCAACAGCGGCCGGTTCAGCGTGGCAGCGTGCCGTGGCGTGCTGCTCAGAGAGATTGATT 957
            |||||||:||||||||||||||||||:::|||:::||||||:::|||||||||||||||
Db  337 LeuAsnAsnGlyAlaArgPheGlyMetAlaAlaAlaAlaLeuAlaGlyThrMetLysGlyIleTyrIleIle 356

Qy  958 GAAATGACTGCTGAGTACGCCCTGCACAAGGAAAACAGTTTAACAAGAGGCTCAGTGAATTT 1017
            ::::::||||||||||:::||| |||||||||||||||||||||   :::||:::||
Db  357 AlaLysAlaValAspHisAlaLeuAsnArgThrGlnPheGlyGluLysIleHisAsnPhe 376

Qy 1018 GGATTGATTCAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATG 1077
            |||   |||||||||||||:::|||:::|||||||||||||||||||:||||||||||
Db  377 GlyLeuIleGlnGluLysLeuGluGlyValAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet 396

Qy 1078 ACCTACCTCACAGCAGGGATGCTCGACCAACCTGGCTTCCCGACTGCTCCATGCGAGGCA 1137
            :::||::::: ::    ||:::||||||||||||||||:::|||||:::|||||||||||
Db  397 AlaTyrMetValSerArgAlaAsnMetAspGln---GlySerThrAspPheGlnIleLeuGluAla 415

Qy 1138 GCCATGGTGAAGGTGTTCAGCTCGCAGGCCCTGCCGAGCCAGTGTGTGAGTGAGGGCTGCAG 1197
            ||||||||||||||   :::||||||||||||||:::|||:||||||:::|||||||
Db  416 AlaIleSerLysIleSerGlyLeuAlaAlaLaTrpLysValThrAspGluCysIleGln 435

Qy 1198 ATCCTCGGGGGCTTGGCTACCACAAGGGACTATCCGTACCGACCGCATACTGCGTGACACC 1257
            :::||||   |||:::|||||||||||||:::||||||||:::||||||||||||||
Db  436 IleMetGlyGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeuArgIleLeu 455

Qy 1258 CGCATCCTCCTCATCTTCGAGGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACG 1317
            |||||||||||||||:::|||||||||||||:||||||||||||:::||||||:::|||
Db  456 ArgIlePheGluGlyThrAsnAspIleLeuArgLeuArgValAlaLeuAlaLeuGln 475

Qy 1318 GGTCTGCAGATGCCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAG------ 1371
            |||||||||:::|||||||||||||||:::||||||||:::||||||:::|||
Db  476 GlyCysMetLysLysGlyLysLeuSerGlyLeuLeuSerGlyLeuAlaAsnLysLysAsnProPhe 495

Qy 1372 GCCAAACTGAGCACACCATGGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGCCCGA 1431
            ::::||        |||::|||||||:::||||||||||||:::|||||||:::|||
Db  496 GlyAsnAlaGlyLeuLeuLeuGlyGlyLeuGluAlaGlyLysLysGlyLeuGlnLeuLeuArgArgArgGlyLeu 515
```

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Qy 1432 ACTGTGACCTGGGCTGACAGGCAACCATGGAGTTGTGCACCCCAGTCTTGCGGGACAGT 1491
            ||||:|   |||   |||||:||||:::||||||||||:::|:||||||   ||||||||
Db  516 GlySerGlyLeuSerLeuSer--------GlyIleValHisGlnGluLeuSerArgSer 532

Qy 1492 GCCACAAGTTGAGGAGAGACACCTACTGCTTCGCCGGACGTGAGACACTGCTGCTC 1551
            |||   :::          ::   |||
Db  533 GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValGluAlaLysLeuIle 552

Qy 1552 CGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGAGGACGTGGCCCAACATCCTC 1611
            :::      |||   ||||||||:::  |||   :||||||:::|||:::|||||||||
Db  553 LysHisLysLysAspIleIleAsnGluGlnLeuLysLeuGlnLnArgLeuAlaAspSerAla 572

Qy 1612 ATCAACCTGTATGGCGATGACCGGCCTGTCGCCGCGGCCAGCCGCCTCCATCCGCCATTGGG 1671
            |||||||:||||:||||:::||   ||:::|||:::|||||||:::||||||||||||
Db  573 IleAspLeuTyrAlaMetValAlaMetValValLeuSerArgAlaSerArgLeuSerGluGluSerGluGly 592

Qy 1672 CTCCCGACCAACCACGACCAGAGGTTCTTCTTGCCCAACACCCTCTGCTGGAAGCT----- 1725
            |||||||:::|||:::|||||||||||||||||:::||||||||||||||:::
Db  593 HisProThrAlaGlnHisGluLysMetLeuCysAspSerrpCysIleGluAlaAlaAlaAla 612

Qy 1726 ---TACTTGCAGAATCTCTTCAGCCTGTCCTCAGCTGGACAAGTATGCTCCAGAAAACCTA 1782
                   :::||||:::   ::|||||   ||||||:::||||||||||||||:::
Db  613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlnGlu---Leu 630

Qy 1783 GATGGACAGATTAAGAAAGTGTCCCAGAGCATCCTTGAGAAGCGGAGCCTATATCGTGCC 1842
            |||||||||||||:||:::||||||:::|||:::|||||||:::||||||||||||||
Db  631 PheArgAsnPheLysSerIleSerLysAlaLeuLeuValGluLeuGlyValGlyValThrSer 650

Qy 1843 CACCCTCTG 1851
            ::::||||
Db  651 AsnProLeu 653
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RESULT 10

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ACDV_MACFA
ID   ACDV_MACFA              STANDARD;      PRT;    655 AA.
AC   Q8HXY7;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD) (QccE-11706).
GN   Name=ACADVL; Synonyms=VLCAD;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain cortex;
RA   Kusuda J., Osada N., Hida M., Sugano S., Hashimoto K.;
RT   "Isolation and characterization of cDNA for macaque neurological
RT   disease genes.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC       of different substrate specificities are present in mammalian
CC       tissues.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; AB083302; BAC20581.1; -.
DR   HSSP; Q06319; 1BUC.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW   Oxidoreductase; Transit peptide.
FT   TRANSIT       1     40       Mitochondrion (By similarity).
FT   CHAIN        41    655       Acyl-CoA dehydrogenase, very-long-chain
FT                                specific.
FT   DOMAIN       41    482       Catalytic.
SQ   SEQUENCE   655 AA;  70443 MW;  DCC7AA898EFCB333 CRC64;
```

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Alignment Scores:
Pred. No.:          2.35e-80           Length:      655
Score:              1318.00            Matches:     280
Percent Similarity: 64.72%             Conservative:107
Best Local Similarity: 46.82%          Mismatches:  197
Query Match:        38.50%             Indels:      14
DB:                 1                  Gaps:        8
```

```
US-09-945-326-3 (1-1863) x ACDV_MACFA (1-655)

Qy      88 CTGCGCCACCAGCCCGCCCTGTACGAGCT----------TTCGCCAAAGAGCTTTCCTA 135
              |||    ||:  |||   ||||||:||            :::|||
Db      60 LeuAsnLysAlaLysProAlaLysGluSerLysSerPheAlaAlaAlaMetPheLys 79

Qy     136 GGCAAAATCAAGAAGAAGAAGAAGTTTCCATTCCAGAAGTT---AGCCAAGATGAACTT 192
              ||||    :::||||||          ||||||:|||:           ||||||||
Db      80 GlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGlnGluGlnThr 99

Qy     193 AATGAAATCAATCAGTTCTTGGGACCCGGTGAAAAATTCTTCACTGAAGAGGTGGACTCC 252
              :::            |||     ||||||   ::|||        |||||
Db     100 GluPheLeuLysGluLeuValGluProValSerArgArgPhePheGluGluGluAspPro 119

Qy     253 CGAAAAATTCACCAGGAGGAGGGAAAATCCAGATGAAACTTTGGAGAAATTGAAGAGCCTA 312
              |||      |||   |||||                ::: |||||:|      ||:||||
Db     120 AlaLysAsnAspThrLeuGluMetValGluThrGlnLysLeuGlnGluLysLysGluLeu 139

Qy     313 GGGCTTTTGGGCTGCAAGTCCCAGAAGAAATATGGTGGCTTCTCCAACACCATG 372
              |||||||||||          :::||||| ::|||||||||:||||:||
Db     140 GlyAlaPheGlyLeuProLysSerGlnGluLysTyrGlyGlyValGlyLeuCysAsnThrGln 159

Qy     373 TACTCAAGACTAGGGGAGGATCATCAGCATG--GATGGGTCCATCACTGTGACCCTGGCA 429
              ||:||||||              |||  |||     :::   ||||:||||: :::|||||
Db     160 TyrAlaArgLeuValGluIleValGlyMetHisAspLeuAlaValGlyIleThrLeuGly 179

Qy     430 GCGCACCAGGCTATTGGCCTCAAGGGGGATCATCTTGGCTGCACTGAGGAGCAGAAAGCC 489
              |||||||||||||||:::||||| |||||||:||||:||:
Db     180 AlaHisGlnSerIleGlyPheLysGlyIleLeuLeuPheGlyTyrLysAlaGlnLysGlu 199

Qy     490 AAATACTTGCCTAAACTGGCTCCGGGAGCACATTGCAGCCTTCTGCCTCACCGGAGCCA 549
              |||||||||:::|||||||||||||||||||          |||:||
Db     200 LysTyrLeuProLysGluLeuAlaSerGlyGluThrLeuValAlaLeuAlaPheGluThrGluPro 219

Qy     550 GCCAGTGGGAGCGGATGCAGCCACAATCAATCCGAGCCAGCAGCAGAGAGCCAGAAGAAG 609
              :::||||||||||||||||:||||||||||:||: |||       |||   |||
Db     220 SerSerGlySerAspAlaAlaSerIleArgThrSerAlaValProSerProCysGlyLys 239

Qy     610 CACTACTACATCCTCAATGGCTCCAAGGTCTGATTACTAATGAAGACTGGCCAATATTTT 669
              :::||||||:|||:||||
Db         ...
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Db     240 TyrTyrThrLeuAsnGlySerLysSerLeuTrpIleSerAsnGlyGlyLeuAlaAspIlePhe 259
Qy     670 ACTGTGTTTGCAAAGACTGAGGTCGTTGAT---TCTGATGATCAGTGAAAAGAACAAAATC 726
              ::: ||| ||||||                |||  ||||||||||:||
Db     260 ThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValAlaValLysGluLysIle 279

Qy     727 ACAGCATTCATAGTAGAAAAGAGACTTGGTGGAGTCACTAATGGAAACCCGAAGATAAA 786
              |||||||||||                |||  ||||||||:||||||:||||||
Db     280 ThrAlaPheValGluArgGlyPheGlyGlyValThrHisGlyProProGluLysLys 299

Qy     787 TTAGGCATTCGGGGTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTG 846
              :::||||||        |||||||:   ||||       :::|||:||||:||
Db     300 MetGlyIleLysAlaSerAsnThrAlaGluValValLeuPheAspGlyValArgValProSer 319

Qy     847 GAAAACATCCTTGGAGAGGTGGGATGGGGTTAAGTGGCCATGAACATCCTCAACAGC 906
              ||||||||||:||||||      :::|||   ||||||||||||||:||||||:
Db     320 GluAsnValLeuGlyGlySerGlyPheLysGlyValAlaMetHisIleLeuAsnAsn 339

Qy     907 GGCCGGTTCAGCATGGGCAGCGTCGTGCTGGGCTGCTCAAGAGATTGATTGAAATGACT 966
              |||||||       ||||||||||||||     |||      |||:||:
Db     340 GlyArgPheGlyMetAlaAlaAlaLeuAlaLeuGlyThrMetArgGlyIleIleThrLysAla 359

Qy     967 GCTGAGTACGCCTGCACAAGAACAGTTTAACAGAGGCTCAGTGAATTGGATTGATT 1026
              :::||||||                |||||||||||||||:::||:||||||||
Db     360 ValAspTyrAlaThrAsnArgIleGlnPheGlyGluLysIleHisAsnPheGlyLeuIle 379

Qy    1027 CAGGAGAAATTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACCTC 1086
              ||||||         |||  :::||||||||  |||||||||||||||
Db     380 GlnGluLysLeuAlaArgMetValMetLeuGlnTyrValThrGluSerMetAlaTyrMet 399

Qy    1087 ACAGCAGGAGGATGCTGACCAACCTGCTTTCCGACTGCTCCATCGAGCCAGCCATGGTG 1146
              :::            ||||||||||:||||
Db     400 ValSerAlaAsnMetAspGln--GlySerThrAspPheGlnIleGluAlaAlaIleSer 418

Qy    1147 AAGGTGTTCAGCTCCGAGGCCGCCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCCTCGGG 1206
              ||||||:||   |||||||||||||||||:::          :::||||:
Db     419 LysIlePheGlySerGluAlaAlaTrpLysValThrAspLysValCysIleGlnIleMetGly 438

Qy    1207 GGCTTGGCTACAAGGGACTATCCGTACGAGGCCATACTGCGTGACACCCGCATCCTC 1266
              ||||:::|||  :::||||||||||:|| |||||||::||  ||||:||
Db     439 GlyMetGlyPheMetLysGluProLysValLeuArgAspLeuValLeuArgArgIlePhe 458

Qy    1267 CTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGGAACATCGCCCCTGACCGGGTCTGCAG 1326
              |||     :::||||||      |||||:|||||||        |||||||
Db     459 ArgIlePheGluGlyThrAsnGluIleLeuArgLeuHisValAlaLeuGlnGlyIleCysMet 478

Qy    1327 CATGCCGGCCGCCATCCTGACTACCAGGATCCATGAGCTTAAACAG-----GCCAAAGTG 1380
              |||||||||||||||:::|||          |||||       ||||||
Db     479 AspLysGlyGlyLeuGlySerGlyLeuGlySerAlaLeuLysAsnProPheGlyAsnAla 498

Qy    1381 AGCACAGTCATGAGCGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGGCCGAACTGTCGAC 1440
              |||:||||||   |||||||||||||||||||:::|||
Db     499 GlyLeuLeuGluGlyAlaGlyAlaGlyGlnAlaGlyArgArgAlaGlyLeuGlySerGly 518

Qy    1441 CTGGGGCTGACAGGCAACATGGAGTTGTGCACCCCAGTCTTGCCGACAGTGCCAACAAG 1500
              ||||||:::||||||||| |||||     |||:::||||||||||||||
Db     519 LeuSerLeuSer-------GlyIleValHisProGluLeuSerArgSerGlyLeuGlu 535

Qy    1501 TTTGAGGAACACCTACTGCTTCGGCCGACCGTGGAGCACACTGCTGCTCCGCTTTGGC 1560
              ||||||||||||||||||||:::|||||||||||:||||||||||||||||:
Db     536 AlaValGlnAlaLeuGluGlnPheAlaThrValGluAlaLysLeuLeuLysHisLys 555

Qy    1561 AAGACCATCATGAGAGACGCAGCCGGGTGGCCAACATCCTCATCAACCTG 1620
              |||||||||||||||:::||||||||||||||||:::
Db     556 LysGlyIleValAsnGluGlnProLeuLeuLeuGlnArgLeuAlaAlaAspGlyAlaIleAspLeu 575

Qy    1621 TATGGCATGAGCGGATGCAGCCGTGCTGTCGCCGGGCCAGCCGTCCATCCGGCTCCGCAAC 1680
              :::|||||||||||||||||||||||||     |||||||||||:||:
Db     576 TyrAlaMetValValValLeuSerArgAlaSerArgSerLeuSerGluGlyHisHisThr 595

Qy    1681 CACGACCACCAGAGTTCTTCGTGCCAACACTTCTGCGTGGAAGCTTACTTGCAGAATCTC 1740
              ||||||||||||||||||||:::||:||||||:::||||||||:::|:||||:
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Db      60 LeuAsnLysAlaLysProAlaLysGluSerLysSerPheAlaAlaAlaMetPheLys 79
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```
Db    596 AlaGlnHisGluLysMetLeuCysAspThrTrpCysIleGluAlaAlaAlaAlaArgIleArg 615
Qy   1741 TTCAGCCTCTCAGCTGGACAAGTATGCTCCAGAAAAC---CTAGATGAGCAGATTAAG 1797
               :::::: |||                    :::::: |||
Db    616 GluGlyMetAlaAlaLeuGlnSerAspProArgGlnHisGluLeuTyrArgAsnPheLys 635

Qy   1798 AAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCCACCTCTG 1851
               :::||||::: :::::||||:::        ::: ::||||||
Db    636 SerIleSerLysAlaLeuValGluArgGlyGlyValValThrAsnAsnProLeu 653
```

RESULT 11
ACDV_HUMAN

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ID   ACDV_HUMAN     STANDARD;      PRT;    655 AA.
AC   P49748; O76056; Q8WUL0;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE   precursor (EC 1.3.99.-) (VLCAD).
GN   Name=ACADVL; Synonyms=VLCAD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=9397809; PubMed=7668252;
RA   Aoyama T., Souri M., Ueno I., Kamijo T., Yamaguchi S., Rhead W.J.,
RA   Tanaka K., Hashimoto T.;
RT   "Cloning of human very-long-chain acyl-coenzyme A dehydrogenase and
RT   molecular characterization of its deficiency in two patients.";
RL   Am. J. Hum. Genet. 57:273-283(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND VARIANTS.
RC   TISSUE=Placenta;
RX   MEDLINE=96254975; PubMed=8845838; DOI=10.1093/hmg/5.4.461;
RA   Andresen B.S., Bross P., Vianey-Saban C., Divry P., Zabot M.-T.,
RA   Roe C.R., Nada M.A., Byskov A., Kruse T.A., Neve S., Kristiansen K.,
RA   Knudsen I., Corydon M.J., Gregersen N.;
RT   "Cloning and characterization of human very-long-chain acyl-CoA
RT   dehydrogenase cDNA, chromosomal assignment of the gene and
RT   identification in four patients of nine different mutations within the
RT   VLCAD gene.";
RL   Hum. Mol. Genet. 5:461-472(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Peripheral blood;
RX   MEDLINE=96125338; PubMed=8554625;
RA   Orii K.O., Aoyama T., Souri M., Orii K.E., Kondo N., Orii T.,
RA   Hashimoto T.;
RT   "Genomic DNA organization of human mitochondrial very-long-chain acyl-
RT   CoA dehydrogenase and mutation analysis.";
RL   Biochem. Biophys. Res. Commun. 217:987-992(1995).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Liver, Lung, and Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=95286809; PubMed=7769092;
RA   Aoyama T., Souri M., Ushikubo S., Kamijo T., Yamaguchi S.,
RA   Kelley R.I., Rhead W.J., Uetake K., Tanaka K., Hashimoto T.;
RT   "Purification of human very-long-chain acyl-coenzyme A dehydrogenase
RT   and characterization of its deficiency in seven patients.";
RL   J. Clin. Invest. 95:2465-2473(1995).
RN   [6]
RP   REVIEW ON VARIANTS.
RX   MEDLINE=9138660; PubMed=9973285;
RA   Andresen B.S., Olpin S., Poorthuis B.J.H.M., Scholte H.R.,
RA   Vianey-Saban C., Wanders R., Ijlst L., Morris A., Pourfarzam M.,
RA   Bartlett K., Baumgartner E.R., de Klerk J.B.C., Schroeder L.D.,
RA   Corydon T.J., Lund H., Winter V., Bross P., Bolund L., Gregersen N.;
RT   "Clear correlation of genotype with disease phenotype in very-long-
RT   chain acyl-CoA dehydrogenase deficiency.";
RL   Am. J. Hum. Genet. 64:479-494(1999).
RN   [7]
RP   VARIANTS VLCAD DEFICIENCY GLU-130 DEL; LYS-299 DEL; GLN-382 AND
RP   TRP-613.
RX   MEDLINE=96108970; PubMed=8554073;
RA   Souri M., Aoyama T., Orii K., Yamaguchi S., Hashimoto T.;
RT   "Mutation analysis of very-long-chain acyl-coenzyme A dehydrogenase
RT   (VLCAD) deficiency: identification and characterization of mutant
RT   VLCAD cDNAs from four patients.";
RL   Am. J. Hum. Genet. 58:97-106(1996).
RN   [8]
RP   VARIANT VLCAD DEFICIENCY HIS-450.
RX   MEDLINE=98206416; PubMed=9546340;
RA   Smelt A.H., Poorthuis B.J.H.M., Onkenhout W., Scholte H.R.,
RA   Andresen B.S., van Duinen S.G., Gregersen N., Wintzen A.R.;
RT   "Very long chain acyl-coenzyme A dehydrogenase deficiency with adult
RT   onset.";
RL   Ann. Neurol. 43:540-544(1998).
RN   [9]
RP   VARIANTS VLCAD DEFICIENCY.
RX   MEDLINE=9177129; PubMed=10077518;
RA   Mathur A., Sims H.F., Gopalakrishnan D., Gibson B., Rinaldo P.,
RA   Vockley J., Hug G., Strauss A.W.;
RT   "Molecular heterogeneity in very-long-chain acyl-CoA dehydrogenase
RT   deficiency causing pediatric cardiomyopathy and sudden death.";
RL   Circulation 99:1337-1343(1999).
CC   -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC       fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC       ETF.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC       step.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P49748-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P49748-2; Sequence=VSP_007734;
CC         Note=No experimental confirmation available;
CC   -!- DISEASE: Defects in ACADVL are the cause of very long chain acyl-
CC       CoA dehydrogenase deficiency (VLCAD deficiency) [MIM:201475].
CC       VLCAD deficiency is an autosomal recessive disease which leads to
CC       impaired long-chain fatty acid beta-oxidation. It is clinically
CC       heterogenous, with three major phenotypes: a severe childhood
CC       form, with early onset, high mortality, and high incidence of
CC       cardiomyopathy; a milder childhood form, with later onset, usually
CC       with hypoketotic hypoglycemia as the main presenting feature, low
CC       mortality, and rare cardiomyopathy; and an adult form, with
CC       isolated skeletal muscle involvement, rhabdomyolysis, and
```

DB: 1   Gaps: 8

US-09-945-326-3 (1-1863) x ACDV_HUMAN (1-655)

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Qy   109  CGAGCTTCGCCAAAGAGCTTTCCTAGGCAAAATCAAGAAGAAGAAGTTTCCCATTT  168
          :::|||||  |||  ::::||| ||  | || | ||| || ||||| |||||||||
Db    71  LysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnValPheProTyr   90

Qy   169  CCAGAGTTAGCCAAGATGAACTTAATGAA---ATCAATCAGTTCTTGGGACCCGTGGAA  225
          |||  |||    ||| ::: :::  :: | ||| :::  ||| :: ::  |||||
Db    91  ProSerValLeuAlaAsnGluGlnThrGlnPheLeuLysGluLeuValGluProValSer  110

Qy   226  AAATTCTTCACTGACGAGGTGGACTCCCGAAAAATTGACCAGGAAGGAAAATCCCAGAT  285
          :::  |||| :|: ::|| ||||||  ||| || ||| ||  :: :: || :: |||
Db   111  ArgPheGluGluProAlaValAsnAspProAlaLysAsnAspAlaLeuGluMetValGluGlu  130

Qy   286  GAAACTTGGAGAAATTGAAGAGCCTAGGGCTTTTGGCGAAGTCCAAGTCCCAAGAGAATAT  345
          |||||| ||  |||||||||||  || |||  ||||  ||||| |||| ||||||||||
Db   131  ThrThrTrpGlnLysLeuLysGluLeuGlyLeuGlyAlaPheGlyLeuGlnLysProSerGluLeu  150

Qy   346  GGTGGCCTGGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATG--  402
          ||||||| |||||:::::||  || || || |||  ||| :: :: || || ||  ||
Db   151  GlyGlyValGlyLeuAlaSerProAsnThrGlnThrArgAlaArgLeuValGluValGlyMetHis  170

Qy   403  GATGGGTCCATCACTGTGACCCTGGCAGCGCACCAGGCTATTGGCTTCAAGGGGATCATC  462
          :: :: ::|||:::||::|::|| ::||||  || ::|| ||| :: :: || :: ||
Db   171  AspLeuGlyValGlyIleThrLeuGlyLeuAlaHisGlnSerIleGlyPheLysGlyIleIleLeu  190

Qy   463  TTGGCTGGCACTGAGGACGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGAGCAC  522
          ||||||| ::|| :: :: ::|||  || ::||  :: || || || :: :: ::|||||
Db   191  LeuPheGlyThrArgAlaGlnLysGlyLeuTyrLeuProLysLeuAlaSerGlyValGluThr  210

Qy   523  ATTGCAGCCTTCTGCCTCACGGAGCCAGCCAGTGGGAGCCGATGGCAATCGCGAGC  582
          :::||:::| ::|:::|::|| :: ::|||| :: :: || || || :: ::|||||
Db   211  ValAlaAlaPheCysLeuThrGluLeuThrGluProSerSerGlySerAspAlaAlaSerIleArgThr  230

Qy   583  AGAGCCACACTAAGTGAAGACAAGAGAGCACTACATCCTCAATGGCTCCAAGGTCTGGATT  642
          ||||:::|||  :: ::|||||||||||  ||:::|::| :: ||| :: || |||||| |
Db   231  SerAlaValProSerProCysGlyLysTyrLysTyrThrLeuAsnGlySerLysLeuTrpIle  250

Qy   643  ACTAATGGAGGACTGGCCAATATTTTACTGTGTTGCAAAGACTGAGGTCGTTGAT--  699
          ::|| :: :: || ||||||||  || || :: :: || ||  :: || :: || ||
Db   251  SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrGluValThrAspPro  270

Qy   700  TCTGATGGATCAGTGAAAGACAAAATCACAGGATTCATAGTAGAAGAGACTTTGGGTGGA  759
          :: ::||||:::|||||||||||  ||||:::|||  :: :: ::|||||  ||||::||
Db   271  AlaThrGlyAlaValLysGluLysIleThrAlaPheValValGluGluThrLeuGlyGly  290

Qy   760  GTCACTAATGGGAAACCCGAGATAAATTAGGCATTCGGCGGCTCCAACACTTGTGAAGTC  819
          ||:::||:: :: |||  || :: ::||  || || :: :: || ||  ||||||||||
Db   291  IleThrThrHisGlyProProGluLysMetGlyIleGlyLysAlaSerAsnThrAlaGluVal  310

Qy   820  CATTTTGAAAACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTCGGAGATGGGGTTT  879
          ||||||||| :: || :: || || || :: :: ||||:::|:::||  || :: ||||
Db   311  PhePheAspGlyValArgValProSerGluAsnValLeuGlyValGlySerGlyPhe  330

Qy   880  AAGGTGCCATGAACATCCTCAACAGGGCCGGTTCAGCATGGCACTCGTGGCTCGGG  939
          |||||| ||:|| :::::||  ||::|||  || :: |||  ||::|::||||||
Db   331  LysValAlaMetHisIleLeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGly  350

Qy   940  CTGCCAAGAGATTGATTGAAATGACTGCTGAGTACGCCTCGACAAGGAAACAGTTTAAC  999
          ::|::||:: :::::||  :::||:::|::|:::| || :: :::|||::||
Db   351  ThrMetArgIleTyrIleLeuAlaLysAlaValAspHisAlaThrArgLysGlnPheGlyIle  370

Qy  1000  AAGAGGCTCAGTGAATTTGATTGATTCAGGAGAAATTTGCACTGATGGTCTCAGAAGGCT  1059
          ::|:::| :::||||  :::|||  || :: :: ::|||  ::|:: ||  |||||||||
Db   371  GluLysIleHisAsnPheGlyLeuIleGlnValGluLeuAlaArgMetValMetLeuGln  390

Qy  1060  TACGTCATGGAGAGTATGACCTCACCTCACAGCAGGGATGCTGGACCAACCTGGCTTTCCC  1119
          ||||||:::||::| ::::|  ||||::|:::  ||::|:::  ::  ||||||||||||
Db   391  TyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln--GlyAlaThr  409

Qy  1120  GACTGCTCCATCGAGGCAGCCAGCCATGGTGAAGGTGTTCAGCTCCGAGGCCGCCGCAGTGT  1179
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DR   EMBL; D43682; BAA07781.1; -.
DR   EMBL; L46590; AAA79002.1; -.
DR   EMBL; X86556; CAA60253.1; -.
DR   EMBL; D78298; BAA29057.1; -.
DR   EMBL; D78279; BAA29057.1; JOINED.
DR   EMBL; D78280; BAA29057.1; JOINED.
DR   EMBL; D78281; BAA29057.1; JOINED.
DR   EMBL; D78282; BAA29057.1; JOINED.
DR   EMBL; D78283; BAA29057.1; JOINED.
DR   EMBL; D78284; BAA29057.1; JOINED.
DR   EMBL; D78285; BAA29057.1; JOINED.
DR   EMBL; D78286; BAA29057.1; JOINED.
DR   EMBL; D78287; BAA29057.1; JOINED.
DR   EMBL; D78288; BAA29057.1; JOINED.
DR   EMBL; D78289; BAA29057.1; JOINED.
DR   EMBL; D78290; BAA29057.1; JOINED.
DR   EMBL; D78291; BAA29057.1; JOINED.
DR   EMBL; D78292; BAA29057.1; JOINED.
DR   EMBL; D78293; BAA29057.1; JOINED.
DR   EMBL; D78294; BAA29057.1; JOINED.
DR   EMBL; D78295; BAA29057.1; JOINED.
DR   EMBL; D78296; BAA29057.1; JOINED.
DR   EMBL; D78297; BAA29057.1; JOINED.
DR   EMBL; BC000399; AAH00399.1; -.
DR   EMBL; BC012912; AAH12912.1; -.
DR   EMBL; BC020218; AAH20218.1; -.
DR   PIR; S54183; S54183.
DR   HSSP; Q06319; 1BUC.
DR   Genew; HGNC;92; ACADVL.
DR   H-InvDB; HIX0013488; -.
DR   Reactome; P49748; -.
DR   MIM; 201475; -.
DR   GO; GO:0005739; C:mitochondrion; TAS.
DR   GO; GO:0004466; F:long-chain-acyl-CoA dehydrogenase activity; TAS.
DR   GO; GO:0015980; P:energy derivation by oxidation of organic c. . .; TAS.
DR   GO; GO:0006635; P:fatty acid beta-oxidation; TAS.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   Alternative splicing; Cardiomyopathy; Disease mutation; FAD;
KW   Fatty acid metabolism; Flavoprotein; Mitochondrion; Oxidoreductase;
KW   Polymorphism; Transit peptide.
FT   TRANSIT   1   40   Mitochondrion (By similarity).
FT   CHAIN   41   655   Acyl-CoA dehydrogenase, very-long-chain

Alignment Scores:
Pred. No.:   655
Score: 1.12e-79   Length: 655
                1308.00   Matches: 276
Percent Similarity: 64.97% Conservative: 106
Best Local Similarity: 46.94% Mismatches: 194
Query Match: 38.21% Indels: 12

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Db    410   AspPheGlnIleGluAlaAlaIleSerLysIlePheGlySerGluAlaAlaTrpLysVal   429
            |||                                            |||:::  ||||||||||||
Qy   1180   GTGAGTCAGGGCCTGCAGATCCTCCGGGGGCTTGGCGTACACAAGGGACTATCCGTACGAG   1239
            |||    :::||||||:::||||||||:||||:|:   :::::   :::::::
Db    430   ThrAspGluCysIleGlnIleMetGlyGlyMetGlyPheMetLysGlyProGlyValValGlu   449

Qy   1240   CGCATACTGCGTGACACCCGACATCCTCCTCATCTTCGAGGAACCAATGAGATTCTCCGG   1299
            |||:::||  ||||   ||:::   |||  :|::  ||||||||:|||::||||  |||
Db    450   ArgValLeuArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArg   469

Qy   1300   ATGTACATCGCCCTGACGGGGTCTGCAGCATGCCGCCGCCTGACTACCAGGATCCAT   1359
            |||::::::::||||||   ||||||:|||:::   ||||:   |||:
Db    470   LeuPheValAlaLeuGlnLeuGlyCysMetAspLysGlyLeuLeuSerGlyLeuGlySer   489

Qy   1360   GAGCTAAACAG------GCCAAAGTGAGCACAGTCATGATACCCGTTGGCCGGAGGCTT   1413
            |||||                     :::::      ||||||::|||
Db    490   AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeu   509

Qy   1414   CGGGACTTCCCTGGGCCGAACTGTGGACCTGGGCGTGACAGGCAACCATGAGTTGTGCAC   1473
            ||||||:::                               |||:::||||:||
Db    510   ArgArgArgAlaGlyLeuGlyLeuSerGlyLeuSerLeuSer-------GlyLeuValHis   526

Qy   1474   CCCAGTCTTGCGGACAGTGCCAACAAGTTTGAGGAGAAACACCTACTGCTTCGGCCGGACC   1533
            |||:::    |||
Db    527   ProGluLeuSerArgSerGlyGluLeuLeuAlaValAlaArgAlaLeuGluGlnPheAlaThrVal   546

Qy   1534   GTGGAGACACTGCTGCTCCGCTTTGGCAAGACCATCATGAGGAGGAGCCAGCTGGTACTGAAG   1593
            :::        |||  |||    |||::    |||
Db    547   ValGlyAlaLysLeuIleLysHisLysLysGlyIleValAlaAsnGluGlnPheLeuLeuGlnGln   566

Qy   1594   CGGGTGGCCAACATCCTCATCAACCTGTATGGCATGACGGCCGTCGTGTCGGGGCCAGC   1653
            |||:::    |||
Db    567   ArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValValLeuSerArgAlaSer   586

Qy   1654   CGCTCCATCCGCCATTGGGCTCCGCAACCACGAGGTTCTCTTGGCCAACACCTTC   1713
            ||||||:::::     |||    :::|||    ::||||:
Db    587   ArgSerLeuSerGluGluHisGlyHisProThrAlaGlnHisHisGluLysMetLeuCysAspThrTrp   606

Qy   1714   TGCGTTGGAA------GCTTACTTGCAGAATCTCTTCAGCCTCTGGACAAGTAT   1767
            ||||||                     :::            :::      :::
Db    607   CysIleGluAlaAlaAlaArgIleArgGluGlyMetAlaAlaLeuGlnSerArgAspProTrp   626

Qy   1768   GCTCCAGAAAACCTAGATGCAGCAGATTAAGAAAGTGTCCCAGCAGCATCCTTGAGAAGCGA   1827
            |||                       |||
Db    627   GlnGlnGlu---LeuTyrArgAsnPheLysSerIleSerLysLysAlaLeuValGluArgGly   645

Qy   1828   GCCTATATCTGTGCCCACCCTCTG   1851
            |||      :::::||||||
Db    646   GlyValThrSerAsnProLeu   653
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RESULT 12
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ID   Q9V8T1
AC   Q9V8T1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG7461-PA.
GN   ORFNames=CG7461;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merklulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K.H., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
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Q9V8T1   PRELIMINARY;   PRT;   655 AA.

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RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; AE003796; AAF57579.1; -.
HSSP; Q06319; 1BUC.
DR   IntAct; Q9V8Ti; -.
DR   FlyBase; FBgn0034432; CG7461.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_N.
DR   InterPro; IPR006092; Acyl-CoA_dh_M.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE   655 AA;  71326 MW;  00916BD701E127CB CRC64;

Alignment Scores:
Pred. No.:                                  Length:       655
Score:                    7.8e-79           Matches:      280
Percent Similarity:       1295.50           Conservative: 104
Best Local Similarity:    61.84%            Mismatches:   212
Query Match:              45.09%            Indels:       25
DB:                       37.85%            Gaps:         9
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US-09-945-326-3 (1-1863) x Q9V8Ti (1-655)

```
Qy     40 GCTCGTGCCTGCCGGGGTCTGGTGGTC---------TCTACCGGGAACCGG   81
             ||||||||| |||||    :::  ::: ||||||
Db     44 AlaSerLeuCysArgGlnIleAlaThrHisSerProLysLeuGlyAlaGluSerAsnArg   63

Qy     82 CGGGCTACTGCGCACCAGCCGCCCGCTGCACGAGCTTTCGCCAAAGAGCTTTCCTAGCAAA  141
             ::: |||        |||                     :::||||
Db     64 SerLysGluLysAlaSerGluAsn---GluSerPheMetAlaAsnIlePheArgGlySer   82

Qy    142 ATCAAGAGAAAGAGAGTTTTCCCATTTCAGAAGTTAGCCAAGATGAACTTAATGAAATC  201
             ::|||||||||:::|||:|||||||:::||
Db     83 LeuValSerSerGlnValPheProTyrProAspValLeuThrArgAlaGluGlnLysGluLeu  102

Qy    202 --AATCAGTTCTTGGACCCGTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGAAAA  258
                  ::  ||||  ::: |||       :::  ||||
Db    103 ThrAsnSerLeuIleAspProGluProPheGluArgPheSerAspValAsnAspAlaAlaArg  122

Qy    259 ATTGACCAGGAAGGGAAATCCCAGATGAAACTTTGGAGAAATTGAAGAGCCTAGGGCTT  318
             |||    ||    ::: |||
Db    123 AsnAspAlaAsnSerLysIleAspAspThrThrSerPheAlaLeuTrpSerAlaLeuGlyAla  142

Qy    319 TTTGGCTGCAAGTCCCAGAAGAATATGGTGGCCGTTCTCCAACACCATGTACTCA  378
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Db    143 PheGlyIleGluValProSerGluLysAsnThrGlnTyrGly  162

Qy    379 AGACTAGGGGAGATCATCAGCATG---GATGGGTCCATCATGTGACCCTGGCCAGCGCAC  435
             |||  ::: |||||||:::|||||
Db    163 ArgLeuCysAlaIleGlyValTyrAlaGlyAsnAspLeuGlyLyleThrIleGlyAlaHis  182

Qy    436 CAGGCTATTGCCTCAAGGGAGGATCATCATCTTGCCTGGCACTAAGTGACAGAAGCACTAC  495
             ||||||||:::||||||        |||
Db    183 GlnSerIleGlyPheLysGlyIleLeuAspLeuLeuTyrArgGlyThrProGluGlnLysGlyLysTyr  202

Qy    496 TTGCCTAAACTGGCTCCGGGGAGCAATTGCAGCCTTCTGCCTCCACGGAGGCCAGCCAGT  555
             ||||||:::||||||            |||
Db    203 LeuProLysValAlaAlaGluValAlaGlnIleValTyrAlaAlaPheAlaLeuHis  222

Qy    556 GGGAGCGATGCAGCCTCAATCCGAGCAGAGCCACTAAGTGACAGAACAGAAGCACTAC  615
             ||||||:::||||||        |||||
Db    223 GlySerAspAlaGlySerIleArgCysArgGlyAlaValLysSerArgAlaValAspGlyLysHisTyr  242
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Qy    616 ATCCTCCAATGGCTCCAAGGTCTGGATTACTAATGAGGACTGGCCAATATTTTACTGTG   675
             :::|||||||||||||||||:::||      :::
Db    243 ValLeuAsnGlySerLysIleTrpIleSerAsnGlyIleAlaGluIleMetThrVal   262

Qy    676 TTTGCAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAATCACAGCA   732
             ||||||:::|||||||           |||
Db    263 PheAlaGlnThrGluGlnValAspProLysThrGlyLuGlnLysAspLysValThrAla   282

Qy    733 TTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAGATAAATTAGGC   792
             |||:::|||||||||||||||||      :::
Db    283 PheIleValGluArgSerPheGlyGlyValThrAsnGlyProProGluGlyLysMetGly   302

Qy    793 ATTCGGGGGCTCCAACACTGTGAAGTCCATTTGAAAACCAAGAACACCTGTGGAAAC   852
             |||:::        ||| :::||||||||||||
Db    303 IleLysAlaSerAsnThrAlaGluValPheGluAspValLysIleProIleGluAsn   322

Qy    853 ATCCTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCTCCAACAGCGGCCGG   912
             |||:::::         ||||||:::||||||
Db    323 ValLeuGlyLysGluGlyAspGlyPheLysLysValAlaMetAsnIleLeuAsnAsnGlyArg   342

Qy    913 TTCAGCATGGGCAGCGTCGTGCGTGGCTGCTCAAGAGATTGATTGAAATGACTGCTGAG   972
             ||||||:::        ::: |||||||
Db    343 PheGlyMetGlyTyrAlaThrLeuSerGlyThrMetLysLysCysIleGluGlnIleAlaThrGlu   362

Qy    973 TACGCCTGCCAAGGAAACAGTTAACAAGAGGCTCAGTGAATTGATTGATTCAGGAG  1032
             ||||||:::        ::: |||||||||||
Db    363 HisAlaAsnAsnArgValGlnPheGlyLeuLysAsnTyrGlySerIleGlnGlu   382

Qy   1033 AAATTTGCACTGATGGTCAGAGGCTTACGTCATCGTGTAGCGAGAGTATGACCTACCTCACAGCA  1092
             ||| ||| ||       :::  :::
Db    383 LysLeuAlaGlnMetAsnIleLeuGlnIleTyrAlaThrGluSerMetAlaPheThrIleSer   402

Qy   1093 GGGATGCTGGACCAACCTGGCTTTCCCGACTGGCTCCATCGAGCAGCCAGCCATGGTGAAGGTG  1152
             ||| :||     :::|||       |||||||
Db    403 GlnAsnMetAsp---AlaGlySerLysAspTyrHisLeuGluAlaAlaIleSerLysIle   421

Qy   1153 TTCAGCTGCCAAGGACCCCTGGAACAGTTTCAGTGTGAGTGAGGCGCTGAGATCGTCGGGGGTTG  1212
             :::||:||||||:::|||:::||||||||||||
Db    422 TyrAlaSerGluSerAlaTrpTyrValCysAspAlaIleGluGlnIleLeuLeuGlyMet   441

Qy   1213 GGCTACACAAGGGACTATCGTGCTGCGAGCGCATACTGGCGTGACACCCGCATCCTCATC  1272
             |||||:::|||||||||||||||:::
Db    442 GlyTyrMetValAlaSpAsnGlyLeuGluValLeuArgAspLeuLeuArgIlePheArgIle   461

Qy   1273 TTCGAGGGAACCAATGAGAATTCTCCGGATGTACATGCCCTGACGGGTCTGCAGCATGCC  1332
             ||||||:::||||||:::|||:::||
Db    462 PheGluGlyThrAsnAspIleLeuGluArgLeuPheIleAlaLeuThrArgGlyIleGlnTyrAla   481

Qy   1333 GGGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAG-----------GCC  1374
             |||  ::: |||:::|||
Db    482 Gly-----------SerHisLeuLysGluLeuGlnIleArgAlaPheLysAsnProSerAla   497

Qy   1375 AAAGTGAGCACAGTCGATGATACCGTTGGCCCGGAGGCTTGGGGACTCCGGGAACT  1434
             ::: |||       |||||||
Db    498 AsnLeuGlyLeuIlePheLysGlyGlnAlaSerArgArg------------AlaAlaSerThr   513

Qy   1435 GTGGACCTGGGGCTGACAGGCAACCATGAGTTGTCACCCCAGTCTTGCGACAGTGCC  1494
             |||||:::|||||||||||||:::
Db    514 ValGlyLeuGlyLysGlyHisIleValGluLysLeuProTyrArg   533

Qy   1495 AACAAGTTTGAGGAGAACACTACTGCTTCCGCCGAGACACTGCTTCGGCTGCTCCGC  1554
             |||||:::|||||||||||
Db    534 LysLysThrAlaHisCysSerLeuHisGluGlyGlnIleSerValGluGluLeuLeuArg   553

Qy   1555 TTTGGCAAGACCATCATGAGAGAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATC  1614
             ::: |||       |||||:::||||||||
Db    554 TyrAsnLysAsnIleValAsnGluLysLeuThrArgLeuAlaAlaAsnAlaAlaIle   573

Qy   1615 AACCTGTATGGCCATGAACGGCCCGTGCTGCTGGTGTCTCGCGGGCCGCCTCCATCCGACCATTGGGCTC  1674
             ::::::|||||||||||||  ::: ::::::
Db    574 AspIleTyrAlaMetValAlaThrGlnSerArgSerArgAlaValAlaAsnLeuAsnLeu   593
```

```
Qy  1675  CGCAACCACCAGCACCAGAGGTTCTCTTGGCCAACACCTTCTGCGTGGAAGGCTTACTTGCAG  1734
                ||||||:::  :::    :::        :::::::|||||||||
Db   594  ProThrAlaGlnHisGluLeuAsnMetThrLysAlaLeuThrIleGlnAlaSerAspArg  613

Qy  1735  AATCTCTTCAGCCTCCTCCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATT  1794
                ::|||:::|||        ::|||||||:::::||||||||||
Db   614  ValIleLysAsnLeuGlnAlaAlaThrSerSerHisHisArgSerLeuAsnGluLysIle  633

Qy  1795  AAGAAAGTGTCCCAGCAGATCCTTGAGAAGCGAGCCTATATCGTGCCACCCTCTGGAC  1854
                ||||||||        |||||
Db   634  SerThrIleAlaLysThrThrLeuGluAsnGlyGlyValThrThrGlyIleLeuLeuAsp  653

Qy  1855  AGG 1857
                :::
Db   654  Gln 654
```

RESULT 13

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Q7Q868
ID   Q7Q868          PRELIMINARY;    PRT;    639 AA.
AC   Q7Q868;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP15352 (Fragment).
GN   Name=agCG50940; ORFNames=ENSANGG00000009991;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008944; EAA10216.1; -.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR009075; AcylCoADH_C like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR   PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
FT   NON_TER        1      1
SQ   SEQUENCE   639 AA;   70246 MW;  46790371A4D12CB5 CRC64;
```

Alignment Scores:
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Pred. No.:           1                      Length:          639
Score:               2.48e-78               Matches:        1288.00
Percent Similarity:  62.66%                 Conservative:    109
Best Local Similarity: 45.19%               Mismatches:      187
Query Match:         37.63%                 Indels:           46
DB:                  2                       Gaps:             11
```

US-09-945-326-3 (1-1863) x Q7Q868 (1-639)

```
Qy   79  CGGCGGCTACTGCGCACCAGCCCG------------------------------------- 102
             |||||        :::|||
Db   28  ArgArgCysLeuSerAlaAlaProGlnAlaLysGlnAlaAlaLysGlnAlaAlaGlnAlaThrPro  47

Qy  103  -------------------CCTGTACGAGCTTTCGCCAAAGAGCTTTCCTAGGCAAAATC 144
                              :::||||||        |||::::::
Db   48  SerGluAlaGluLysArgProAsnMetSerPheLeuThrAsnIlePheArgGlyGlnVal  67
```

```
Qy  145  AAGAGAAAGAAGTTTCCCATTTCCAGAGTAGTAGCCAAGATGAACTTAATGAA---ATC  201
             :::|||||||        ::::|||||||||        :::|||        ---|||
Db   68  GlnProAlaGlnValPheProTyrProGluAlaLeuAspAlaGluGlnLysGluTyrIle  87

Qy  202  AATCAGTTCTGGGACCCGTGGAAAAATTCTTCACTGAGGAGGTGGACTCCGAAAAATT  261
             |||        :::||        |||||||        |||||||||
Db   88  AlaSerPheValAspProValThrLysPheGluValAlaAsnAspProValLysAsn  107

Qy  262  GACCAGGAAGGGAAAATCCCAGATGAAACTTGGAGAAATTGAAGAGCCTAGGGCTTTTT  321
             |||        :::::|||        |||        |||        |||||||
Db  108  AspValAlaAsnAlaSerIleAspGluLysThrCysGluAlaLeuTrpArgAsnAlaPhe  127

Qy  322  GGGTGCAAGTCCCAGAAGAATATGTGGCCTGGCTTCTCCAACACCATGTACTCAAGA  381
             |||        :::|||||||||        :::|||||||||
Db  128  SerLeuMetValProProAspTyrGlyIleGlyLeuLeuAsnAsnThrGlnThrTyrSerArg  147

Qy  382  CTAGGGGAGATCATC---AGCATGACGATGGTTCCATCACTGTGACCCTGCACGCGCACCAG  438
             :::    :::|||        ---|||||||        :::|||||||||
Db  148  MetCysAspIleIleGlyGlnHisGlnAspLeuGlyLeuIleGlyIlePheIleGlyAlaHisGln  167

Qy  439  GCTATTGGCCTCAAGGGATCATCTTGGCTGCACTGAGGAGCAGAAAGCCAAATACTTG  498
             :::|||||||        :::        :::|||        |||||||
Db  168  SerIleGlyPheLysGlyLeuLeuLeuTyrGlyAspGlnArgGlnLysGlnLysTyrLeu  187

Qy  499  CCTAAACTGGCGTCCGGGAGCACATTGACCACCTTCTGCCTCACGGAGCCAGTGGGG  558
             :::|||||||        |||||||        :::|||||||
Db  188  ProMetValSerThrGlyLysValTyrAlaAlaPheAlaLeuThrGluProSerSerGly  207

Qy  559  AGCGATGCAGCCTCAATCCGGGAGCAGAGCCACACTAAGTGAAGACAAGAAGAGCACTACATC  618
             |||||||        :::|||        |||||||||        :::|||
Db  208  SerAspAlaGlySerIleArgCysArgAlaValLysSerAlaAspGlyLysHisTyrVal  227

Qy  619  CTCAATGGCTCCAAGTCTCGATTACTAATGGAGGACTGGCCAATATTTTACTGTGTTT  678
             |||||||||        :::|||||||||        :::|||||||
Db  228  LeuAsnGlySerLysSerArgLeuLeuMetGluAspTrpProAsnIleLeuLeuCysLeuGly  247

Qy  679  GCAAAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAAGACAAAATCACAGCATTC  735
             :::|||        ---|||||||        :::||||||
Db  248  AlaGlnThrGluValGluAspProLysThrGlyGlnLysLysValThrAlaPhe  267

Qy  736  ATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATT  795
             |||||||||        :::|||||||||        :::|||||||
Db  268  IleValGluArgGlyPheGlyGlyValSerSerGlyTyrProProGluAsnLysMetGlyIle  287

Qy  796  CGGGGCTCCAACACTTGTGAAGTCCATTTGAAAACACCAAGATACCTGTGGAAAACATC  855
             :::        :::|||||||        ::::::
Db  288  LysCysSerAsnThrAlaGluValProGluAspValLysIleProAlaGluAsnVal  307

Qy  856  CTTGGAGAGGTCGGAGATGGGTTAAGGTGGCCATGAACATCCTCAACAGCGCCGGTTC  915
             |||||||        :::|||||||        |||        :::|||||||
Db  308  LeuGlyGluValGlyAspGlyLeuArgTrpProMetAsnIleLeuAsnSerAlaGlyArgPhe  327

Qy  916  AGCCATGGCAGCGCGTGCTGCTCAAGAGATTGATTGAAAATGACTGCTGAGTAC  975
             :::        ::::::|||||||        :::||||||
Db  328  GlyMetAlaAlaThrLeuSerGlyThrMetArgAlaCysIleGlnLysAlaAlaGluHis  347

Qy  976  GCCTGCACAAGGAGAAACAGTTTAACAAGAGGCTCAGTGAATTGATTCAGAGAGAAA  1035
             |||        :::||        |||||||        :::|||||||
Db  348  AlaThrAsnArgValGlnPheGlyArgLysIleGluThrPheGlyValGluGlnGluLys  367

Qy  1036  TTTGACTGATGGCTCAGAAGGCTTACGTCATGAGGAGTATGACCTACCTCACAGCAGGG  1095
              |||        :::||||||        |||||||||
Db  368  LeuAlaArgMetAlaMetHisHisTyrValThrGlnSerMetAlaTyrMetIleSerGly  387

Qy  1096  ATGCTGGACCAACCTGCGTCTTCCCGACTGCTCCATCGAGGCAGCCATGGTGAAGGTGTTC  1155
              :::|||        ::::::|||||||        :::|||||||
Db  388  AsnMetAsp---ThrGlySerLeuAspTyrHisLeuGlnAlaAlaIleSerLysValPhe  406

Qy  1156  AGCTCCGAGGCCGCCTGGCAGTGTGTGAGGTGGCTTGGGGGCTTGGC  1215
              :::|||||||        |||||||||
Db  407  AlaSerGluSerAlaTrpTyrValCysAspGluAlaIleGlnIleIleLeuGlyMetGly  426
```

```
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
KW   FAD; Flavoprotein; Oxidoreductase.
FT   NON_TER       1
SQ   SEQUENCE   604 AA;   65510 MW;   F48852A94F3EF51A CRC64;
```

Alignment Scores:

```
Pred. No.:                              Length:                 604
Score:                     2.32e-77     Matches:                269
Percent Similarity:         64.72%      Conservative:           107
Best Local Similarity:      46.30%      Mismatches:             170
Query Match:                37.20%      Indels:                  35
DB:                            2        Gaps:                    10
```

US-09-945-326-3 (1-1863) x Q70870 (1-604)

```
Qy    97 AGCCCGCCTGTACGA---GCTTTCGCCAAAGAGCTTTTCCTAGGCAAAATCAAGAAGAAA 153
            ::::||| |||     ||||:||| ||||| |||||| |||| |||:||||:::
Db    17 AlaProThrValAsnThrSerPheMetAlaAsnLeuPheArgGlyIleGluProLeu 36

Qy   154 GAAGTTTCCATTCCAGAA---GTTAGCCAAGATGAACTTAATGAAATCAATCAGTTC 210
            :::|||||||||||||||:::     |||:||     ||||||:::
Db    37 GlnValPheProPheProAspSerLeuAsnProAspGlnLysGlySerLeu 56

Qy   211 TTGGGACCCGTGGAAAAATTCTTCACTGAGAGGTGGACTCCCGAAAAATTGACCAGGAA 270
            ::: |||    ||||||||||:|::    |||   :||||||:||:||:||||
Db    57 IleAspProValThrLysPhePhe---AspGlyTyrAspProValLysAlaGluLysAsn 75

Qy   271 GGGAAAATCCCAGATGAAAACTTGGAGAAAATTGAAGAGCCTAGGGCTTTTGGGCTGCAA 330
            ::: ||||      :::|||     |||:||||||:||
Db    76 GlyGlyGlyProAspGluAlaThrPheGlnSerMetTrpGluMetGlyLeuMetGlyMetGln 95

Qy   331 GTCCCAGAAGAAATATGTGGCCGGCCTTCTCCAACACCATGTACTCCAAGACTAGGGGAG 390
            :||||||||||||:|||||||    ::||||:||||||:||||||:::
Db    96 AlaProGluLeuTyrGlyValGlyLeuAlaLeuProAsnThrGlyTyrAlaArgMetGlyGlu 115

Qy   391 ATCATC---AGCATGCGATGGGTCCATCACTGTGACCCTGGCACCAGGCTATTGGC 447
            ::::: :|  |||    |||||:||    |||:|||||||||||:::||||||
Db   116 LeuValGlyAlaAlaAlaAspLeuGlyLeuAlaValValPheGlyAlaHisGlnSerIleGly 135

Qy   448 CTCAAGGGATCATCTTGGCTGGCACTGGAGGAGCAGAAAGCCAAATACTTGCTAAACTG 507
            ||||||:||||    |||:||||||||||||||:|::||||||||||||||:|:|
Db   136 TrpLysGlyValLeuLeuTyrGlyThrGlyGlyGluGlnLysLysArgLysTyrLeuProGlnVal 155

Qy   508 GGGTCCGGGAGCACATTGGCACCTTCGCCTTCTGCCTCACGGAGCCAGCGATGCA 567
            :::||||||||||||||:|||||||||:|||:||||||||||:::|||:||||||
Db   156 ValThrGlyThrGlyThrIleAlaCysPheCysProSerLeuThrGluProSerGlySerAspAla 175

Qy   568 GCCTCAATCCGGAGCAGAGCCACACTAAGTGAAGCAAGAAGCACTACATCCTCAATGGC 627
            ||||| |||||:||      |||   |:||||||||||:|||   ||||||||||||||
Db   176 GlySerIleArgSerArgAlaValLysSerAlaAspGlySerHisTyrValLeuAsnGly 195

Qy   628 TCCAAGGTCTGATTACTAATGCAGGACTGGCCAATATTTTTACTGTGTTTGCAAAGACT 687
            |||||||||:||| |:||:||:||||||||||||||||:::|||||||:|:|||||||
Db   196 SerLysIleTrpIleSerGlyValGlyLeuGlnLysAspIlePheThrValPheAlaGlnThr 215

Qy   688 GAGGTCGTTGAT---TCTGATGGATCCAGTGAAAGACAAAATCACAGCATTCATAGTAGAA 744
            ::::||||||||    |||:||||    ||||||:||:|||||||||:||||||:||:||||
Db   216 GluValThrAspProLysThrGlyGlnLysAspLysAspLeuValThrAlaPheIleValGlu 235

Qy   745 AGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCC 804
            |||||||:|||||||||:|||::|||||:||:||||||||:|:|||:||||:|||:||||:::
Db   236 ArgGlyPheGlyGlyValThrSerGlyProProGluAspProGluAspProGluGlyIleLysCysSer 255
```

```
Qy  1216 TACACAAGGGACTATCCGTACGAGCGGCATACTGGCTGACACCCGCATCCTCCTCATCTTC 1275
             :::  ::||| |||||||||:|||    ||||  |||||||   ||||||:::|||  |||
Db   427 PheMetLysAspCysCysGlyLeuGluArgValMetArgAspLeuArgIlePheArgIlePhe 446

Qy  1276 GAGGGAACCAATGAGATTCCGGATGTACATCGCCGTGACGGGTCTGCAGACATGCCGGC 1335
             :::||| ||||||||||||||||:|||||||||:||||:|||:||||:||:||||:::
Db   447 GluGlyThrAsnAspIleLeuArgPheValAlaLeuThrGlyIleLeuArgGlnAlaGly 466

Qy  1336 CGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCC-----AAAGTGAGCACAGTC 1389
             ||:|||||||||||||||:::||||||||||:||||||       :::  :::
Db   467 -----------SerHisLeuLysGluGlnArgAlaPheLysAspAlaThrAsn 482

Qy  1390 ATGGATACCCGTTGGCCCGGAGGCGCTTCGGGGACTCCCTGGGACCGTGGACCTGGGGCTG 1449
             |||  |||:::||| ||||||||||||:|||||||:::|||:|||||||||||||:::
Db   483 MetGlyLeuIlePheLysGluGlyGlySerArgArgAlaIleArgSerIleArgGlyTyrGlyGly 502

Qy  1450 ACAGGCAACCAATGGAGTTGTGCACCCCAGTTCTGCCAGACAGTGCCAACAAGTTTGAGGAG 1509
             |||||:  |||||||||:||:||:::|||||:|:|||||:|||||||||||:::||:|||:::
Db   503 ThrArgLeuSerArgAlaPheValAlaAlaAspProLeuLysValProAlaLysGlnCysSerGlu 522

Qy  1510 AACACTACTGCTTCGGCCGAGACCTGGAGACACACTTGCTGCTCCGCTTTGCAAGACCATC 1569
             ||||||||:||||:||||||:||||||||:||||||||||:||||||||||||:::
Db   523 CysIleAspLeuProPheGlyGlyThrGlnThrGluSerLeuLeuLeuIleLysTyrArgGlyLeuLysIle 542

Qy  1570 ATGGAGGAGCAGCTGGTACTGAAGGCGGGTGGCCAACATCCTCATCAACCTGTATGGCATG 1629
             :::::||||||||||| ::::|||  ||||   :|||:|||||::::||||:::
Db   543 ValAspGluGlnPheLeuLeuLysAsnArgLeuAlaAlaIleAspThrTyrAlaMet 562

Qy  1630 ACGGCCGTGTCGCGGGGCCAGCCGCTCCATCCGCATTGGCTCCGCAACCAGACCAC 1689
             ||:||||||:||||||||||||:|||||||||:|||::::||||||:::
Db   563 AlaValValLeuSerArgAlaThrArgSerValArgLysAspLeuProSerGluAlaGluHis 582

Qy  1690 GAGGTTCTCTGCCAACACCTTCGCGTGGAAGCTACTTGCAGAATCTCTTCAGCCTC 1749
             :::||||||:||||||:::  |||:||||||| ||||:||||:::
Db   583 GluValLeuMetThrLysMetCysHisGlnIleSerAspArgValAlaArgValAsnIle 602

Qy  1750 TCTCAGCTGGACAAGTATGTCCAGAAAACCTAGATGAGCAGATTAAGAAA------GTG 1803
             ||:||:||||||||:|||||||||||||:||      |||||||:::|||||
Db   603 ArgLysIle------------AsnThrAspSerPheValLysAsnTyrGlyVal 616

Qy  1804 TCCCAGACAGATCCTTGAGAAGCGAGCCTATATCTGTGCC---------- 1842
             ::::||||:::||:::
Db   617 MetSerGlnIleAlaLysAsn-------IleCysAlaAsnAsnGlyIleIleAlaHisAsn 633

Qy  1843 CACCCTCTGAC 1854
             ::|||||||||
Db   634 AsnProLeuAsp 637
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RESULT 14

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Q70870
ID   Q70870            PRELIMINARY;       PRT;   604 AA.
AC   Q70870;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP15349 (Fragment).
GN   Name=agCG55939; ORFNames=ENSANGG00000009986;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008944; EAA10215.1; -.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
```

RESULT 15
Q19057

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ID   Q19057               PRELIMINARY;       PRT;   613 AA.
AC   Q19057;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein E04F6.5.
GN   Name=E04F6.5; ORFNames=E04F6.5;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   WormBase Consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Pauley A.;
RT   "The sequence of C. elegans cosmid E04F6.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RG   WormBase Consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR   EMBL; U28943; AAA68357.1; -.
DR   PIR; T15905; T15905.
DR   HSSP; Q06319; 1BUC.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   InterPro; IPR006092; Acyl-CoA_dh_N.
DR   InterPro; IPR009075; AcylCoADH_C_like.
DR   InterPro; IPR009100; AcylCoA_dehyd_NM.
DR   Pfam; PF00441; Acyl-CoA_dh_1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR   PROSITE; PS000073; ACYL_COA_DH_2; 1.
KW   FAD; Flavoprotein; Hypothetical protein; Oxidoreductase.
SQ   SEQUENCE   613 AA;   66171 MW;   C1F2883EC34551B CRC64;
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Alignment Scores:
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Pred. No.:                                     Length:            613
Score:                         4.24e-73        Matches:           272
Percent Similarity:            1210.50         Conservative:      109
Best Local Similarity:         61.16%          Mismatches:        205
Query Match:                   43.66%          Indels:             37
                               35.36%
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Qy   805  AACACTTGTGAAGTCCATTTGAAAACACCAGATACCTGTGGAAAACATCCTTGGAGAG 864
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Db   256  AsnThrAlaGluValTyrPheaspValLysIleProAlaGluAsnValLeuGlyLysGly 275

Qy   865  GTCGGAGAGTGGGTTAAGGTGGCCATGAACATCCTCAACACGCGGCCGGTTCAGCATGGGC 924
               |||:::|||     |||||||     ::|||||     :|||| ||
Db   276  GluGlyAsnGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArgPheGlyMetSer 295

Qy   925  AGCGTCCTGGCTGGGCTGCTCAAGAGATTGATTGAAAATGACTGCTGAGTACGCCTGCACA 984
               ::||||     :::      |||
Db   296  GlyThrLeuAlaGlyThrMetAlaHisCysIleArgLysAlaAlaGluHisAlaThrThr 315

Qy   985  AGGAAACAGTTTAACAAGAGGCTCAGTGAATTGAATTGGATTGATTCAGGAGAAATTTGCACTG 1044
               ||||||     :::||||     |||     :::|||||
Db   316  ArgValGlnPheGlyGlnLysIleGluGluAsnPheGlyAsnValGlnGluLysLeuAlaArg 335

Qy   1045 ATGGCTCAGAGAGGCTTACGTCATGAGGAGTATGAACCTACCTCACAGCAGGGATGCTGGAC 1104
               ||||:::||||     ::|||||||     :||||| :::|||
Db   336  MetAlaMetHisGlnTyrValSerGlnSerMetGlyTyrMetIleSerGlyAsnMetAsp 355

Qy   1105 CAACCTGGCTTTCCCGACTGCTCCATCGAGGCAGCAGCCATGTGAAGGTGTTCAGCTCCGAG 1164
               ||||:::     ||||||:::     |||||||
Db   356  ---AlaGlyHisThrAspTyrHisLeuGluAlaAlaIleSerLysIleSerPheSerSerGlu 374

Qy   1165 GCCGCCTGGCAGTGTGTGAGTGAGGCGCTCGAGATCCTTCGGGGGCTTGGCTACACAAAGG 1224
               |||     :::     ||||     ||:::|||
Db   375  AlaAlaTrpTyrValCysSerGluAlaIleGlnIleLeuGluGlyLeuGlyAsnGlyPheMetLys 394

Qy   1225 GACTATCCGTACGAGCGCCATACTGCGTGACACCCGCATCCTCCTATCTTCGAGGGAACC 1284
               ||||:::     |||||||     :|||
Db   395  SerSerGlyLeuGluLysGluGlyPheLeuLeuArgAspIleArgIleTyrArgIlePheGluGlyIleGlyAla 414

Qy   1285 AATGAGATTCTCCGATGTACATCGCCCTGACGGGTCTGCAGCATGCCGGCCGCCATCCTG 1344
               |||:::     |||||||:::     |||
Db   415  AsnAspIleLeuArgLeuPheValThrLeuThrArgLeuThrGlyTyrIleGlnTyrAlaGly----------- 431

Qy   1345 ACTACCAGGATCCATGAGCTTAAACAG-------GCCAAAGTGAGCACA 1386
               :::     :::     ||||||
Db   432  ---SerHisLeuLysGluLeuGlnIleArgAlaPheLysAsnProThrAlaAsnLeuGlyLeu 450

Qy   1387 GTCATGGATACCGTTGGCCCGGAGGCTTCGGGACTTCCCTGGCCGGAACTGTGGACCTGGGG 1446
               ||||||     ::|||
Db   451  IlePheLysGluGlySerArgArgArgAlaValAlaValArgSerIleedIy-------- 466

Qy   1447 CTGACAGGCAACCATGGAGTTGTGCACCCCAGTTCTTGCCGGACAGTGCCAACAAGTTTGAG 1506
               ||||     :::|||||
Db   467  GlyThrAspLeuSerThrPheValValAspProLeuLysGlySerAlaAlaLeuCysAla 486

Qy   1507 GAGAACACCTACTGCTTCGGCCGCGTCGAGACACCTGCTTCCCGCTTGGCAAGACC 1566
               :::     ||||||:::     |||
Db   487  AspSerIleAspArgPheSerLysThrIleGluAlaLeuLeuLeuHisGlyLysLysGly 506

Qy   1567 ATCATGGAGGAGCAGCAGCTGGTACTGAAGCGGGTGGCCAACATCCTCATCAACCTGTATGGC 1626
               ||||:::     ::|||
Db   507  IleValAspGlnGlnPheLeuLeuLeuIleArgLeuLeuArgLeuAlaAspSerAlaIlePheTyrGly 526

Qy   1627 ATGACGGCCGTGCTGTCGCGGGCCAGCGCCGTCATCCGCACCATTGGGCTCCGCAACCACGAC 1686
               ||||     ::|     :::|||
Db   527  MetSerCysValLeuSerArgAlaSerArgLysAlaValAlaArgGluAsnAsnProSerAlaGlu 546

Qy   1687 CACGAGGTTCTCTTGCCCAACACCTTCTGCGTCGGAAGCT-------- 1725
               ||||     :::|||
Db   547  HisGluLeuMetAlaLysAlaLysTrpCysValGluAlaAsnAspArgValArgIleAsn 566

Qy   1726 --------TACTTGCAGAATCTCTTCAGCCTCTTCAGCTGAC 1761
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Db   567  IleArgArgValAlaAsnAsnGlyValPheValLysAsnTyrAspThrMetSerAlaIleAla 586

Qy   1762 AAG 1764
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Db   587  Lys 587
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DB: 2   Gaps: 14

US-09-945-326-3 (1-1863) x Q19057 (1-613)

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Qy      19  TTCCTGGCACCAGCGCTGCGGCTCGTGCCGCCGGGGTCTGGTCGTGTCTTCACCGCGAAC  78
                |||::::::||:||    |||  ||||::    ::|:
Db      16  PheIleArgLeuSerHisSerAlaAlaAlaLys----------AspAlaLysPro  31

Qy      79  CGGGCGGCTACTGCGCACCAGCCGCCCGTACGAGCTTCGCCAAAGAGCTTTCCTAGGC  138
                ::::::::||    |||   ::|||  |||||  |||
Db      32  LysLysValAlaAlaAlaValAspSerPro------SerPheValMetAsnLeuPheArgGly  49

Qy     139  AAAATCAAGAGAGAAGAAGTTTTCCCATTTCCAGAAGTTAGCCAAGATGAACTTAATGAA  198
                |||::  :|||||:||||
Db      50  LysAlaValThrArgGlnValPheP.roTyrProLeuAsnMetThrAspGluGlnLysGlu  69

Qy     199  --ATCAATCAGTTCTTGGGACCCTGGAAAAATTCTTCACTGAAGAGGTGGACTCCCGA  255
                :  ::  |||:|||||||
Db      70  ThrLeuGlyMetValMetSerProLeuValGluValAsnAspValVal  89

Qy     256  AAAATTGACCAGGAAGGGAAAATCCCAGATGAAACTTGGAGAAATTGAACAGCCTAGGG  315
                 |||::  ||||||
Db      90  LysAsnAspGluThrSerAspIleProArgAlaValValLeuAspGlnPheAlaGluLeuGly  109

Qy     316  CTTTTTGGGCTGCAAGTCCCAGAAGAATATGGTGCCTCGGCCTTCTCCAACCACCATGTAC  375
                ::  ||||||                   ::|:::||
Db     110  ThrPheGlyValProProGluLeuGlyLySerGlyPheAsnAsnGlnMet  129

Qy     376  TCAAGACTAGGGGAGATCATC---AGCATGGATGGGTCCATCACTGTGACCCTGGCAGCG  432
                ||||||||||:  :||       |||
Db     130  AlaArgValAlaLaGluIleValAlaTyrAspLeuGlyPheGlyValMetGlyValAla  149

Qy     433  CACCAGGCTATTGGCCTCAAGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAA  492
                ||||||||||::||||      |||||||::
Db     150  HisGlnSerIleGlyTyrLysGlyIleLeuLeuLeuGlyThrGluGluGlnLysGlnLys  169

Qy     493  TACTTGCCTAAACTGGCGTCCGGGGAGCACATTGCAGCCTTCTGCCTCACGGAGCCAGCC  552
                ||||||||:::||                ||||::|::
Db     170  TyrLeuProAspLeuAlaThrGlyLysPheAlaAlaPheAlaLeuThrGluProThr  189

Qy     553  AGTGGGAGGCCGATGCAGTCCAATCCGGGAGCAGAGCCACCAAGTGAAGACAAGAAGCAC  612
                ::||||:||||||||::||                |||   ||| |||:|:||
Db     190  ThrGlySerAspAlaSerValArgThrArgAlaGlaGluLeuSerArgAlaAspGlyLysHis  209

Qy     613  TACATCCTCAATGGCTCCAAGGTCTCGATTACTAATGGAGGACTGCCCAATATTTTTACT  672
                ||||:|||||||||||||     |:|||||||
Db     210  TyrIleLeuAsnGlyGlyLyValSerIleTrpIleSerAsnGlyGlyLeuProAsnPheThr  229

Qy     673  GTGTTTGCAAAGACTGAGGTGTCGTTGATTCTGATGATCAGTGAAGACAAAATCACCAGCA  732
                |||||:||                 |||||||:::||
Db     230  ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysAspLysMetSerAla  249

Qy     733  TTCATAGTAGAAAGACTTTGGTGAGTCACTAATGGGAAAACCCGAAGATAAAATTAGGC  792
                ::::|||           |||:|  |||||                  ::|CAC  1845
Db     250  PheIleValGluArgAlaPheGlyGlyValThrSerGlyValThrSerGlyGlyLeuThrSerGlyMetGly  269

Qy     793  ATTCCGGGCTCCAACACTTGTGAAGTCCATTTGAAACACCAAGATACCTGTGGAAAC  852
                ||||::::: |||::|:::  :||||||
Db     270  IleLysGlySerAsnThrArgGluValHisLeuLysHisGlnAspThrCysGlyAsn  289

Qy     853  ATCCTTGGAGAGGTCGGAGAGATGGGTTTAAGTGCCATGAACATCCTCAACAGCGGCCGG  912
                ::  |||:::|||||:::||||:||||:||||||:
Db     290  LeuLeuGlyLysGlyGluGlyGlyPheLysValPheLysValAlaMetAsnIleLeuAsnSerGlyArg  309

Qy     913  TTCAGCATGGAGCAGCCGTCGGCTGCGGCTGCTCAAGAGATTGATTGAAATGAATGAAG  972
                :::  |||||: :||::   ||||||||
Db     310  PheGlyIleProAlaAlaCysSerThrGlyAlaMetLysHisCysIleGlnLysThrValAsp  329

Qy     973  TACGCCTGCACAAGGAAACAGTTTAACAGGAGGCTCAGTGAATTTGATTCAGGAG  1032
                ::   |||||||||:::||::
Db     330  HisIleThrArgValGlnPheGlyLysLysLeuGlyLeuGluPheGlyAsnIleGlnGlu  349

Qy    1033  AAATTTGCACTCATGATGGCTCAGAAGGCTTACGTCATGGAGAGTAGTCATGACCTACCTCACAGCA  1092
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Db     350  LysLeuValGluMetIleSerLysLeuTyrArgAlaThrGluSerIleLeuValTyrMetLeuSer  369

Qy    1093  GGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCAGCCATGGTGAAGGTG  1152
                ::  ||||||:::                   |||||::
Db     370  SerAsnMetAspArg---GlyIleLysGluTyrGlnLeuGluLysGluAlaAlaIleGlyLysLysVal  388

Qy    1153  TTCAGCTCCGAGGCCCGCCTGCCCAGTGTGACTGAGGGCGTCGAGATCCTCCAGACTTTGAG  1212
                |||   :||:||||                   ::|||::
Db     389  LeuAlaSerGluAsnAlaTrpLeuValCysAspAlaIleGlnValHisGlyValHisGlyMet  408

Qy    1213  GGCTACCAAGGGACTATCCGTACGAGCGCATGCTGGCACCCGCATCCTCCTCATC  1272
                |||::: :|||||                   ||||||||
Db     409  GlyPheMetArgGluThrGlyLeuArgValLeuArgArgValLeuArgIleLysPheArgIle  428

Qy    1273  TTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCCTGACGGGTCTGCAGCATGCC  1332
                |||||:|||                   |||||::
Db     429  PheGluGlyTyrAlaAsnAspValLeuArgLeuPheIleAlaLeuThrGlyAlaGlnHisAla  448

Qy    1333  GGCCGCATCCTGACTACCAGGATCCATGAGCTTAAACAGGCCAAAGTGACAGCAGTCATG  1392
                |||::||::::||                   |||||||
Db     449  GlyLys---------HisLeuAlaGluGlnAla------SerGlyValGly  460

Qy    1393  GATACCGTTGGCGGAGGCTTCGGAGGACTCCCGGACGCTGTGACCAGTGCCAACAAGTTTGAG  1452
                ::  |||                   |||
Db     461  GlyLeuIleGlyLeuLeuValAlaValSerArgValThrGly---------GlyAsnThr  475

Qy    1453  GGC---AACCATGA---GTTGTGCACCCAGTCTTGCCAGAGTGCCAACAGTTTGAG  1506
                ||:::||||                   :||
Db     476  GlySerAsnPheGlyGlnValValAspAlaSerLeuGlnAsnSerAlaLysValLeuAsp  495

Qy    1507  GAGAACACCTACTGCTTCGGCCGGACGTGGAGACACTGCTGCTCCGCTTGGCAAGACC  1566
                |||::||||||::                  |||
Db     496  GlnGlnIleAlaLeuPheGlyGlnThrValGlnGlyLeuLeuMetLysHisLysGlyGly  515

Qy    1567  ATCATGGAGGAGCAGCTGGTACTGGAGCGGGTGGCCAACATCCTCATCAACCTGTATGGC  1626
                |||::::: ::                   :|||||
Db     516  IleIleAspArgArgGlnTyrGluMetHisArgValAlaAlaAlaIleAlaIleTyrSer  535

Qy    1627  ATGACGGCCGTGCTCGTCGCGGCCAGCCGCTCCATCCGCATTGGGCTCCCAACCACGAC  1686
                ::  |||:::||                   ::|||
Db     536  SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLysAsnLysSerSerAlaAsp  555

Qy    1687  CACGGAGGTTCTTCGGCCAACACCTTCGCGTGGAAGCTTACTGCAGAATCCTTCAGC  1746
                :::  :|||  ::::|||
Db     556  PheGluArgLysValAla---ThrTyrTyrValAspLysAlaMetLys---------Ser  571

Qy    1747  CTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGTGAGCAGATTAAGAAAGTGTCC  1806
                :::||||||                   |||
Db     572  SerAsnArgPheLeuLysAspAlaGlySerGlyValGlnAsnAlaSerLysValAlaThr  591

Qy    1807  CAGCAGATCCTTGAGAAGCGAGCCTATATCTGTGCC----------CAC  1845
                ::|||:::                   |||
Db     592  IleGluSerLeuAlaLysGlu------ValCysGlyAsnGlyGlyLeuThrLeuGlnHis  609

Qy    1846  CCTCTGGAC  1854
                ||::|||
Db     610  ProValGlu  612
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Job time : 358.736 secs

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